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A_Geneseq_36:R14480
A_Geneseq_36:W44941
A_Geneseq_36:R88912
A_Geneseq_36:R88911
A_Geneseq_36:R88910
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A_Geneseq_36:W10653
A_Geneseq_36:W15326
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A_Geneseq_36:W13009
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A_Geneseq_36:R06400
A_Geneseq_36:R06379
A_Geneseq_36:R06399
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A_Geneseq_36:W35856
A_Geneseq_36:P93323
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A_Geneseq_36:W13825
A_Geneseq_36:R99462
A_Geneseq_36:R05159
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Database sequences: 188963
Database length: 23686106
Search time (sec): 139.200000
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Query: US-09-323-427-1
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A_Geneseq_36:R06427
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A_Geneseq_36:R42452
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-Q=/ggn2_1/UsPTQ_spool_US09323427/runat_14042000_170513_19878/app_query.fasta.1
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-DB=A_Geneseq_36 -QFMT=fastan -SUFFIX=backtrans.rag
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-COOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.000 -GAPOP=6.000 -FGAPOXT=7.000 -YGAPOP=10.000
-YGAPOXT=0.500 -PGAPOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=20
-THR_SCORE=pct -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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_Geneseq_36:P81184
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0.10779 369
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                                                                                                                                           C. difficile toxin A. Fusion F
Clostridium difficile toxin A.
Human CD45 for use in T lymphoc
Bovine peptidyl-glycine alpha-a
Newcastle disease virus immunog
Newcastle disease virus glycopi
Haematopoietin receptor Hu-Bl. 2
Haematopoietin receptor Hu-Bl. 2
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E. coli colitose or glucose tra
GAP protein Ira2. Blocking Ras
Enzyme involved in eicosapenta
S. putrefaciens EPO biosynthes
                                                Haematopoietin receptor Hu-Bl.2
Oat phytochrome A apoprotein.
Carbamoyl-phosphate-synthetases
Candida albicans histidine kir
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A_Geneseq_36:R11110
A_Geneseq_36:R10322
A_Geneseq_36:R80530
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alignment_block:
US-09-323-427-1 x R20112
                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP-465404-A.
08-JAN-1992.
27-MAY-1991; 8
01-JUN-1990; 10-AUG-1990; 30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                               peptide(s) e.g. human calcitonin.
Claim 4; Page 18; 28pp; English.
The sequence was deduced from a cDNA insert from pAE-III-202-4
(FERM BP-3172). The vector serves as a source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyOH -> R-NH2. It can be used to produce peptides wit amidated C-termini, e.g. calcitonin, growth hormone, LH-RH.
                                                                                                                                             313
                                                                                                                                                                         526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA encoding peptidyl hydroxy:glycine N-C lyase (PHL) used to prepare PHL which can be used in the amidation of peptide(s) e.g. human calcitonin.
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N-PSDB; Q20269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CIBA ) CIBA GEIGY AG.
Iwasaki Y, Shimoi H, S
Kawahara T, Kangawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region
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AE-III (peptidylhydroxyglycine N-C
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                                                                                                            lAlaAspGlyTyr......
                                                                                                                                           AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
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                                                                                                                                                                                                TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 312
Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                           AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                    ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
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Ratio:
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! Type A alpha-amidating enzym
! B. sphaericus SLP. Host cel
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1243 CTCAATGTTTATGGGTTTAAGCATTGCATTT...GCTGCCGTCATTA 1289
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                                                                                                                                                GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT
                                                                                                                                                                                                                                                                                                                                                                            TGATATCAACACCCTTGAA.....ATTAGCGATGATAATCAAGCTT 1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCG 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGCTGATGGATGTCTTGATAAATATTTG.....CTAAATAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaGlyValSerThrGlnGluLysGlnAsnValValGlnGluIleAsnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alGlnGlyPheMetLeuAsnPheSerAsnGlyAsp.......
                                                                                    {\tt ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVal}
                                                                                                                                                                                                                                                               TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT
                                                                                                                                                                                                                                                                                                                      a {\tt GlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV
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                                                                                                                                                                                                      lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......GlyTyrSerAlaProV
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alignment_block:
US-09-323-427-1 x P81184
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: P81184 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful as antigenic protein for vaccine
Disclosure; Fig 1; 13pp; English.

cDNA was prepd. from FIPV straim 79-1146. N81533 gives the sequence
of the peplomeric gene in three reading frames. The top reading
frame is an open reading frame of 4356 nucleotides and has a coding
capacity for a precursor polypeptide having a mol. wt. of 160,470
(1452 AAs). The beginning and the end of the E2 gene are indicated
in the FT of N81533. The first 18 N-terminal AAs have a strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoded by the 2nd reading frame of FIVP strain 79-1146.

Vaccine; peplomeric protein; E2 gene. Feline infectious peritonitis virus.

EP-264999-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydrophobic character and presumably comprise a cleavable signal peptide. The extreme carboxy-terminal part comprises a region of 20 hydrophobic AAs, which presumably serves as a transmembrane anchor. The FIPV peplomeric protein has 35 potential glycosylation sites, of which 22 are in the N-terminal part (pos. 1-790) which corresponds to the S-part of the IBV E2 (see P81183). N.B. IBV = infectious bronchitis virus. "X" in the AA sequence denotes the translation
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De Groot RJ, Spaan WJM, Van Der Zeijst BAM:
WPI; 88-114147/17.
N-PSDB; N81533.
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05-SEP-1986; NL-002244
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29-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                  194 ACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                  109 lyAsnHisLeu
                                                                                                                                                                                                                                      uAspThrProLysPheLysCysArgCysAsnAsnAlaLeuIle.ValAsn 78
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                                                                                                                                                           LeuLysGluLysGluLeuAsnGluMetVal.....ValGlyLeuLe
                                                                                                                                                                                                   ATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGAT 343
                                                                           uArgLysGlyLysLeuLeuIleArgAsnAsnGlyLysLeuLeuAsnPheG
                                                                                                                   CAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTC 393
                                       ACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCAC 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1594 AA;
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0.376
45.783
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    .ValAsn
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1109 396	CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA	1068 380
1067 380	GCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA :::	1019 363
1018 363	CACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCC::::::::::	969 349
968 348	CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGAC ::::: 1::::::::::::::::: 1aLeuLeuProGlyAsnThrValLeuHisMetLeuThrLysValPhe	928 333
927 333	V 14	887 316
316	GGCTGGCCAAGAAGCTCACGT:: ::: lleThr*	837 313
836 312	GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATA ::: :::::::: ::: erGlyMetMetThrLeuLeuGlnLeuIleLeuValValValleu	787 298
786 298	rgarggr ::: luglnLy	744 281
281	rProProThrSerGlyIleProHisValArgValLeu1	0 4
743 264 743	AATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGG !!!	702 248 743
701 248	ArgLeuIleGlyMetMetCysAsnLysGlyProPhe**	698 231
697 231	CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC ::::: ::::::::::::::: valValasnHisTyrTyrPheMetCysMetValSe	4 4
647 214	TGC heIleLeuLeuTrpLysProTrp	639 198
638 198	CAGTATGCCGTTATGAAATTT ::::: rAlaLeuGluGlnLeuGluLeuLeuProPheSerI	618 181
617 181	CTGCT7 GluVal***LeuLe	579 165
578 164	AAACAGTTAGTGCACAGATTGAGGTATCTG	535 148
534 148	TATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTA :::::::::::::::::::::::::::::::::	489 131
488 131	GTGGTATTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCAT	444 115

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seq_documentation_block:
ID R87953 standard; Protein; 332
AC R87953;
              seq_name: A_Geneseq_36:R87953
                                                                             W09530432-A1.
16-NOV-1995.
09-MAY-1994; E01479.
R 09-MAY-1994; W0-E01479.
A (BOEF) BOEHRINGER MANNHEIM GMBH.
Nacannehrl R, Huston J, Junghans U, K
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Mueller HW; WPI; 95-403938/51.
Proteoglycan cpds, partic chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
                                                                                                                                                                                                                                                                                                                       20-MAR-1996 (first entry)
Bovine neurotrophic biglycan.
Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
neurotrophic; central nervous system; CNS; memory loss; dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 l***ArgLysLeuLeuValSerGlyAlaIlePheIleLeuMetValT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 hrIleSerLeuAlaHisPheLeuLeuValValTyrLeuLeu
                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                               region
                                                                                                                                                                                                                                                                                    Bos taurus.
                                                                                                                                                                                                                                                                                                           learning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTTCTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAAATATATA 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heHis***IleGlnGlnValValSerPheLeuLysPheHisValIleVal 494
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/label= Hypervariable_region
                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                        Kappler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567
                                                                                                        Koops
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alignment_block:
US-09-323-427-1 x R87953
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                                                                                                                                             1423
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Bovine biglycan (R87953) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients
                                                                                                                                                                                                                                                                                     160 GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 1262
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                                               ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 1522
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                                                                                                                                          ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC 1472
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LeuAspHisAsnLysIleGlnAlaIleGluLeuGluAspLeuLeuArgTy
                                                                                           lyIle.....ProLysAspLeuProGluThrLeuAsnGluLeuHis
                                                                                                                                                                                         rLeuArgIleSerGluAlaLys....
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0.798
40.468
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Gaps: 13
Percent Identity: 20.401
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seq_documentation_block:
ID R87951 standard; Prot
AC R87951 standard; Prot
BI (first e
DT 20-MAR-1996 (first e
DE Rat neurotrophic; central
KW Biglycan; proteoglyca
KW learning.
OS Rattus Sp. Locat
FT Peptide 1. .3
FT peptide 1. .3
FT region /1abe
FT region /1abe
FT region /1abe
PD 16-NOV-1995.
PP 09-MAY-1994; WO-E01479.
PR 09-MAY-1994; WO-E01479.
PR 09-MAY-1994; WO-E01479.
PR N-PSDB; T08788.
PT for maintain structur
PT memory deficit(s) in
PS Claim 1; Page 44-45;
CC neurotrophic activity
Obtd. by expression o
CC calls, can be used to
CC and function of CNS n
pathological and/or t
CC degenerative diseases
CC in the elderly and in
SQ Sequence 369 AA;
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                                                                                                       Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia Claim 1; Page 44-45; 60pp; English.
Rat biglycan (R87951) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. Recombinant biglycan, obtd. by expression of encoding cDNA (708768) in eukaryotic host cells, can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also
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09-MAY-1994; E01479.
09-MAY-1994; WO-E01479.
(BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat neurotrophic biglycan.
Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
                                                    be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory
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          in the elderly and in patients with dementia. Sequence 369 AA;
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alignment_scores:
Quality: 95.50
Ratio: 0.789
Percent Similarity: 40.468
Alignment_block:
US-09-323-427-1 x R87951
Align seg 1/1 to: R87951 from: 1 to: 369
1005 AAACAGGTGGTGCCGCAAGCAAAACCTGCTGCAGCTACGTTTA 1054
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seq_name:
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                                                                                                                     TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 1691
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                                                                       leThrLysValGlyIleAsnAspPheCysProMetGlyPheGlyVal 328
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                       A_Geneseq_36:R87952
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R87952 standard; Protein; 369
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Human biglycan (R87952) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to
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Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
neurotrophic; central nervous system; CNS; memory loss; dementia
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16-NOV-1995.
09-MAY-1994; E01479.
09-MAY-1994; WO-E01479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with dementia.
Sequence 369 AA;
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                         GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 1312
                                                                                                                                                                                                                       CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 1212
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                                                                                                                        AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 1262
                                                                                                                                                                                                                                                                                                                        CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 1162
                                                                                                                                                                                                                                                                                                                                                                                                                    ....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 1112
                                                                                                                                                                      sAsnHisLeuValGluIleProProAsn.......
                                                                                                                                                                                                                                                                  ProLeuArg.....LysLeuGlnLysLeuTyrIleSerLy 148
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hrl R, Huston J, Junghans U,
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                                The sequence encodes a derivative of the mature C-terminal alpha-amidating enzyme from plasmid pxA/99. amidating enzyme from plasmid pxA457. The plasmid was screened from an E.coli library using plasmid pxA457 to screen a larger library. Although pxA799 is similar to pxA457 at the N-terminus, it has an ar
                                                                                                                                                                                                                                          Recombinant C terminal alpha amidating enzymes and their precursors deoxyribonucleic acid enco Disclosure; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka S,
WPI; 89-017279/03.
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Expression plasmid pUCP1CI799
alpha-amidating; pAX799; alpha
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; N94527
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17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
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Sequence 693 F
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seq_documentation_block:

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alignment_block:
US-09-323-427-1 x P94854
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.

Plasmid pXA799 contains a sequence derived from Xenopus laevis. The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.

Although the gene product is similar to that of pXA457 at the N-terminus, it has an area of hydrophobic elements suggesting a membrane function. See also N93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P94854; standard; protein; 875 AA.

P94854;
27-JUN-1990 (first entry)
C-terminal prepro-C-terminal alpha-amidating enzyme of pXA799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-1989.
15-JUL-1988; 306508.
17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-amidating; pAX799; alpha amide; Synthetic. EP-299790-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka
WPI; 89-017279/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; N90791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGACATGTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT
                                                                                                                                                                                                    {\tt leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla}
                                                                                                                                                                                                                                                                                                                                           Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lAlaAspGlyTyr......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
   laValSerTyrAlaPro
                                                                 uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
                                                                                                  AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
                                                                                                                                  AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                                    AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
                                                                                                                                                                                                                                                                       nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
                                                                                                                                                                                                                                                                                                                                                                          AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
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                                                                                                                                                                                                                                       ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
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alignment_block:
US-09-323-427-1 x R73053
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                                                                                                                 Align seg 1/1 to: R73053
                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP-649900-A.
26-APR-1995.
07-SEP-1994;
08-SEP-1993;
                                                                                                                                                                                                                                                                           3mu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alpha-
amidase enzyme (AE)) were suspended in F-12 medium to which aliquots
of trichostatin were added. Cells were cultured for 3 days at 37 deg
and then assayed for AE. Without trichostatin, AE productivity was
708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities
were respectively 866, 1897, 1894 and 3359 U/ml.
                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q87970.

Increasing protein prodn. from cultured animal cells - by a trichostatin to the medium, effective at low concn. and injurious to host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-1995 (first entry)
Peptidyl C-terminal alpha-amidating enzyme.
Peptidyl C-terminal alpha-amidating enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R73053 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trichostatin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furukawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FURU/) FURUKAWA K. (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
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lAlaAspGlyTyr....
                              AGGACATGTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                         TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 312
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                                                          CysGlnProThrAspValAlaValAspProTleThrGlyAsnPhePheVa
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JP-257881.
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SECOND SE
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Purified RNA polymerase II holo:enzyme - comprises RNA polymerase and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SWI/SNF proteins Claim 11; Fig 10a-b; 154pp; English.

Novel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W13825;
04-JUN-1997 (first entry)
Yeast transcription regulatory factor SRB8.
Transcription regulatory factor; suppressor c
SRB8; RNA polymerase II; holoenzyme; SWI/SNF.
Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                 06-MAR-1997.
28-AUG-1996; U14192.
31-AUG-1995; US-521872.
11-OCT-1995; US-540804.
26-JAN-1996; US-590399.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                      N-PSDB; T59908
                                                                                                                                                                                                                   Chao DM, Koleske AJ,
WPI; 97-179258/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 886
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                                                                                                                                                                                                                                                       Thompson CM,
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alignment_block:
US-09-323-427-1
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Percent Similarity:
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  434
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                                                                                          nTyrAsnMetValLeuArgAsnValMetGluTyrAspValLysPheTyrG
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luIlePheAsnPheAspGlnValValGluIleThrGluGlnIleLysMet
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1032 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG

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seq_name: A_Geneseq_36:R99462
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                                                                                                               1723 GCATTATTGCAATTAAA 1739
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                                                         InLeuIleSerLeuLys 714
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seq_documentation_block:
ID R99462;
AC R99462;
AC R99462;
DT 30-JAN-1997 (first entry)
DE Biosynthetic enzyme of icosapentaeno:
KW foodstuffs; animal feed; lipid balance antiinflammatory; anticancer agent.
SS Shewanella putrefaciens.
PN W9621735-A1.
PN W
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US-09-323-427-1 x R99462
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Percent Similarity:
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Biosynthetic enzyme of icosapentaenoic acid synthase.
Icosapentaenoic acid synthase; EPA; drugs; agrochemicals; foodstuffs; animal feed; lipid balance correction; antihypertensive; antiinflammatory; anticancer agent.
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The DNA sequence (T34137) which encodes the biosynthetic enzymes of icosapentaenoic acid (EPA) can be used to transform Escherichia coll. The DNA sequence allows efficient microbial production of EPA, which is a raw material for drugs, agrochemicals, foods and animal feedstuffs. EPA is also useful for lipid balance correction and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAGA ) SAGAMI CHEM RES CENTRE.

Kato S, Kondo K, Yamada A, Yazawa K;

WPI; 96-342288/34.

N-PSDB; T34137.

Production of icosapentaenoic acid using transformed E. co

DNA coding for icosapentaenoic acid synthase derived from
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                                                                                                                                                                                                                                                            IleSerIleAsnProAsnProLysValAspSerAspLeuGlnLeuLys..
                                                                                                                                                                                                                                                                                                                                                  ATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                        lnLysLeuValGlnGlyThrLeuValAsnThrGluAsnGluValCysThr
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                                                                                 .....GlnAlaAlaMetGlnLeuA
                                                                                                                                                                           TCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTG
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Gaps: 23
Percent Identity: 18.400
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1098 GAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCA
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                                                    oThrGlnAlaProAlaProLysAlaGlnPro.....AlaProValT
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                                                                                                                                                                                                                                                                                              erGlnValValGlnSerGln.....Thr
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                                                                                                                                                                            AlaValGlnProValIleSerThrGlnValAsnHisValSerGluGlnPr 1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGAC 968
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                                                                                                                 .....TCTGCAGAACCGGAGAATATCATTGATGTAC 1097
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seq_documentation_block:
ID R05159 standard; prot
AC R05159;
DT 09-OCT-1990 (first e
DE Sequence of human bon
KW Osteoporosis; rheumat
KW 14herosclerosis; peri
OS Homo sapiens
PN US7432044-A.
PR 3-NOV-1989; US-432044
PR 3-NOV-1989; US-432044
PR 3-NOV-1989; US-432044
PR 3-NOV-1989; US-432044
PR 17-APR-1990 US-432044
PR 3-NOV-1989; US-432044
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1163 CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 1212
                                                                                                                                                                                                                                          1068 .....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 1112
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Disclosure; p; English.

Probes and Abs raised to the proteins can be used to determine their levels useful in diagnosis of associated conective tissue diseases states such as osteoporosis, osteo/rheumatoid arthritis, Paget's disease, artherosclerosis and periodontal disease.

Paget's disease, artherosclerosis and periodontal disease.
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                                                                                                                                                                                                                                                                                                        102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bone matrix DNA and proteins - used in detection, diagnosis and treatment involving skeletal and/or connective tissue disease states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of human bone proteoglycan I (biglycan).
Osteoporosis; rheumatoid arthritis; Paget's disease;
atherosclerosis; periodontal; human bone matrix; proteoglycan.
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3-NOV-1989; US-432044.
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                                                                                                                     CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 1162
                                                                                                                                                                                euValLeuValAsnAsnLysIleSerLysIleHisGluLysAlaPheSer 135
                                                                                                                                                                                                                                                                                                     eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 119
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                                                          ProLeuArgAsnVal......GlnLysLeuTyr1leSe 146
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Gaps: 14
Percent Identity: 19.732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1423 ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC 1472
                                                                                                                                                                                       Feline infectious peritonitis 1 virus spike protein. Feline infectious peritonitis 1 virus; FIPV-I; spike vaccine; prevention; treatment. Feline infectious peritonitis 1 virus. J07327683-A. 19-DEC-1995.
DNA encoding feline infectious peritonitis I virus spike protein used in a vaccine for prevention and treatment of FIPV-I infection Claim 1; Page 14\cdot17; 23pp; Japanese.
                                                                                         10-JUN-1994; 129300.
10-JUN-1994; JP-129300.
10-JUN-1994; JP-129300.
(KITA) KITASATO KENKYUSHO SH.
WPI; 96-072341/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy
                                                                           N-PSDB; T10166
                                                                                                                                                                                                                                                                                                                                                                        R88469 standard; Protein; 1464
                                                                                                                                                                                                                                                                                                                           14-AUG-1996 (first entry)
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| eThrLysValGlyValAsnAspPheCysProMetGlyPheGlyVal 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host cell with the spike protein DNA and expressing the sequence such that the spike protein can be isolated.
                                                                                                                                           903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 818
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TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC
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                                              GlyAlaArgLeuGluSerLeuMetLeuAsnAspMet.....
                                                                                          GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA
                                                                                                                                                                                     TA.....AATGCT.....GAT
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                                                                                                                                                                                                                                                                                                                              TyrIleGlnIleGlnValLysProValValValAsp.....CysAlaTh
                                                                                                                                                                                                                                                                                                                                                                                 TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 744
                                                                                                                                                                                                                                                                                                                                                                                                                             hrGlyAsnIleSerIleProLysAsnPheThrValAlaValGlnAlaGlu
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                                                                                                                                         euThrGlnTyrThrSerAlaCysGlnThrIleGluAsnAlaLeuAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ... GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT
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                               races or patient samples

Disclosure; Fig 7; 165pp; English.

This is the amino acid sequence of the protein encoded by the wbdM gene of a gene cluster (see x06748) involved in the biosynthesis of the Escherichia coli Olll O antigen. The protein shows high homology with TrsE of Yersinia enterocholitica, and is predicted to be a colitose or glucose transferase. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in testing food or faecal-derived samples, or samples from patients.

The O antigen is a major virulence factor of enteropathogenic E.
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O antigen; Oll1 antigen; wbdM gene; colitose transferase;
glucose transferase; diarrhoea; haemorrhagic colitis; diagnosis Escherichia coli.
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(UNSY ) UNIV SYDNEY.
Reeves PR, Wang L;
WPI: 99-059669/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; X06748.
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22-JUL-1997; AU-008162.
01-MAY-1997; AU-006545.
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alignment_block:
US-09-323-427-1 x W88310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 TGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG...ATCGTGCAT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProAspIle.....IleHisSerHisMetPheHisAlaAsn..
                                                                                                                                                                                                                                            ACTGTGGAA.....ATTCTAAATGCTGATGGATGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAG
euLeuIleAlaGlyAspGlyAlaLeuArgAsnLysLeuLeuAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erLysGluAlaValGlnGluPhe.....IleAlaArgLysAlaThrPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gLeu.....SerAspPheLeuAlaSerIleThrThrAsnValS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrAlaHisAsnLysAsnGluGlyGlyAsnAlaArgMetPheCysTyrAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuThrGlyIleSerGluValLysProThrGlnAsnIleAsn....
                                                                                               aIleAsnHisLeuIleLeuSerLysThrSerAsnCysAsnAspPheIleL
                                                                                                                                               TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGAT.....
                                                                                                                                                                                               LeuValGluAlaLysAspTyrProAsnLeuLeuAsn.....Al
                                                                                                                                                                                                                                                                                               spSerThrAlaValLeuLeuAlaVal...
                                                                                                                                                                                                                                                                                                                                              CTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                            pPheAspIleAsnValArgLysLysThrArgAspAlaPheAsnLeuLysA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                       ......AAATGGACATGCGATTCTGAAACCGTTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCAATTTGCTATCATTGGTCAGCCAGTTTATCAT........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lePheSerArgPheIleArgMetLeuIleProAlaValProLeuIleCys 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erPhePheArgAlaLeuPheGlnValLysLysIleIleValAlaLeuLys
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0.533
46.281
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18
21.763
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     240
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38 ACTGCAGCAACAACAACAACAACAAACA
⊶. ,
alignment_block:
alignment_scores: Quality: 89.00 Length: 752 Ratio: 0.264 Gaps: 42 Percent Similarity: 44.814 Percent Identity: 18.617
241

82 2316	ACAGGAAGCAATCTTAG	131
132	TTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATG	2
2325	::: ::::: eAspGluSerLysLysMetLysAsnSerSer	2341
17	CGTCTTATTGCTTTCTGTACTACACCTTATTGCATTGTTTTTTCG	20
221	ATTCCGGTTGACAAT	235
2358	HisPheHisArgSerProGluValTyrValProGluAspThrThrThrP	w
236	GGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA	280
2375	roGluLeuThr	2391
281 2392	ACAATCAATTTAATACACGTAATGCATTCGAAGGACATGTTTATGT::::	327 2408
328	GTTGCC	356
2408		2424
357	I GCCGGAATT	391
2425	HisValTyrLeuAlaAspAspGluGluGlyProGluAs	2441
392	\TTTGATTCATGCAATGTTGCGCGTACAC	135
2441	lePheArgIleLeuIleArgLeuSerValArgGluThrA	2458
3	CACGTGGTATTTTTGTAACAACAACTGTTGTCATTT	476
U	enysalavaliyimettiniyivaliipheuheuheuhspasp	4
2475	Glv#rcArtCAFTATTTGTTACCAAAGTTGATCGTGCATArtCGA 	520
521	rgctttacarggaag	542
2491	AspSerGluAsnArgAspTrpLysLysThrIleSerLeuLeuThrV	2508
543	CTGATAAAACAGTTAGTGCAC	563
2508	alLeuProThrThrGluValAlaAsnAsnIleIleGlnLysIleLeuAla	2524
564	G	613
614	AACC	
2537		2544
664 2544	AGTTCAATTIGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG :::::::::::::::::::::::::::::::::::	713 2560
714	TTCTGAAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTGTC	763
2561	ValGlnMetTyrLeuProGluIleLeuPheIleValSe	2575
76	GATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	13
814	_eumeurreaspydroryrroargorumeuargserser CTTGATAAATATTTGCTAAATAATTTGGAATATCCAACA	363
Ē	CITGALAAALAITIGCIAAALAAITIGGAATATCCAACAGAITIAATGG	

99	1477 AAACTTCTTCTATCGCTTTTATA
1476 2857	1451 TAATACAATAAGTGATATTTTCATCA 14
.450 840	1401 AATAACTAATTTTAGCTAACAAATATATAGTAGTAGGAAATAATTACTG 14 ::::: ::: 2829LeuSerGlyIleValTrpAsnGluAspAsnPheTh 28
00	1360 TAAAACTGCCATATATATTCGTTTCTTATCATCCTTCT 14 :: :: ::: ::: :: 2813 eulysGlyArgLysPheAlaHisThrPheLeuSerLysIleGluAsn 28
13	1326CATAAAAATAATGTTAGAATCATCGAAGCAATAA 13
96	1287 TTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGG 13 ::::::
286	1252 TATGGGTTTAAGCATTGCATTGATTGCTGCCGTCA 12 :: :: 2766 herrpPheSerThrLeuPheLeuGluSerArgHisProIle 27
	1236TTGGCTTCTCAATGTT 12
35 49	1215 ATGGAATCT
214 732	1171 TCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAA 12 :: ::: :: ::: 2716 euCysLysAlaMetLeuIleGluThrMetLysValIleAlaGluProLys 27
.70	1121 ATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT 117 :::
99	1086 TCATTGATGTACGAACTGATATCAACACCCTTGAA 11 ::: ::: 2683 LysTyrValLeuGluSerValPheThrSerAsnSerPheLeuSerAlaar 26
	1042 GCAACTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAATA 10 :::::: :::::::::::::::::::::::::::::
1041 .	1023
649	2 ⊢
ω	49 AAATAGCGAATGTTCGACCACAATGTTCAGAAC
48 616	914 TATCAATGCCAGATCAGTATTACCATTAAAGAACC 94
13	864 CTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGATC
597	::: ::: 92 euLeuMetAsnValCys

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seq_documentation_block:
ID R42452 standard; Prot
AC R42452
DT 27-MAY-1994 (first e
DE Enzyme involved in ei
KW EPA; eicosapentaenolic
KW Hoolipemic; hypoglyc
KW foodstuff; additive.
OS Shewanella putrefacie
PN W9323545-A.
PF 14-MAY-1993; J00641.
PR 15-MAY-1993; JP-14794
PA (SAGA) SAGAMI CHEM R
PPI Kato S, Kondo K, Ya
DR WPI; 93-386577/48. Ya
DR N-PSDB; O51128.
PT Gene coding for eicos
PT recombinant prodn. of
PS Claim 6; Page 52-63;
CC EPA is useful as a dr
CC hypoglycemic, antihyp
CC a pesticide and is us
CC sequence 1634 AA;
                                                                                                  alignment_scores:
Quality:
Ratio:
alignment_block: US-09-323-427-1 \times R42452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: A_Geneseq_36:R42452
                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2974 IleCys.....AlaLeuArgPheTyrSerValIleArgAsnGluTleAr 2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2957 erArgPheArgPheAlaLeuIleIleArgHisLeuLeuThrLysLysPro
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                                                                                                                                                                                                                                                                       (SAGA) SAGAMI CHEM RES CENTRE.

(SAGA) SAGAMI CHEM RES CENTRE.

KRATO S, KONDO K, Yamada A, Yazawa K;

WPI; 93-386577/48.

N-PSDB; Q51128.

Gene coding for eicosa penta:enoic acid synthetase - is isolated from pseudomonas, Alteromonas or Shewanella and used for recombinant prodn. of eicosa-penta:enoic acid Claim 6; Page 52-63; 106pp; Japanese.

EPA is useful as a drug, having anticoagulant, hypolipemic, hypoglycemic, antihypertensive and anticancer activity. It is also a pesticide and is useful as a nutritional foodstuff and animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2857 ysSerThrAlaPheAspPheLeuLysMetMetPheArgAsnSerTyrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzyme involved in eicosapentaenoic acid (EPA) synthesis.
EPA; eicosapentaenoic acid synthetase; drug; anticoagulant;
hypolipemic; hypoglycemic; antihypertensive; anticancer; pesticide;
foodstuff; additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1993; J00641.
15-MAY-1992; JP-147945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shewanella putrefaciens.
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27-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R42452 standard; Protein; 1634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rLeuTyrGlnGlyAlaIleLeuPheLysCysSerValThrAspGluProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysIleLeuLeuGluTrpLeuSerSerAspAsnGluAsnAlaAsnIleTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTTATTCTAACAGTTTATCATTTGTGATAAT...ATCACAAATTATAC 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alAspPheGluGlyGluMetValAsnIleGluAsnLysAsnThrIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATAGTTTCGT.....TTGTTATTATCATCATTATCAACTTGTCCT 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uLeuTyrPheValLeuAsnCysAsnGlnPheGluGluLeuLeuGlyAspV 2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGCATACTATTGTAAATGTTTCATCA.....TTAGGCCATG 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluHisGlnIleAsnGlnLysSerAspHisTyrLeuCysTyrMetPheLe 2890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....TTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTT 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ........GCTTCTGAAAAGCTTATTCATTAT...TCAGTAATCTTTTA 1537
                                                                       88.00
0.376
46.800
                                                                       Length: 500
Gaps: 23
Percent Identity: 18.200
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Align seg 1/1 to:

R42452

from:

ب

to: 1634

781	GGGGGTTGTCCATTCCTGCTTTGTCGATCATGGTAAACGGTGAT 	738
	AlaLeuSerAsnPhePheAlaAlaGlnGlnGlnThr	1068
737	CCAGTTTATCATAAATGGACATGCGATTCTGAAA	688
687 1068	TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA ::: ::::::::::::::::: ::: ! ::: ValSerLysAsnSerLysProAlaValGlnSerIleSerGlyAs	638 1054
637 1053	CTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATT::: ::: ::: ::::::::::	588 1037
587 1037	AGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAA ::::: :::: :::::::: :::::::::	541 1020
540 1020	TTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGA	491 1004
490 1003	TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTA ::: ::: ::: hrGlyIleValThrSerGlnIleGluHisValIleGluGluLysIleVal	452 987
987	${\tt aAsnHisIleSerLysAlaThrArgAlaLysMetAlaLysSerLeuGluT}$	970
451		451
451 970	GTTGCGCGTACACGATCTCTGAATCCACGTGGTATT	416 954
415 953	CCGGAATTTCACTTCCATTTGATTCATGCAAT	384 938
383 938	TCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTG	334 932
333 931	ATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGG	284 916
915	lnLysLeuValGlnGlyThrLeuValAsnThrGluAsnGluValCysThr	899
283		281
280 899	TGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA	235 884
234 884	GCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAA	185 873
184 872	TTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATT :::	135 859
134 859	AATAATAACCCCATCAAGTGGAGGAAGAAGAAGAAGCAATCTTAGTTT	85 843
84 843	CCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA	35 827

1297 1265	TGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATT ::: ::: :: :::: ::: ::: laGluThrAlaLeuSerAlaThrLysValGlnAlaThrMetLeuGluVal	1248 1249
1249	nThrSerValAlaThrThrThrProSerAlaPheSerA	1236
1247		1198
1236		1228
1197		1148
1227		1211
1147		1098
1211	oThrGlnAlaProAlaProLysAlaGlnProAlaProValT	1197
1097		1067
1197	AlavalGlnProvalIleSerThrGlnValAsnHisValSerGluGlnPr	1181
1066		1019
1180		1173
1018	GGAGCTGTTAAAACAGGTGGTGCC	969
1173	aProAlaIleHisAsnGluAlaIleGInS	1163
968	AAATAGCGAATGTGTTCGAC	919
1163		1147
918		869
1146	lnAlaGlnThrLeuGlnSerHisThrGlnPheLeuGluMetGlnAlaGly	1130
868		845
1130		1113
844		811
1113		1097
810		782

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Database sequences: 133990
Database length: 13297546
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Query length: 1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search time (sec): 99.320000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19887/app_query.fasta.1
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-MATRIX=blosum62 -TRANKS-human40_cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA: *
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415-751-6 -
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Quality:
                          alignment_block:
                                                                                                            US-08-415-751-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                 US-09-323-427-1/rev x US-08-415-751-6
                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
COMPUTER: P
                                                                                                                       NAME/KEY:
                                                                                                                                 NAME/KEY:
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                              STRANDEDNESS:
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                                                          Ratio:
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-415-751-6
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/cgn2_6/ptodata/1/iaa/FCTUS9_COMB_pep:US-08-97-302-5 + 81.50
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-872-302-5 + 81.00
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-392-806A-6 + 81.00
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/071,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/01
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/88
FILING DATE: May 29, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01
FILING DATE: 03-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6, Application US/08415751
o. 5643772
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hana Dolezalova
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                    (415) 324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEECH, JAMES
                                                                                                                                                                                                                                                ss: single
linear
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                                                                                                                                                                                           Cryptosporidium parvum
                                                                                                                                   identified as Xaa.
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NUMBER: 07/891,301
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121.50
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CRYPTOSPORIDIUM ANTIBODIES, DNA
AND RNA ENCODING THEM, HYBRID
VECTOR AND TRANSFORMED HOST AND
METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/415,751
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Percent Identity:
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seq_name:
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                                                                                                                                                                                                                                                                                                                                                                  135 AAAACTAAGATTGCTTCCTGTCTTCCTCCACTTGATGGGGTTATTAT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 CAATAAGACGAATCATCATTTCAGAAGATTTAGTAAATTCGATTTTTAGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 ATTGTCAACCGGAATCGAATAAGACAATGCAATAAGTGTAGTACAGAAAG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 GACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTAAAATTG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 ACGTCCACCTTCATCATT.....ACGGCAACCTTCTTGATCATAAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 leSerTyrLeuSerCysLeuArgThrTrp...........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 CGCGCAACATTGCATGAATCAAA...TGGAAGTGAAATTCCGGCAACTTG 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 TGACAACAGTTGTTGCTACAAAATACCACGTGGATTCAGAGATCGTGTA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            561 GCACTAACTGTTTTATCAGCTTCCATGTAAAAGCATTGTACTCGATATGC
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                                                                                                                                                                                                                                                      GGTTGGTCCACCATCCAA.....AATTTCATAACGGCATACTGGCATCG 612
                                                                                                      u***CysCysCysCysCys 215
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                                                                                                                                                       ... TGCTGCAGTCGGTGT 32
                                                                                                                                                                                                                                                                                                              ......ValSerLeuGlySerSerSerCysArgTrp...HisCys 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGTTATTGAAGTTGGTCCACATTCAATTTCTGGCTCACCTTCGACACC
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alignment_scores:
Quality:
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US-08-415-751-35
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                                                                                                                             Align seg 1/1 to: US-08-415-751-35 from: 1
                                                                                                                                                                 US-09-323-427-1/rev x US-08-415-751-35
                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/08415751 Patent No. 5643772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 324-1678 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING CO...
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/071,880
                                                      135 CysCysCysLeuAsnTrpThrLeuTrpTrpTyrGlyCysCysCysCy 151
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                          124 TGCTTCCTGTCTTCCTCCACTTGATGGGGTTATTATTGCTGTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Hana Dolezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
74 TTGTTTGTTGTTTGTTGTTGTTGTTGCTGCAGTCGGTGT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hana Dolezalov
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/071,880 FILING DATE: June 1, 1993 APPLICATION NUMBER: 07/891,301
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/415,751 FILING DATE: 03-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2: PHILLIPS, MOORE, LEMPIO & FINLEY 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEECH, JAMES
NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                             Positions coded by nonsense codons are identified as Xaa.
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                                                                                                                                                                                                                                                                                                                                                                                                 Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette -
                                                                                                                                                                                                                 109.00
6.056
58.065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRYPTOSPORIDIUM ANTIBODIES, DNA AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPEPTIDES BINDING ANTI-
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5
                                                                                                                                                                                                                   Percent Identity:
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                                                                                                                             to: 362
                                                                                                                                                                                                                   31
0
51.613
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151 sCys***LeuTrpTyrAsnCysCysCysCysPheCysCys 165

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COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, Barbara G.
REFERENCE/DOCKET NUMBER: 035.002
TELECOMMUNICATION UNFORMATION:
TELEPHONE: 510-651-3708
TELEPHONE: 510-655-3542
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 mnino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-477-451-8 from: 1 to: 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-323-427-1/rev x US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08477451 Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    1216 ATTTTGTACTGCAGCAAGTAT......TACAGGTTGTCCATTATGTT 1176
                                                                                                                                                                                                               1125 CTAATTTCAAGGGTGTTGATATC.....AGTTCGTACATCAATGATATT 1082
                                              1031 CAGGTTTTGCTGCGGCACCACCTGTTTTAACAGCTCCGAATCCTTGTGGT 982
                                                                                                                                    1081 CTCCGGTTCTGCAGATCTTTTCTTGAGTAAACGAAGTTGCGCAGCTGCAG 1032
                                                                                                                                                                                                                                                                                                                   1175 GCAGAAGTGCACGGTGACGTAAATCAACTGGCAAAGCTTGATTATCATCG 1126
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                                                                                                                                                                              774 alAsnPheLeuSerGlnPheLeuIleProLysProTyrLeuThrGluIle
804 uProTyrAsnThrGlnThrThrCysTyr......
                                                                                      791 IleAsnPheIleMetProPhe......GlnArgGluAlaArgCysLe
                                                                                                                                                                                                                                                                         761 sLysThrCys......PheSerPheTyrArgLeuIleGluIleV 774
                                                                                                                                                                                                                                                                                                                                                             745 IleValPheCysArgIlePheGluLeuValTyrArgLeuLeuIleAlaLy 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 4560 Hort
CITY: Emeryville
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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Ratio:
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41.501
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Helicobacter Pylori Cagi Region
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Gaps: 24
Percent Identity: 22.075
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0	alaGluIleLeu	N i
145	ТСАGААGАТТТАGТАААТ	194
1020		1005
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245	TTATTGAAGTTGGTCCACATTCAATTTCTGGCTCAC	295 291
٠ ٧	Tregra Sercys1) a
9	CTTTCACATAAACATGTCCTTCGAATGC	4. 0
ω	LeuIlePheAlaIlePheGl	00
4	ATTCCGGCAACTTGACGTCCACCTTCATCATTACGGCAACCTTCT	9
981	SLe	969
392	ATTCAGAGATCGTGTACGCGCAACATTGCATGAATCAAATGGAAC	441
969		957
442	ATGAAACGAAATGACAACAGTTGTTGTTACAAAAATACC!	491
956	TyrArgLeuIleGluIleIleAsnPheIleArg.	946
492	CCATGTAAAAGCATTGTACTCGATATGCACGATCAACTTTGGTA	541
945	luIleGlyArgLeuLeuTyrProThrGluIleThrArgCysPheSerHis	929
542	GATTTCAGATACCTCAATCTGTGCACTAACTGTT	583
929	uLeuGlyGlnLeuLeuLeuGluIleP	917
584	GTTTGAAAAGCAGTTGT	617
916	eArg	903
618	GGTCCACCATCCAAAATTTCAT	652
902	ysLeuArgProIleThrAspGlySerIleH1sThrIleLeuAsnGlyLeu	886
653	TAAACTGGCTGACCAATGATAGCAAATTGAACTGGTTGACCGG	699
986	uAspValArgLysValPheArgLysSerCysGlyPheC	873
700	\GAAAGTATCAACGGTTTCAGAATCGCATGTCC	749
873	leSerLysPheCys	857
750	CACCGTTACCATCATCGAC	781
856	<pre>!!!::: IleAsnGlyPheValPheGl</pre>	848
782	AAGAGCACATCCATCAGCATTTAGAATTTCCACAG	831
847	eIleAsnPhe	844
832	TGAGCTTCTTGGCCAGCCATTAAATCTGTTGGATATTCC.	881
844	LeuSerValAsnGlyPhePheLysAlaSerCysLeuProCysPheLeuPh	828
882	3GCATTGATAGAAAAGCTGTGATCGATCCGCATATTTGTAI	931
827	LeuIleGluSerValAsnPheCysIleTyrLeuPheSerAsn	814
932	TCTGAACATTGTGGTCGAACACATTCGCTATTTGGTTCTTTAATGGTAAT	981

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seq_documentation_block:
    Sequence 2, Application US/07707367
    Patent No. 5196316
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-07-707-367-2
                                                                                              TELEFAX: (919)541-868:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1096 lAlaAla 1098
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                                     SEQUENCE CHARACTERISTICS:
LENGTH: 935 amino acids
TYPE: AMINO ACID
                                                                                                                                                      REGISTRATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-18110/A/CGJ 44
TELECOMMUNICATION INFORMATION:
MOLECULE TYPE:
                                                                                                                                                                                                                  APPLICATION NUMBER: JP 329911/90
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Villamizar, Johnn
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 210535/90 FILING DATE: 10-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 141678/90
FILING DATE: 01-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kangawa, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hawthorne
STATE: New York
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                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATTGCTTCCTGTCTTCCTCCACTT.....GAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
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Shimoi, Hiroko
Suzuki, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kangawa, Kenji
VENTION: No. 5196316el Enzyme and DNA Coding Therefor EQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ghisalba, Oreste
Nishikawa, Yoshiki
Kawahara, Takashi
                                                                                                                       (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                    linear
                                                                                                                                        (914)785-7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us/07/707,367
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alignment_block:
US-09-323-427-1 x US-07-707-367-2
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Quality:
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692 lyAspAlaHisAlaAsnAlaValTrpLysPheSerProSerLysAlaGlu 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           612 nPheValLys...GlnTleLysHisGlnGluPheGlyArgGluValPheA 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457
                                                    891 ATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT.....
                                                                                                                                                                             841 GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT 890
                                                                                                                                                                                                                                                                                                                                                          652 alGlnGlyPheMetLeuAsnPheSerAsnGlyAsp......
                                                                                                                                                                                                                                                                                                                                                                                                                     747 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646 r.....GlyTyrSerAlaProV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           697 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  628 laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             580 leProHisSerLeuThrMetValProAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 nTrpGlyGluGluThrSerSerAsnValProArgProGlyGlnPheArgI 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA.... 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 lAlaAspGlyTyr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gly......ValLeuTyrAlaValAsnGlyLysProTyrTy
                                                                                                                                                                                                                                                                                                AATGCTGATGGATGTCTTGATAAATATTTG.....CTAAATAATTT 840
                                                                                                                  eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG
                                                                                                                                                                                                                                        .....IleLeuAspThrPheIleProAlaArgLysAsnPh
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Percent Identity: 19.437
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16,
                                                                                                                                      COUNTRY: U.S.A.
ZIP: 20036-8218
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757 AlaGlyValSerThrGlnGluLysGlnAsnValValGlnGluIleAsnAl
                                           FILING DATE: 24-MAY-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 HisArgSerValLysLysAlaGlyIleGluValGluGluIleThrGluTh
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                                                                                                                                                                                                                                                                                                                                                                STREET: 1233 20th
CITY: Washington
                                                                                                                                                                                                                                                                                                                                              STATE:
                           APPLICATION NUMBER:
                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lSerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI 840
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                                                                                                                                                                                                                                                                                                                                                                                           E: Wegner, Cantor, Mueller & Player, P.C 1233 20th Street, N.W.
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IFUKU, Ohji
KATO, Ichiro
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OKAMOTO, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUSE, Yuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAMINUMA, Toshihiko
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     15-AUG-1989
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                           JP 1-209687
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alignment_block:
US-09-323-427-1 x US-08-070-301-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: (202) 887-040
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           679
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02-AUG-
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APPLICATION NUMBER:
FILING DATE: 31-OCT-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           664
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728 uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                               363 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 989 amino acids
                                   AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
                                                                           AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                           leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
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                                                                                                                   AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
                                                                                                                                                                                                                                       \verb|nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI|
                                                                                                                                                                                                                                                                                                                     Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                 ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 499
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43.103
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seq_documentation_block:
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Patent No. 5919666
GENERAL INFORMATION:
                                                                                                                                                                  APPLICATION NUMBER: US 08/521,872
FILING DATE: 21-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,265
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GIANABAN, PALTICIA
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-03A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                     TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino aci
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APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 5919666el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Young, Richard A. APPLICANT: Koleske, Anthony
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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TOPOLOGY: 1
LECULE TYPE:
                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 11-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..........MetIleAsnPheSerAsnGlyAsp.......
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Two Militia Drive
                                                                         1226 amino acids
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                    linear
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alignment_block:
us-09-323-427-1 x Us-08-540-804-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-540-804-12
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                                                     1132 TAATC.....AAGCTTTGCCAGTTGATTTACGTCACC 1163
                                                                                                                                                                                                                                                                                      1032 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 108.
                                                                                                                                                                                                                          451 ArgIleLeuSerAsn.......AspIleThrAsnLeuGl 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384
472 etValAlaGluTrpTyrLeuSerHisLeuCysSerGlyIleLeuSerSer 488
                                                                                                                                                                                                                                                                                                                                           434 luIlePheAsnPheAspGlnLeuValGluIleThrGluGlnIleLysMet 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 nTyrAsnMetValLeuArgAsnValMetGluTyrAspValLysPheTyrG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 HisValGlnLeuLeuTleAsnLeuLysIleSerProLeuMetLysSerGl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              639 TGGATGGTGGACCAACCGGTCAACCAGTTCAAT.....TTGCT 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 TGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 uTrpSerIleHisProSerArgGlnPheAspHisTyrGluSerAsnGlnL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 CATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA....
                                                                                                                                                                     AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.....ATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAC...AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...SerThrAspGluAspLeuHisGluPheGlnIleGluAspAlaIleTr 338
                                                                                                                                                                                                                                                                                                                                                                                                   AG....GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....PheSerAlaGlnLysArgValValSer 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG 776
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                                                                                                             .LysThrProLeuSerIleLysIleM
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24
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-218-265-12
                                                                                                                                                                                                                                                                        Sequence 12, Application US/08218265 Patent No. 5922585
                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1184 GGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACC 1233
                                                            APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 592585el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 IleLeuLeuCysTyrGlnLysLeuPheSerGlnPheIleAsnAspHisIl 552
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCATTATTGCAATTAAA 1739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCCTATTTTA 1622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGCTTTTATAGCTTCTGAAAAGCTTATTCATTATTCAGTAATC..... 1532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....CTGCCATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA 1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....MetLeuLeuIleAlaThrAsnLeuLysGluTyrIleLysPheMe 693
                                   OF SEQUENCES:
                                                                                                                                                                                                    Young, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-218-265-12
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US-09-323-427-1 x US-08-218-265-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/218,.
APPLICATION NUMBER: US/08/218,.
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
NAME: Granahan, Patricia
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-861-624
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 CATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino aci
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 TyrValAspGlnAsnProLeuThrMetHisLysIleIleGlnLeuIleLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 uTrpSerIleHisProSerArgGlnPheAspHisTyrGluSerAsnGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Mil:
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTT
                                        TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu
                                                                                                                           GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT
                                                                                                                                                                                                                TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG
                                                                                                                                                                                                                                                      pSerLeuValPheGlnLeuAlaLysAsn......
                                                                                                                                                                                                                                                                                                  ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 726
                                                                                                                                                                                                                                                                                                                                                                                     TGGATGGTGGACCAACCGGTCAACCAGTTCAAT.....TTGCT 676
                                                                                                                                                                                                                                                                                                                                         ...SerThrAspGluAspLeuHisGluPheGlnIleGluAspAlaIleTr
                                                                                                                                                                                                                                                                                                                                                                                                                                euValAlaLysLeuLeuLeuArgIleAsn......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......GTGCACAGATTGAGG......TATCTGAAATCACAAC
                                                                                                                                                                     .....PheSerAlaGlnLysArgValValSer
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.IleThrTyrGlyIleIleLysValProThrTyrIleArgLysL
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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Gaps: 24
Percent Identity: 19.836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1164 GTGCAC.....TTCTGCAACATAAT 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1082 AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 1131
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                                                                        lAsnIleArgPheLeuLeuHisAsnSerGluIleIleAspThrAsnThrS
                                                                                                                                                                                                                             SerAsnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGCTTTTATAGCTTCTGAAAAGCTTATTCATTATTCAGTAATC..... 1532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAATACAATAAGTGATATTTTC.....ATCAAAACTTCTTCTA 1488
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                                                                                                                                                 .....TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....CTGCCATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA 1409
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alignment_block:
US-09-323-427-1 x US-07-906-349A-6
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Quality:
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                                                                                                                                                                                  Percent Similarity:
                                                                                Align seg 1/1 to: US-07-906-349A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Margolis, B
TITLE OF INVENTION: A
TITLE OF INVENTION: IC
TITLE OF INVENTION: TA
NUMBER OF SEQUENCES: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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573 ThrThrAlaAlaAlaThrCysAlaCysThrGlyCysThrGlyCysThrCy
                                        982 ACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 18-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 419 Seven CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 30-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                     Ratio:
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                             801 amino acids
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18-JAN-1991
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A NOVEL EXPRESSION-CLONING METHOD FOR IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES
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                                                                                                                                                                                    Percent Identity:
                                                                              from: 1
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: 1252-1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                            TELEFAX: (415) 324-16
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1182 ATGGACAACCTGTAATACTTGCTGCAGTACA 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-1677
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OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 385 Shered CITY: Palo Alto
      NAME/KEY:
                                          ORGANISM:
                                                                                                  TOPOLOGY:
                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                               NAME: Hana Dolezalova
                                                                                                                                                      ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-415-751-35
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5643772
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                                                                                                                                                      362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
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                                                                                                linear
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                                        Cryptosporidium parvum
Positions coded by nonsense codons
                                                                                                                                                                                                                                    (415)
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                                                                                                                single
                                                                                                                                                                                                                  324-1678
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CRYPTOSPORIDIUM ANTIBODIES, DNA
                                                                                                                                                                                                                                                                                           30,518
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alignment_block:
US-09-323-427-1 x US-08-415-751-35
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                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-303-238-3
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                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Applic Patent No. 5654270
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 .....TyrGly......CysCysCysCysCys***LeuTrpTyrAs 157
                                                                    NUMBER OF SEQUENCES: 8
                                                                                                                      APPLICANT: PIERSCHBACHER, MICHAEL D. APPLICANT: BOKDER, WAYNE A. TITLE OF INVENTION: INHESITORS OF CETITLE OF INVENTION: AND METHODS FOR
                                                                                                                                                                                                                       APPLICANT: LONGAKER, MICHAE: APPLICANT: WHITBY, DAVID J. APPLICANT: HARPER, JOHN R.
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                                                                                                                                                                                                                                                                    APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
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                     STREET:
                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnThrIle***HisLeuLysAsnArgCysLysTyrGlnSerThrHisHis 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *****LeuGlnPhe.AspLeuCysValLeu********Trp***ArgLe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....LeuValGlu*****LeuGlnLeuArgLeuValValLeuLeu* 97
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                  E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE, SUITE 700
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1.220
49.669
                                                                                                                      INHIBITORS OF CELL REGULATORY FACTORS AND METHODS FOR PREVENTING OR REDUCING
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                                                                                                                        REDUCING SCARRING
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TELEFAX: 619-535-8949;
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-238-3
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    Quality:
    Ratio:
Percent Similarity:
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US-09-323-427-1 x US-08-303-238-3
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION UMBER: 34,202
REFERBICE/DOCKET NUMBER: P-LA 9453
                            1313 CCAAATCAGAAGGCATAAAAATAATGTTAGA......ATCA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                     1113 CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 1162
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                                                                                                                                                   1263 GCATTGCATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 1312
                                                                                                                                                                                                                                                     1213 AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 1262
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
162 lGluLeuArgIleHisAspAsnArgIleArgLysValProAsnGlyValP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 119
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TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:::::: |||::::||||:::||| 102
86 LysGluIleSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspIl 102
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COUNTRY: UN
ZIP: 92122
                                                                                                                                                                                                  CALIFORNIA
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                                                                                                    .....IleProProAsnLeuProSerSerLeu.....Va 162
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0.738
41.472
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Percent Identity: 19.732
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236 LeuAspHisAsniySileGinAlaileGluLeuGluAspLeuLeuArgTy 252 1523 TTCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCATTAGGCC 1572 1111 :::::::::::::::::::::::::::::::::	heSerGlyLeuArgAsnMetAsnCysIleGluMetGlyGlyAsnProLeu
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seq_documentation_block:
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; Patent No. 5587311
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                                                                 GENERAL INFORMATION:
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      APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                        yLeuProAspLeuLysLeuLeuGlnValValTyrLeuHisSerAsnAsnI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAATCAGAAGGCATAAAAATAATGTTAGA.....ATCA 1347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 1522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isAsnGlnIleArgMetIleGluAsnGlySerLeuSerPheLeuProThr 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyIle.....ProLysAspLeuProGluThrLeuAsnGluLeuHis 235
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                                                                                             // Application US/08325071
5587311
COBON, Stewart Gary MOORE, Joanna Terry
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alignment_scores:
Quality:
Ratio:
                                                                      alignment_block:
US-09-323-427-1 x US-08-325-071-67
                                                                                                                                                                                                                 US-08-325-071-67
                                                                                                                         Percent Similarity:
                                            Align seg 1/1 to: US-08-325-071-67
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 650 amino acid
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
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APPLICATION NUMBER: US 0.
FILING DATE: 07-AUG-1992
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                 304 TGCATTCGAAGGACATGT.....
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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TELEFAX: 904136
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                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/111 BIAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEMP, David Harold
SRISKANTHA, Alagacone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1987
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14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: AU PI4912
16-OCT-1987
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                                                                                                                 Length: 359
Gaps: 22
Percent Identity: 21.727
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418	lLeuArgLysLeuGlnAlaCysGluHisProIleGlyGluTrpCysMetM .	401
1051	ACTTCGT	045
401	IleLysAlaArgLeuIleAlaGluLysProLeuSerLysTyrVa	387
1044	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA	995
386	alPheLysValGluIleLeuAsnCysThrGlnAsp	375
994	AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC	945
944 375	GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG (895 360
360	::: ::	351
894	TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC	845 5
844 350	GTGCTCTTGATAAATATTTGCTAAATATTTGGAA i ::::: ;::: ysLeuLeuAsnGluTyrTyrThrValSerPheThrProAsnIleSer :	810 334
334	pLysSerArgLysProGlyProAsnValAsnIleAsnGluC	320
800		772
772 320	TTTGTCGATGATGGT	758 304
303		290
757	CATGCGATTCTGAAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC	708
707 290	TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA : : : : : : : : : : : :	658 283
283	GluAspCysArgValGlnLysGlyThrValLeuCysGluCysProTrpAs	267
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616	AGGTATCTGAAATCACAACTGCTTTTCAAAACTCAAATTGTCCCGATG	570
569 250	329 CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG 56 	529 233
233		217
528	TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG	479
478 217	yProAspGlyGlnCysLysAsnAlaCysArgThrLysGluAlaGlyPheV	460 200
200	ProProAlaAspSerTyrCysSerProGlySerProLysGl	187
459	ACGATCTCTGAATCCACGTGGTATTTTTGTAAC	427
186		173
ν γ		777
376 173	TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGAGGT :::::	327 163
163	CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy	147

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seq_documentation_block:
; Sequence 22, Application US/08477451
; Patent No. 5928865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter P
NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
Ratio:
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; MOLECULE TYPE:
US-08-477-451-22
                                                                                                                                                                                                                 alignment_block:
US-09-323-427-1 x US-08-477-451-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/477,
APPLICATION UNMBER: U5/08/477,
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BAIDATA G.
REGISTRATION NUMBER: 03113
REFERENCE/DOCKET NUMBER: 0335.
TELECOMMUNICATION INFORMATION:
TELEPAN: 510-651-2708
TELEPAN: 510-655-3542
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                        Align seg 1/1 to: US-08-477-451-22
                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1129 TGATAATCAAGCTTTGCCAGTTGAT 1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052 .....GAACCG 1078
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                333 GTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 451
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LENGTH: 485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 yGlnAsnLysCysValLysValAsp 459
                                           383 GCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA..... 425
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CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
                                                                                       10 ValIleLeuValTyrProIleLeuPheLeuPheAlaLeuIleIleLys..
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STRANDEDNESS: sir
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linear
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0.393
40.426
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BER: 0335.002
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Gaps: 28
Percent Identity: 18.085
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326	09 rLysSerAspLysThrAlaAsnLysMetSerValSerGlnValArgLeuT	30
1025	90GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAA	99
309	93 SerīleLysAsnMetGlySerAlaLeuValGlyAsnGlyPheGlySerSe	29
989	81 AACCACAAG	98
292	76 etAspAsnIleLysAsnPheMetAlaGluValLeuLysAsnGlyPheAsp	27
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938	+1000Mo+	912
259		24
911	0	87
869 243	20 TAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	82 22
226	10 ProAsnLysGlnGluLeuThrGlnProLysIleLysGlyLeuIleMetGl	21
819	0 GG	77
209	4/ TCCATTCCTGCTTT	19
۱ (د	9 ULEUITEALAPNEHISG	
746	6	71
179	6 euValTrpTrp.GlnAsnIlePheValCysAspTrpT	16
715	2TGGTCAGCCAGTTTATCATAAATGGA	83
166	::: ::: 9 ulleLeulleLysIleCysTyrAsnGlulleLysThrLysArgIle	14
681	8	65
149	3 ysIleCysValSerAsnLeuPheLeuIleTrp.TrpTrpPheSerLys	13
657	10 CCCGATGCCAGTATGCCGTTATGAAATTTTTGGATGGTGGACCAACCGG	61
133		116
609	6 C	59
116	.06LysLeuAlaTyrLeuLysLysProIleTyrPh	10
595	TTT	54
105	92 ysProTyrLeuLysThrLysIlePheLeuSerAlaTyrThr	9
545	ь 1	49
92	spheLeuLysThrPheArgGluIleSerLeuPheProAs	7
495	1 ACAACTGTTGTCATTTCGTTTCATCCATTAT	46
75	9 LeullelleLeuMetThrGlnTrpGlnAsnTrpPheLeuPheValGlnLy	υj
460	7	44
58	<pre>2 erIleIleSerLysTyrTyrLeuLeuSerHisAlaLysPheThrMet</pre>	4
446	CGATCTCTGAATCCACGTG	42

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seq_documentation_block:
   Sequence 61, Application US/08325071
   Patent No. 5587311
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: COBON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1300
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                APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1600 CATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAAT 1649
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                                                                                                                                                                                                                                  APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: JOHNSON, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: WILLADSEN, Peter
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCAT 1599
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|lePheThrThrAspLeuAlaPheCysGlu......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpCysIleAsnTyrLeuLysValLysPhePheHisLeuSerArgArgAla 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...SerIleThrSerIleGlnTyrValAlaIlePheArgAsnAsnProIl 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....LeuProThrLeuLys.....A 391
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alignment_block:
us-09-323-427-1 x us-08-325-071-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-325-071-61 from: 1 to: 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: AU PH9196
FILING DATE: 27 NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/111 BIAU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5390
TELEPAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION UNMBER: US 07/926,368
APPLICATION UNMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                               377 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 426
                                                                                                                         327 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 376
                                                                                                                                                                                                                                     304 TGCATTCGAAGGACATGT.....TTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: AU P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
                                                                                             82 sGluLysAsnLeuLeuGlnArgAsp.
                                                                                                                                                                                        66 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 82
92 rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
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Gaps: 22
Percent Identity: 22.284
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	TGATAATCAAGCTTTGCCAGTTGAT 1153	1129
70	euLeuLysAsnGlnGluAlaAlaTyrLys	35
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53	tTyrProLysLeuLeuIleLysLysAsnSerAlaThrGluIleGluGl	ω
1078	TTACTCAAGAAAAGATCTGCA	1052
337	ysLeuGlnAlaCysGluHisProIleGlyGluTrpC	320
1051	ACTTCGT	1045
320	IleLysAlaArgLeuIleAlaGluLysProLeuSerAsnHisVa	306
1044	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA	995
305	alPheLysValGluIleLeuAsnCysThrGlnAsp	294
994	AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC	945
944 294	GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG :::::::::::::::::::::::::::	279
279	PheAspSerAspHisCysLysTrpTyrGl	7
894	:: ફ	845
269		253
. u	alASHITEASHG	010
809	AACGGTGATACTGTGGAA	ა - 7
239	heMetAspCy	223
772	TTTGTCGATGATGGT	758
757 222	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC	708 209
209	histeuvaibiyasp	
	ACCAGTTCAATTTGCTATTGGTCAGCCAGTTTATCATAAATGG	0 0
202	ysGlyThrValLeuCysGluCysProTrpA	186
657	CAAC	617
185	ysGlnThrCysAr	169
616	AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG	570
169	ProArgGl	152
569	CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	529
528 152	TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG :::	479 136
136	yProAspGlyGlnCysIleAsnAlaCysLysMetLysGluAlaGlyPheV	119
478	AACTGTTGTCATTTCG	463
119	ProProAlaAspSerTyrCysSerProGlySerProLysGl	106
462	ACGATCICIGAATCCACGTGGTATTTTTTGTAACAAC	427

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seq_name: /cgn2_6/ptodata/l/laa/5A_COMB.pep:US-08-325-071-63
seq_documentation_block:
    sequence 5, Application US/08325071
    Patent No. 5587311
    Patent No. 558731
    Patent No. 558731
    Patent No. 558731
    Patent No. 558731
    Patent No. 55873
    Patent No. 5587
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alignment_scores:

895 GGAT 360 uAsp	845 TAT ::: 351 Phe	810 GTG 334 YSL	773 320 pLy	758 TTT 304 Phe	708 CATGC 290 hrCys	658 TCAAC : 283 nGln.	617 CCAGT 267 GluAs	570 AGGTA :: 250 erHis	529 C 233 sPr	479 TTT 217 alc	463 200 yPr	427 ACG 187 Pro	377 CAAG 173 rgCy	327 TGA 163 SG1	304 TGC 147 Cys	Align seg 1	alignment_bl US-09-323-4	Percent Sim
ATCGATCACAGCTTTTCTA spargValLeuGl	CCAACAGATTTAATGGCT::: 	CTCTTGATAAATATTTGCT :::::: euLeuAsnGluTyrTyrTy	ACGGTGA sserArgLysProGlyPr	'GTCGATGATGGT 	GATTCTGAAACCGT ::: IleSerAspCysVa	CAGTTCAATTTGCT	GTATGCCGTTATGAA spCysArgValHisLys	TATCTGAAATCACAACTG ::: isThrValSerCysThrA	TTTTACATGGA -:: OArgGlyPheThrValal	CATCCATTATTTGTTACC ::: } ysGluHisGlyCys.Arg	A/ - - - 	ATCTCTGAATCCACGTGC ::::: ProAlaAspSer	TTGCCGGAATTTCAC :::::::: scysGlnGlyTrpAs	AAAGGTCTTTATGATCAAG ::::: ::: uLysAsnLeuLeuGlnAr	ATTCGAAGGACATGT ::: valProThrThrCysLeu	/1 to: US-08-325-	ock: 27-1 x US-08-325-0	Quality: 89.00 Ratio: 0.614 imilarity: 40.390
TCAATGCCAGAT::: ::: uAlaIleArgTh	GGCCAAGAAGCT	TAAAT ::: yrThrValSerF	TACTGTGGAAATTCT ::: oAsnVal	rMetAsnArgGlnSerCy	ATACTTTCTGCGCGG spLysLysCys	ATCATTGGTCAGCCAGTTTATC	ATTTTGGAI ::: GlyThrValLeuCys	CTTTTCAAACTCAAATTGTC 	AGCTGATAAAACAGTT aGluAspGlyIleThr	CAAAGTTGATCGTGCATAT ::::::::::::::::::::::::::::::::::	.AACTGTTGTCAT ::: eAsnAlaCysLysMetLysG	GGTATTTTTGTAACAAC ::: ::: TyrCysSerProGl	CCATTTGATTCATGC <i>t</i> :: hrAlaas	AAAGGTTGCCGTAATGAT gasp	ArgProAspLeuThrCy	071-63)71-63	Length Gaps Percent Identity
CAGTATTACCATTAAAG 944 rSerlleGlyLysGluV 375	ATACAAATATGC 894 + /sLysTrpTyrGl 360	AATTTGGAA 844 :::::: ProAsnIleSer 350	PARATGCTGATGGAT 809		GTCCATTCCTGC 757 ::: HisGluGlu 303	ATCATAAATGGA 707	NGGTGGACCAACCGG 657 :: GluCysProTrpAs 283	GTCCCGATG 616 CysargProThr 266	AGTGCACAGATTG 569 ::: : CysLysSerIles 250	TCGAGTACAATG 528 ::: rGluCysThrCy 233	TTCG 478 		AATGTTGCGCGTAC 426 :: snCysSerAlaAla 186	GAAGGTGGACGT 376 ::: serA 173	TTATG 326 SLysAspLeuCy 163	to: 650		359 359 31 22 71 22.284

	TGATAATCAAGCTTTGCCAGTTGAT 1153 ::: ::::::: yGlnAsnLysCysValLysValAsp 459	1129 451
451		435
1128	1079 GAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGA 1128	1079
434	418 etTyrProLysLeuIleLysLysAsnSerAlaThrGluIleGluGlu 434	418
1078	1052GAACCG 1078	1052
418	401 lLeuArgLysLeuGlnAlaCysGluHisProIleGlyGluTrpCysMetM 418	401
1051		1045
401	IleLysAlaArgLeuIleAlaGluLysProLeuSerAsnHisVa	387
1044	995 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 1044	995
386	375 alPheLysValGluIleLeuAsnCysThrGlnAsp	375
994	GCGAATGTGTTCGACCA	945

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pir2:S72284
pir2:F71606
pir2:B26696
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pir2:S27799
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Database length: 47169319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pir1:RNZQBF
pir2:S78177
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-Q-/cgn2_1/USPMO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.1
-DB-PIR_62 -QFMT=fastan -SUFFIX-backtrans.rpr -GAPOP=12.000
-GAPEXT=4.000 -MINAATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALION=200 -THR_SCORE=pct
-MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2:A36054
2:S05356
2:S17855
1:VGBE11
2:E71615
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2:C71607
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2:S55098
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2:F71613
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2:C70126
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2:H71616
       2:H71606
2:B42239
2:S20811
2:S32793
2:I51703
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:: S23344
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Compugen Ltd.
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EScore Len
2.2e-119 42
7.1e-75 96
0.0164 17
0.0164 7
0.0904 7
0.0908 8
0.1293 1
0.01293 1
0.01293 1
0.01394 8
0.2325
8 0.2508
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1.46 1.29
2.975 1.36
2.9885
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3.61 0.8984
3.61 0.8984
3.62 0.9685
1.63 0.8984
3.64 1.25
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3.65 0.862
2.975 1.36
3.66 1.29
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5 | hypothetical protein PFB0470w

6 | probable membrane protein YMR21

2 | hypothetical protein PFB0315w

9 | hypothetical protein PFB0370w

1 | hypothetical protein PFB0870w

9 | twitchin - Caenorhabditis eleg

18 | mucin, submaxillary - pig
                                                                                                                                                            Itranslation initiation factor I mucin homolog - boyine
hypothetical protein (clone plk peptidylglycine monoxygenase (glycoprotein H precursor - saim probable amine transporter PEH S-layer protein precursor - BH S-layer protein precursor - BH S-layer protein protein PEH S-layer protein protein PEH S-layer protein protein PEH S-layer protein protein (mu spransporter peh S-layer protein protein (mu spransporter peh S-layer protein protein PEH S-layer protein PI S-layer protein Totein T-9 - Salm orderin protein T-9 - Salm orderin protein S-BH S-S-W bypothetical protein T-9 - Salm orderin PEH S-W bypothetical protein T-9 - Salm orderin PEH S-W bypothetical protein T-9 - Salm orderin PEH S-W bypothetical PEH S-W bypothet
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) hypothetical protein PFB0800c
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seq_documentation_block:
cuticle protein cut-1 - Caenorhabditis
C:Species: Caenorhabditis elegans
C:Date: 07-Apr-1994 #sequence_revision
C:Accession: A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Sebastiano, M.; Lassandro, F.; Bazzicalupo, P. Dev. Biol. 146, 519-530, 1991
A;Title: cut-1 a Caenorhabditis elegans gene coding A;Reference number: A49772; MUID:91323673
A;Accession: A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-423 <SEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block: US-09-323-427-1 \times A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:M55997
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snPheAsnThrargAsnProPheGluGlyHisValTyrValLysGlyLeu
                                                          ATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTTCATCCA 487
                                                                                                                                                                                                                                                                                                                                      AATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGA
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             TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA 687
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LeuAspGlyGlyProSerGlyGlnProIleGlnPheAlaThrIleGlyGl
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! biglycan precursor - human
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R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P. submitted to the EMBL Data Library, July 1991 A;Description: CUT-1 a Caenorhabditis elegans ge A;Reference number: S27799 A;Accession: S27799 A;Molecule type: DNA
                                                                                                             seq_documentation_block:
cuticlin 1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
C;Accession: S27799
                                                                                                                                                                                                                          seq_name: pir2:S27799
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A;Cross·references: EMBL:M55997; NID:g156271; PID:g156272 C;Genetics: A;Gene: CUT-1 A;Introns: 245/3
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122 876 105

726 55 39

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72

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C;Accession: S72284

R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyt J. Mol. Biol. 261, 155-172, 1996

A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa A;Reference number: S72277; MUID:96346169

A;Accession: S72284
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DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid
N;Alternate names: RNA polymerase rpoc2
C;Species: plastid Plasmodium falciparum
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Genome: plastid A;Note: this apparently degenerate plastid is referred to as the apicoplast C;Keywords: nucleotidyltransferase; plastid; transcription
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A;Note: biosynthesis of this protein involves a -1 frameshift in the codon for residue
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
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US-09-323-427-1 x S72284
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Ratio:
Percent Similarity:
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530 TTTTACATGGAAGCTG......ATAAAACAGTTAGTGCACAGAT 567
                                                                                                                                 483 ATCCATTATTTG...TTACCAAAGTTGATCGTGCATATCGAGTACAATGC 529
                                                                                                                                                                                                                                                               445 TGGTATTTTTGTAACAACAACTGTTGTCATTTCGT......TTC 482
                                                                                                                                                                                                                                                                                                                                                                                                       395 CTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACG 444
                                                              58 IleTyrLeuLeuIleLeuTyrLysAsnLysIleAsnAsnIleTyrAsnAs
                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                     28 .PheLysIleLeuHisGluLeuLeuTyr.....LeuGlyTyrGluT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LysLysLeuLeuIleIlePheLysTyrAsnIleSer......
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Gaps: 34
Percent Identity: 21.078
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seq_documentation_block:
probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: F71606
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.: Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743
A;Accession: F71606
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:F71606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leIleLeuAsnAsnAsnAsnLysTyrAsnVallleTyrPheLeuIle 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACTGTAATA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..........IleLysTyr.TyrAsnTyrSerAsnIleGlnLeuLeuIleL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sCysAsnPheIleTyrAsnSerIleSerLysAsnPheLysTyrAsnLeuA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euIlePheLeuMetAsnLysIleLeuTyrAsnTyrAsnAsnIleLeuPhe 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGCAACATAATGGACAACCTGTAATAC.....TTGCTG 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ePheLysLeuIleIleAsnPheLysLysTyrIleAsnIleLysPheAsnL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ......IleIleIleLysLysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rTyrLeuTyrTyrTyrHisIleLysPheTyrAsnLeuTyrAsnLysGlyI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573
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A;Cross-references: GB:AE001417; GB:AE001362; NID:g3845271; PID:g3845273; TIGR:PFB077
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0770c
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alignment_block:
US-09-323-427-1 x F71606
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Ratio: 0.492
Percent Similarity: 46.654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: F71606
                                                                                                                                                                                                               631
                                                                                                                                                                                                                                                                                                                      615 snAsnLeuPheGlyAla.SerAsnLysLeuThrSerHisHisGluAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        536 CysAsnAsnHisThrSer...AspAsnAsnThrCysAsn......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 sThrCysAsnAsnHisThr.....CysAsnAsnHisThrCysAsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 CACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 AsnThrCysAsnAsnHisThr......CysAsnAsnHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 TCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA 425
                                                                                                                                                                                                                                                                                                                                                                                                                       sAspGly.....LeuTyrLeuAsnThrLysSerTyrAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            snLysLysGluThrHisAsnAsnPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTTGGAATATCCAA
                                                    CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT 1048
                                                                                                                                                                                                                                                                                                                                                                       CAGATTTAATG...GCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGAT.....
LeuAsnGluTyrPhe...
                                                                                                                                                           AAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG 998
                                                                                                                                                                                                               eLysLysIleIleGluLeuAsnThrThrLysLeuValGluGluArgAsnA
                                                                                                                                                                                                                                                                    CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....SerHisAsnAspThrGlnGluAsnAsnIleMetLysAsnLy 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGATGATGGTAACGGTGATACTGTGGAA.....ATTCTAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....TCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....AsnAsnHisThrLeuGlyAsnPro 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGC 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....AsnHisThrCys...AspAsnAsnThrCys......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGC 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....AsnHisThrCysAsnAsnHisThr 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACA
                                                                                                         .SerLeuLeuAspIleAsnGluTyrAsnAsnAsnSerAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
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Gaps: 31
Percent Identity: 21.654
..AspAsnLeuIleGluAsnAsnIleLe
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hypothetical protein 1 (CYb-COII intergenic region) - Leishmania tarentolae mitochondriC; Species: mitochondrion Leishmania tarentolae
                                                          seq_documentation_block:
                                                                                                                     seq_name: pir2:B26696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1649 TATCACAAATTATACCTTGTATTGCCCCAATTTTTATGGGCATCATTTCCT 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1520 TTATTCAGTAATCTTTTATATGCATACTATTGTAAA.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1453 ATACAATAAGTGATAT.....TTTCATCAAAAC.......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049 CGTTTACTCAAGAAAGATCTGCAGAACCGGAGAATA.......
                                                                                                                                                                                                                                                    1699 ATTCTGTAAACAATTCA 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1292 ACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGCATAAAAATAATGTTA 1341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      843 ysTyrAlaProTyrPhePheLeuThrPheAlaValIleProSerPheLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761 rAspTyrLysMetTyrPhe...LysLeuPheGluHisLysAsnIleIleP 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693 leMetAsnLysLeuMetTyrThrAsnValSerAsnAsnGluArgTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATATAGTATGTAGG......AAATAATTACTGTA 1452
                                                                                                                                                                                   yrAsnAsnAsnAsnAsn 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerPheIle.,PheLeuSerSerPhePheGluValValLeuSerThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAA 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleIleArgAsn...IleTyrPhePheLeuCysAlaLeuSerGlyArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lTyrAsnGluValPheGluIlePheLeuArgAsnIleLysGlnProAspL 843
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                                                                                                                                                                                                                                                                                                            .....LysAsnIleSerLysLeuProAsnPhePhe.AsnIleLysGluT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....TGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCA 1598
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alignment_scores:
Quality:
Ratio:
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C;Superfamily: hypothetical protein 1 (CYb-COII intergenic region)
C;Keywords: mitochondrion
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A;Title: Comparison of the maxicircle (mitochondrial) genomes of Leishmania tarentola A;Reference number: A92643; MUID:87194837
A;Accession: B26696
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US-09-323-427-1 x B26696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-443 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: B26696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT
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AACCGTTGATACTTCTGCGCGGTTGTCCATTCCTGCTTTGTC.....
                                        \verb|nLeuIleAsnPheIleLeuLeuPheValLeuLeuTyrTyrMetIleLeu|.
                                                                                        TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA 720
                                                                                                                                                                                                                                                                                                                                                                   CAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGT 573
                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eIleIleLeuCysAspTyrThrSerLeuPheTyrLeuSerPheAspLeuI
                                                                                                                                 TyrLysIleLeuIleLeuTrpTyr.....TyrTyrMetIleAs
                                                                                                                                                                                TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA 670
                                                                                                                                                                                                                                                                         ATCTGAAATCACAACTGCTTTTCAAACTCAAATTG...TCCCGATGCCAG
                                                                                                                                                                                                                                                                                                                    eIleSerIleLeuPheGluLeuPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                 PheMetPheLeuHis......ValIleHisIleLeuPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heAspThrArgPheValPheMetIleIleIleMetGlnTyrIleIleIle 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuPheLeuTyrLeuIleHisIleIleLeuPheLeuLeuLeuTyrSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leTrpLeuIleIleIleAsnIleIleIleLeuThrIleLeuAspSerTyr
                                                                                                                                                                                                                           ....SerLeuLeuLeuPheLeuIleLeuIleSerSerArgPheGly 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....LeuPheLeuPheCysPhePhePheLeuPheCysPheLeuAsnP
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44.485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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763
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618	GTTTGTTATTATCATCATATCAACTTGTCCTAT 1	1585
56		340
584	TATTGTAAATGTTTCATCATTAGGCCATGAATAGTTTC 1	1547
546 39	ATAGCTTCTGAAAAGCTTATTCATTATTCAGTAATCTTTTATATGCATAC 1 ::: ::: :::	1497 329
1496 328 ,	ACTGTAATACAATAAGTGATATTTTCATCAAAACTTCTTCTATCGCTTTT ::: sTyrasnGluasnTyrPheLeuIleAsnPheIlePhe	1447 . 316
316	eullelleLeuTyrTyrPhePheIleValTyrAsnMetPheAspIle.Ly	300
300	AsnPheHisLeuIleTyrSerLeuSerLeuIleIleI	288
1396	GAAGCAATAATAAAACTGCCATATATATTCGTTTCTTCTTATCATCC	1350
287		274
273	alAsnAsnPheSer	1300
1299	TTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTC	1250
65	uIleGlyLeuAsnSerPheAlaIleValSerLeuLeuPheValLeuSerV 2	248
1249	TTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTTGGCTTCTCAATG	1200
48	::: :::::::: yrileilepheileLysLeuile.IleileGlnSerIleThrCysValLe	232
1199	CCGTGCACTTCTGCAACATAATGGACAACCTGTAATAC	1162
32	::: :: :::	219
1161	ACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCA	1112
18	:::	210
1111	AAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAAC	1062
209	: :	206
1061	TGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGA	1012
205	 1Phe	204
1011	GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGG	962
204	::: 	203
961	TCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGT	912
02	TyrIleArgLeu	199
11	GGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGATC	862
198	uPheLysLeuTyrIleAlaIleLeuIleLeuPheLeuGluGlnLeu	183
		2
811	GATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	764 167
167		153

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A;Cross-references: EMBL:x95275; NID:g1171583; PIDN:CAA64572.1; PID:e220243; PID:g117 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996 R;Gardner, M.J.; Williamson, D.H.; Wilson, R.J.M. submitted to the EMBL Data Library, March 1990 A;Reference number: S10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-323-427-1 x RNZQBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: this apparently degenerate plastid is referred to as C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase; plastid; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite A;Reference number: S72277; MUID:96346169
A;Accession: S72282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Plasmodium falciparum plastid C;Species: plastid Plasmodium falciparum C;Date: 31-Dec-1990 #sequence_revision 15-May-1998 #text_change 11-Jun-1999 C;Accession: S72282; S10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X52177; NID:g9879; PIDN:CAA36427.1; PID:g9880 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 328-1024 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1024 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1643 TGATAATATCACAAATTATACCTTGTATTGCCCAATTTTTATGGGCATCA 1692
                                                         119
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                                                                                                                   237
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                                                                                                                                                                                                                                                                                                                                                    197 ACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 AATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 yPhePheLeuLysValPheCysLeuLeuLeuHisLeuSerTyrLeuGlyI 373
                                                                                                                                                                                                                                                                                                                                                                                                              70 AsnIleAsnAsnLeuLeuLysIleIleLeuThrLeuLysLeuAsnPheIl
                                                                                                                                                                          roPheIleTyrAsnAsnIleIleIleLeuAsnGlyLeuTyrLysThrCys 118
                                                                                                                                                                                                                                                                                          eAsn...IleAsnLysIleIleLysPheAsnIleLeuIlePheIleLeuP 102
                                                      IleGlnLeuPheLysLysAsnAsnLysIlePheIleIleLysPheLysAs 135
                                                                                                                .....GTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .PheIlePheSerTyrGlnPhe
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Ratio:
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0.373
45.113
. ATTTTAATACACGTAATGCATTCGAAGGACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 665
Gaps: 28
Percent Identity: 17.594
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321
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A.; W

1052		1052
390	sGlyLeuValAsnTyrLeuT	374
1052	AGCTGCGCAACTTCGT	1035
7	:::::::::::::::::::::::::::::::	357
0	CAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAGCAAAAACCTGCT	985
984 357	eLvsIleAsnMetIleThrThrGlvLeuAsnSerTvsPheTleLeuAsnSe	975 340
340	lAsnAsnLeuSerGluIleAsn	324
974	ACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACA	933
N	uGluAsnIleAsnIleAsnProLe	310
932	CAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT	œ
882	AATAATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGT AATTATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGT .::::	833 295
295	PheLysTyrGlnLeuLeuAsnIl	281
832	TTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCT	783
280	leLysSerLys	277
782	TCTGCGCG	733
732 277	AAATGGACATGCGATTCTGAAACCGTTGATAC	701 260
260	eSerIleLysLeuAsnPheSerTyrTyrSerAspPheTyr	244
700	GCTATCATTGGTCAGCCAGTTTATC	672
4.	nIleTyrIleAsnLeuL	ω
671	GATGGTGGACCAACCGGTCAACCAGTTC	622
621 236	GTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGT : :::	572 219
219	nTyrIleLysPheIleTyrSerLysTyrAsnAsnIle	205
571	GCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC	522
204	euPheIleTyrAsnAsnIleIleAsnLysLysIleLeuIle	191
521	TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGT	472
191	rLeuAsnAsnIleTyrIleAsnLysAsnIleSerL	179
471	ACACGATCTCTGAATCCACGTGGTATTTTTG	422
179	::::::: ysPheAsnPheL	163
421	CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT	372
162	THATS THANKS TO THAT I AND ANGETT GCC GTAN TAN THAT GARAGE TO THAT I SHOW THAT	152
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152	:::::: ::::::: ::::::: ::::::	135

	seq_name: pir2:S78177
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	ATTCACTT
646	630 euTyrThrSerLeuHisLeuAsnIleTyrGluIleSerLeuAsnIleIle
1709	1666 TGTATTGCCCCAATTTTATGGGCATCATTTCCTATTCTGTAAAC
630	AlaIl
1665	TTGTGATAATATCACAAATTATACCT
613	ySer1
1634	1602 TTATCAACTTGTCCTATTTTATTCTAACAGTTT
596	580 alasnIleGlyGlnIleLeuAlaIleAsnSerAsnLeuLeuAsnSerGlu
1601	AAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCAT
580	nIleLeuLeuIleTyrLysProIleValTrpValGly
1551	1551
563	547 LeuPheAsnArgGlnIleIleTyrTyrLeuAsnAsnTyrLysLysIleAs
1550	1512 CTTATTCATTATTCAGTAATCTTTTATATGCATACTATT
546	531 luGlyIleVallleTyrValSerCysIleLysIleIleIleArgAsp
1511	ATATTTTCATCAAAACTTCTTCTATCGCTTTTATAGCTTCTC
531	leI
1461	A
514	506 AsnLeuSerAsnIleIleThrAsnTy
1426	TTTCTTCTTATCATCCTTCTAATAACTAATTT
505	489 snLeuMetSerIleLysMetHisThrGlnIleValProIleIleTyrPro
1376	AAGCAATAATAA
489	473 eIleGluAsnLeuIleProPheIleHisTyrAsnAspSerIleArgA
1326	TTTAAATTTCGTCCAAATCAGAAGG
473	467 PheAsnTyrLeuLeuSerPh
1276	ATTG
466	457 snileThrGlnAsnileIleTyrIlePro
1226	1177 ACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCA
457	440 eAsnLysThrThrIleLeuThrIleAsnLysAsnThrPheLysIleCysA
1176	TTCTGC
440	424 PheTyrAsnIleSerPheAsnAsnIleTyrLeuLysLysAsnIleAsnPh
1141	TCAACACCCTTGAAATTAGCGATG
423	:::
1091	
407	390 nIlePheLeuAsnLeuLysTyrLeuPheValIleTyrTyrLysHisIleP

seq_documentation_block:

632 GAAATTTTGGATGGTGAACCAACCGGTCAACCAGTTCAAT	TGCACAGATTGAGGTATCTGAAACTGCACTGCTTTTCAAACTCAAATTG :: ::: :::: hrLysAsnLeuGluTyrIleAsnIleGlnThrIleThrLysIleLysGln TCCCGATGCCAG	CAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTGAT :::::::::::::::::::::::::::::::	AATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTC :::::::::::::::::::::::::::::::::::	alignment_block: US-09-323-427-1 x S78177 Align seg 1/1 to: S78177 from: 1 to: 717 align seg 1/1 to: S78177 from: 1 to: 717 309 TCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGT 358 31: ::::::::::::::::::::::::::::	C:Keywords: mitochondrion alignment_scores: Quality: 108.00 Length: 563 Ratio: 0.414 Gaps: 28 Percent Similarity: 46.359 Percent Identity: 19.538	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-717 < LAN> A;Residues: 1-717 < LAN> A;Cross-references: EMBL:AF007261; NID:g2258325; PID:g2258376 A;Experimental source: ATCC 50394 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997 C;Genetics: A;Genome: mitochondrion	hypothetical protein 717 - Reclinomonas americana (ATCC 50394) mitochondrion C;Species: mitochondrion Reclinomonas americana A;Variety: ATCC 50394 C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 17-Mar-1999 C;Accession: S78177 R;Lang, B.F; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank Nature 387, 493-497, 1997 A;Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniature. A;Accession: S78177 A;Accession: S78177 MUID:97311393
PIleThrAsnLysPheSerLeuTyrIleThrAsnGlnThrLysGlnLysAACAAATATAGTAGTAGGAAATAATTACTGTAATACAATAAGT :::! :::! snIleValAsnIleArgAsnGlnSerGlnLysLysSerAspAsnThrAsn GATATTTTCATCAAAACTTCTTCTTATAGGTTTTATAGGTTCTGAAAAGCT ::::: spepheTyrGlnLeuLeuLysAsnThrGlnLysLleatySGluTy TATTCATTATTCAGTAATCTTTTATATGCATACTATTG :::: TATTCATTATTCAGTAATCTTTTATATGCATACTATTG ::::	1355	1278 CTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCA 1315 :::	1178 CATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCAT 1227 :::	1084 TATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATA 1133	1011 GTGGTGCCGCAGCAAAACCTGCTGCAG	911 TTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATG 960 :::::	269

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seq_documentation_block:
undulin 1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
C;Accession: A40970
R;Just, M:; Herbst, H:; Hummel, M:; Duerkop, H:; Tripier, D:; Stein, H:; Schuppan, D.
J. Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular management in the second second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-323-427-1 x A40970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1699 ATTCTGTA......ACAATTCACTTATTTGCATTATTGCAATTAAA 1739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 TyrLeuLys..... 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 laArgAspIleGlnLysMetProHisGluPhePheIleTyrPheLeuHis 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 GluIlePhe.....LysLysLysIleTyrLysLys 605
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270 AsnSer...MetArgValLysTrpAspAlaValProGlyAlaSerGlyTy 285
                                                                                                                                                                                                                                                                                                       108 GAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATCGAATTTACTAAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 LeuThrGluTyrGlnIleAlaValPheAlaIleTyrAlaHisThrAlaSe
                                                                                                         158 TCTTCTGAAATGATGGTTCTTATTGCTTTCTGTACTACACTTATTGC 207
                                                                                                                                                                                                                                                                                                                                                                                                                      244 rGluGlyLeuArgGlyThrGluThrThrLeuAlaLeuProMetAlaSerA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 CAACAAACAACAACAACAACAACAACAATAATAACCCCATCAAGTGGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TTACCCAAGTTTGAGGTGTCTATAACACCGACTGCAGCAACAACAACAAA
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0.527
51.768
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Gaps: 21
Percent Identity: 21.212
                                                                                                                                                                                                             .LeuLeuLeuTyrAspValThrGlu 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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1012 т	962 G 1 546 1	912 T : 531 T	871 A : 514 r	842 . 498 P	795 T 483 a	773 . 466 u	725 G : 450 T	675 C : 433 h	631 T 417 e	590 G 401 P	540 A : 384 s	490 A 371 .	440 CC 364 Al	390 T : 348 e	340 T 331 e	293 . 319 P	255 A 302 L	208 A 285 r
AACTTCGTTTACTCA 1	GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGG 1 ::: :::::::::	TCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGT 9 ::: :::::::: ThrGluProAlaThrThrIleValProThrThrSerValThrSerVa	AGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTT 9 :! ::::: ::: rGluSerGluVal.ValThrAlaValGlyThrThrLeuAspSerPheTrp 5	GAATATCCAACAGATTTAATGGCT	TAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG 8 ::::::::::::::::::::::::::::::::::	AACGGTGATACTGTGGAAATTC 7 :::	GTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGT7 ::: ::: ::: ThrAspSerPheArgValThrTrpHisProLeuSerAlaAspGluGlyLe 4	CTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACC 7 :: :::	TGAAATTTTGGATGGACGACCAGCTCAACCAGTTCAATTTG 6 :::: ::: ::: :::	GCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTA 6 :::::: ::: PheProLeuLysGlyLeuThrProLeuThrGluTyrThrIleAlaIlePh 4	ACT 5	TATCGAGTACAATGCTTTTACATGG 5 ::: : TyrargileValTyrAsna 3	ACGTGGTATTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATT 4 	TTTCACTTCCATTTCATTCATGCAATGTTGGGGGTACACGATCTCTGAAT 4 ::: ::::::::::::::::::::::::::::::	TGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAA 3 : :: ::: ::: ::: ::: ::: ::: ::: ::	AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTA 3	AAATTGAATGTGGACCAACTTCAATAACAATCAATTTT	CCAG LysG
058	1011 555	961 546)11 530	870 514	841 497	.83	772 466	724 449	674 433	630 417	00	39	89	39	148	339 331	292 318	25 4 302

104 GATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTT 453	
399 leArgThrAspGluLysLysLysGluLeuPhe 409	
54 GCCGTAATGA	
319 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTT 353 :::: ::: ::: 382 nIlebeuAsnLysTyrIleLysAsnGluHisIleValThrLysHisVall 399	
69 CCAACTTCAA :: 66 snAsnAsnAs	
366À 366	366
C	219
365 365	365
69 G	
119 GAAGCAATCTTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAAT 168 ::::: ::: 356 snLysAsnIleTyrGlyAsnAsnAsnAsn	
75 CAACAACAGCAATAATAACCCCATCAAGTGGAGGAAGAAGACAG 118 :::::: ::: : 339 nAsnGluThrAsnAspValLysAsnAsnIleTyrGlyArgLysLysA 356	
25 GTCTATAACACCGACTGCAGCAACAACAACAACAACAACAACAACAA 74 ::: ::: ::: ::: ::: 323 IleTyrLysMetAsnArgGlyAsnAsnAsnIleGlnHisAspAspIleAs 339	ω σ
n seg 1/1 to: C71607 from: 1 to: 1351	Align se
gnment_block: -09-323-427-1 x C71607	alignment US-09-32
ment_scores: Quality: 107.00 Ratio: 0.354 ent Similarity: 43.832 Gent Identity: 19.303	alignment Percent
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tus: preliminary; nucleic acid sequence not shown; translation not shown ecule type: DNA	A; Status:
le: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. le: Chromosome 7 sequence of the human malaria parasite Plasmodium falciparum. erence number: A71600; MUID:99021743	A; Title: A; Referen A: Accessi
dner, M; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; dner, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Caro, S. 1720 1008	R;Gardner
ocumentation_block: hetical protein PFB0745w - malaria parasite (Plasmodium falciparum) cles: Plasmodium falciparum e: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999	seq_docum hypotheti C;Species C;Date: 1
ame: pir2:C71607	seq_name:
059 AGAAAAGATCTGCAGAAACCGGAGAATATCATTGATG 1094 ::: ::: ::: : :	ν σ
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124 676	AAATGGAATCT	1213	
960	TyrGlnLysG	654	
121		1163	
116 654	CCCTTGAAATTAGCGATGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 1 ::: ::: :::	1113 641	
640	spAsnCysThrAsp6	636	
111	CCGGAGAATATCATTGATGTACGAACTGATATCAACA	1063	
106	GCTGCGCAACTTCGTTTACTCAAGAA J ::: ::: uTyrAsnAsnPheLeuPheValTyrValProAspLeuLeuTyrSerGlnA (1037	
619	alHisAsnTyrLeuAsnLysIleAspProLeuLe	603	
103		987	
986	CATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCAC ::: ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	937 586	
586	AAATATGCGGATCGATCACAGCTTTTGTATCAATGCCAGATCAGTATTAC :	573	
5		000	
88e 571	ATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC {	837 566	
566	GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATA (:::	787 553	
55		537	
786		758	
757 536	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGC 7	708 520	
707 520	CCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA ; ;;;;;	503	5₩
503	:::: :::::::::::::::::::::::::::	487	
66		621	
620 486	GGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG (571	o.<
47:	GTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGA: : :: :: :: :: : sAsnAsnIleProMetGluArgIleLysLysGluThrHis 4	521 458	
520	ATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGA (483	
44		425	
48	:: T	454	
42	PheCysThrPheValAsnMetThrThrLeu.LeuTyrGluIleIleL	410	

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hypothetical protein PFB0470w - malaria parasite (Plasmodium falciparum)
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C; Accession: G71613
R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A; Reference number: A71600; MUID:99021743
                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:G71613
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879 luLysGluLys 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleArgIleSerGluTyrValLeuSerLysTyrPhePheArgAsnGlyLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCATCA 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eGluLysAsnLeuSerHisLeuLeuAsnIleTyrTyrGlnHisLysIleV 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGAAAAGCTTATTCATTATTCAGTAATCTTTTATATGCATACTATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....GATATTTTCATCAAAACTTCTTCTATCGCTTTTATAGC 1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleGluThrCysAsnLeuAsnIleTyrAsnAsn......ValAspPr 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alAsnLysAsnAsn......AsnIleCysSerLysIleLysAsn 711
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A;Accession: G71613
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Stolecule type: DNA
A;Residues: 1-1346 <GGAR>
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A;Experimental source: clone 3D7
C;GenetLvs:
A;Genet.pFB0470w
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US-09-323-427-1 x G71613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCG...TCTTATTGCTTTCTGTAC.....TACACTTATTGCATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 etThrSerProLeuTyrTyrTyrTyrTyrTyrTyrTyrAspAsnAspPro
                                           yrLeuTyrLeuGluIleLeuHisArgMetLysIleTyrAsnHisAspIle
                                                                                          {\tt ATCTGARATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG...}
                                                                                                                                             sPhePheIleLeuLysGluAsnTyrTyrTyrLeuSerIleAspAsnLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                              n..........IleSerAspLysIleLeuLysIleIle........G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAGGTGGACGTCAAGTTGCCG...GAATTTCACTTCCATTTGATTCA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGACATGTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euTyrThrSerPheSer.SerLeuSerTyr.Val...ValLysTyrAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ATTTACTAAATCTTCTGAAATGATGAT 174
...TATGCCGTTATGAAATTT.......TGGATGGTGGA
                                                                                                                                                                                         ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG.....T
                                                                                                                                                                                                                                            IleSerLeuSerLeuCysAspIleLysTyrLeuAsnLeuTyrAlaLeuCy
                                                                                                                                                                                                                                                                                                                                              {\tt luGlnAsnLeuAsnHisGluAsnMetLysTyrIleIleHisAsnLeuMet}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luGlnMetPheLeu...LysLysPheLysAspSerLysGlnSer.....
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0.319
46.036
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48
21.280
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ValHisAlaLeuGluSe 8	51
GTCAACCAGTTCAATTTGCTATCATT	82 68
GCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGAT 7	30
OValAspMetLysGluMetCysAsp 8	79
CTTTCTGCGCGCGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGA 7	80
SerAsnAsnLysIleGluLysGluAsnGlyAsnAspAs	96
TAAATATTTG. 8	29
LeuMetLeuGlyLysCysThrHisGluLysAsnLeuT 9	9
CTAAATAATTTGGAA	n 44
luIleLysGlnAsnLeuIleAsnLeuGlu 9	25
.TATCCAACAGATTTAATGGCTGGC	76
lleetiinysetuneuneusetasiiasilaspasiiaspuysmetetunii	7
GIRVIACAARVATGUGGATCGATCACAGCTTTTCTATC 9 ::: :: .AspAsnAsnCysAsnIleIleGlyHisAspLysPhePheSerAsn 9	58
ATGCCAGATCAGTATTACCATTAAAGAACCA	949
snAspGluAsnLysIleLysLysGluLysTyrPheAsnLeuLysAsnGl	175
ATA	54
etValPheLysLysIleGluLysThrGluThrLeuProCysThrL 9	
GTGTTCGACCACAATGTTCAGAAACACAAG :::: ::: IldTyrAspTyrIleAsnPheLeuLeuIleLeuIlePheTyrGln 1	890
GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCT 1	039
nAsnLysIleLysGluCysAspGluLysIleAsnLeu 1	022
GCAACTTCGTTTACTCAAGAAAAGATCTGCAGA	074
LeuPheSerLysAspGluAsnValIleIleThrIleGlnA 1	038
CGGAGAATATCATTGATGTACGAACTGATATCAACACCC 1	115
GAAATTAGCGATGATAATCAAGCTTTGCCAGTT 1	150
TyrValLysAsnLysGlnTyrMetLeuAspLysTyrSerGluMe 1	067
ATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACT 1	200
LeuLysGluAsnLeu 1	072
GTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGT 1	250
PheAsnIleGluSerSerLeuIleGlnLeuPheSer 1	084
TATGGGTTTAAGCATTGCATTGATTGCTGCC 1	282
lePheValAsnLeuLeuGluLysGlyGluAspAspLysGluLeuPheVa 1	0
TCCAAATCAGAAGGCATAAAA 1	332
	YSGGTCAACCAGTTCAATTTGCTATCATT LYSLYMETLYSIIEPHELEULEUSETTYTASNIIEPHEGINLYSM TCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGAT """"""""""""""""""""""""""""""""

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alignment_block:
US-09-323-427-1 x S55098
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    Quality:
    Ratio:
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736 CTGCGCGGTTGTC..........
                                                                                                                                                                                                                                                                                           566 ATTGAGGTATCTGAAATC.....AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 CCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAA 142
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                                CAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTT 735
                                                                                                                                              TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT 685
                                                                                                                                                                                                                      AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 635
                                                                                                                                                                                                                                                        IleLysIleAlaAspLeuGlyAsnAlaCysTrpTyrAspGluHisTyrTh
                                                                                                                                                                                                                                                                                                                                  erAsnSerAsnValSerThrAspIleAsnSerProGluAsnLeuIleGln
                                                                                                                                                                                                                                                                                                                                                                                                     TGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...GlyProTyrIleSerAsnThr...........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euSerThrPheAspIleSerAsnIleSerGlnSerSerAspThrAsn...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTT 392
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                                                                                                                                                                                 rAsnSerIleGlnThrArgGluTyrArgSerPro......GluV
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0.816
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13
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hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 13:Nov-1998 #sequence_revision 13:Nov-1998 #text_change 07:May-1999
C;Accession: C71618
R;Gardner, M.J.; Tettlelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin,
R;Gardner, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
Cience 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: C71618
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1712 <GAR>
A; Cross-references: GB: AEO01386; GB: AEO01362; NID: g3845148; PID: g3845151;
A; Experimental source: clone 3D7
C; Genetics:
A; Gene: PFB0315w
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US-09-323-427-1 x C71618
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1116 rValTyrGluTyrValIleGluLysTyrLysArgValHisValLeuTyrL
                                                                                                                                                                                                                                                                                                                                                                                1150 LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1133 euGlyArgLeuLeuGlnIleValGluLysLeuPheLysLysTyrTleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1102 MetLysLysLysLysThrGlnGluTyrValAspIleGlu.....Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 ATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGA 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                637 yLysTyr 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    591 aCysLeuIlePheGluLeuIleThrGlyAspPheLeuPheGluProAspG
                                                               TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT
                                                                                                                              ysLeuGluPheLeuIleLysLysLysMetGlnHisTyr.....
                                                                                                                                                                                         AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA
                                                                                                                                                                                                                                                        tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 1183
                                                                                                                                                                                                                                                                                                ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TC...CACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATC 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104.50
0.477
44.422
......PheAsnHisIleIleIleAsnSerTyrGl 1205
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Percent Identity:
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` E.

	4.8	<pre>::: ::: ::: </pre> ::: /// :::	4
	1307	TGCTGCCGTCATTATTACCATTTCGTTTAAAT	1275
	1467	 PheGlnPhe	1459
	1274	ACCATTTGGCTTCTCAATGTTTATGGG	1225
	1459	::::: ::: PheValLeuAsnLysIleIleG	1445
	1224	AACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATC	1175
	1445	<pre>LysGlyProGlnIleAsnThrGluArgPheTyrTyrCy</pre>	1429
	1174	TGCCAGTTGATTTACGTCACCGTGCACTTCT	1143
	1428	<pre>:: ::: euIleLysPheLysArgLysGluCysLeuMetLysTyrPheTyrThrL</pre>	1412
	1142	TAATCAAGCTT	1132
	1412	::: AlaIleGluLysGlyIleAsnGlnIleAsp	1395
	1131	ACACCCTTGAAATTAGCGATG	1109
	1395	ysAspAsnLeuIleTyrAlaAsnA	1379
	1108	ACCGGAGAATATCATTGATGTACGAACTGATA	1074
	1378	LeuGlnLysTyrValTyrGluGlnAsnGlu	1367
	1073	TGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCA	1024
	1366	eSerAspAsnHisLysTyrAsnAlaPheLeuLys	1355
	1023	CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGC	978
	1355		1339
	977	ATGTGTTCGACCACAATGTT	957
	1338	rgIleLeuPheGlyTyrLeuArgIleArgAspAsnArgIleAsn	1322
	956	CAGTATTACCATTAAAGAACCAAATAG	928
	1322	spAsnValSerTyrPheCysPheThrMetTyrLys	1305
	927	AGCTTTTCTATCAATGCCAG	906
	1305	${\tt TyrGluArgArgIleLysSerPheIlePheSerLysLeuLysPhe}$	1289
,	905		905
	1288	ysAsnAlaPheAlaTyrThrLeuThrArgValAsnSerIleLeuVal	1272
	905	CCAAGAAGCTCACGTATACAAATATGCGGATCGATCAC	868
	1272	aIleTyrPheArgSerPheValTyrAsnAsnIleLysValSer	1255
	867	GATAAATATTTGCTAAATAATTTTGGAATATCCAACAGATTTAATGG	818
	1255	IleLeuIleLeuTyrLysValLeuLeuSerMetTyrLysLy	1239
	817	ACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCT	774
	773 1238	TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGA ::: ::: euLeuLeuLysGluLysSerAlaTyrGlnAsnHisLeuGlyLysA	1222
	N	uSerSerPheIleAsnTyrGlnIleLysThrAsnAspMetLeuTyrAsn	
	26	CAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACC	00

324	75 TCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTA
274 553	GAAATTGAATGTGGACCAACT
224 548	178 TCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTC ::: ::: :: :: :: :: :: :: :: :: :: :: :: ::
177 531	128 TTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG ::: ::: ::::: 523 ysasnLysLysAsnLysLeu
127 523	81 CAGCAATAATAACCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATC :::: ::: 506 nAsnAsnAsnAsnGlyTyrLysLysLysIleLysAsnLysAsnLysAsnL
80 506	31 AACACCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA
	Align seg 1/1 to: E71604 from: 1 to: 2380
	alignment_block: US-09-323-427-1 x E71604
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yrLysAsp 1517 YrLysAsp 1517 TAGCTAAC 1420 eval 1532 TGATATTT 1470 ::::::: hrLeuTyr 1535 hrLeuTyr 1535 # text_change 07-May-1999 # text_change 07-May-1999 # operasite Plasmodium falciparum. town; translation not shown 13845293; PID:93845297; TIGR:PFB087	1342 GAATCATCGAAGCAATAATAAAACTGCCATATATTTC
1341 1501	1308TTCGTCCAAATCAGAAGGCATAAAAATAATGTTA ::: ::::: ::: ::: 1484 eLysLeuLeuGlnValLeuValGlnLysLysGluLysLysSerValIleA

1182	3 AATCAAGCTTTGCCAGTTGATTTAGGTCACCGTGCACTTCTGCAACATAA ::: ::: ::: :: :: :: :: :: :: ::	1133
800		œ
1132	ATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA	1083
1082 785	TGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGG	774
2 4	National designation of the state of the sta	2 0
1 0	CCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAAACCT	, œ
763	IleTyrLeuAsnAsnA	751
982	TTACCATTAAAGAACCAAATAG	933
750	:::::: :::	737
93	ATACAAATATGCGGATCGATCA	æ .
882 736	AATAATTTGGAATATCCAACAG ::::::::::::::::::::::::::::::::	730
72	TyrPheLeuIleGluAsnIleI	\vdash
832	TAAATGCTGATGGATGTGCTCTT	795
713	lyserileCysA	697
1 0	TITELEURSHMECHISTHESEF	ā
74	TATCATAAATGGACATGCGATTC	9
683	ProTyrHisLeuGl	670
694	GTGGACCAACCGGTCAACCAGTT	645
669	TCAAACTCAAATTGTCCCGATGCCGATATGCCGTTATGAAATTTTGGAT ::::::::::::::::::::::	658
		5
594 658	GATAAAACAGTTAGTGCACAGAT :::: ::: 1ValLeuLeuAspAspT	545 643
643		627
544		495
626	SGlyMet.IleLysGlnGlnHisAsnAsnIleHisAsnThrHisAsnIle	610
404	FER & COLER OLD BENEVOLD AND AND AND AND AND AND AND AND AND AN	A (
444	16 GTTGCGCGTACACGATCTCTGAATCCACG ::::	416 594
593	ysLysTyrAspThrSerTyrSerPheAsn	584
415	GTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATG	375
374 584	TGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTA ::: ::::::: ValLysIleMetValAspLysAsnAsnAspThrG	325 567
567	::: ::: ::::::::::::::::::	554

Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H. ture 342, 45-50, 1989 Title: Sequence of an unusually large protein implicated in regulation of Reference number: \$06797; MUID:90044042 Accession: \$06797 Status: nucleic acid sequence not shown Molecule type: DNA Residues: 806-1175;1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693;569 Cross-references: EMBL:X15423 Experimental source: var. Bristol Benian, G.M.; L'Hernault, S.W.; Morris, M.E. netics 134, 1097-1104, 1993 Title: Additional sequence complexity in the muscle gene, unc-22, and its	A; Accession: S57242 A; Molecule type: DNA A; Residues: 1-6899 < MBN1> A; Cross-references: EMBL:L10351 A; Cross-references: EMBL:L10351 A; Experimental Source: var. Bristol R; Benian, G. Submitted to the EMBL Data Library, November 1989 A; Reference number: S07571 A; Accession: S07571 A; Accession: S07571 A; Molecule type: DNA A; Residues: 792-6839 < MEN2> A; Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898 A; Experimental Source: var. Bristol	bditis elegans myosin-regulati. kinase (EC 2.7 bditis elegans #sequence_revi. \$06791, \$0679 ernault, S.W.; BL Data Library tional sequence \$57242	1524 TCAGTAATCTTTTATATGCATACTATTGTA 1553 11 902 ArgLysIlePheAspTyrTyrThrPheVal 911 seq_name: pir2:S57242	1424 TATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTCA 1473	1373 ALANIGITAGANICALCANGCANIAN	CATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATTG	801SerAsnIlePheValAsnPheArgAsnLysLysCysI 813 1183 TGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCAC 1232 :: :::
H. of m;5696	•	1999 rhabditis eleg					`

A;Reference number: S57218; MUID:93387664
Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <ben4></ben4>
rimental source: var. Bris ent: Lack of unc-22 leads tion:
);Genetics:);Gene: unc-22);Map position: IV
introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 652/3; 6691/3; 6776/1; 6808/3
omology serine/ 58-2450 57,2451
5210,5399
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31 AACACCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA
81 CAGCAATAATAACCCCA 97 ::: 3306 ysSerThralaArgAlaAspSerGlyLysTyrLysIleValAlaThrAsn 3322
98 TCAAGTGGAGGAAGAAGACAGGAAGCTTAGTTTTCTAAAAATC 145 ::: ::::: 3323 GluSerGlyLysAspGluHisGluValAspValAsnTleLeuAspTlePr 3339
146GAATTTACTAAATCTTCTG 164 3339 oGlyAlaProGluGlyProLeuArgHisLysAspIleThrLysGluSer. 3355
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215 TATTCGATTGCGGTTGACAATGGTGT 240 ::::: ::: :::
241 CGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAA 278
279 TAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTAT 325 ::::::::::::::::::::::::::::::::::
326GTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG 369 :::::: 3409 PheArgValLysAlaVal
370 TGGACGTCAAGTTGCCGGAATTTCACTTCCATTGATTCATGCAATGTTG 419 ::: :::::
GTGGTATTTTTGTAACAA(

1039	GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCT	990
3712	<pre>b uValProGlyLysGluTyrAlaPheArgValLysAlaValAsnLeuGlnG</pre>	3695
989	AGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAG	943
942 3695	TrpGlnGluValGlyThrPheProAspCysThrAlaLysValAsnLysLe	908 3679
6 6	GCCAAGAAGCTCACGTATACAAATATGCGGATCGATCACAG :::	3662
ס ס	TGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTG	5 1
		785 3635
784 3634	GTGATACT	777 3618
776 3618	GGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG	742 3601
741 3601	AlaAspValThrAsnThrProThrSerSerAlaIleHisIlePheSerAl	734 3585
733 3584	TATCATAAATGGACATGCGATTCTGAAACCGTTGATACT	695 3568
694 3568		668 3551
3551	ArgMetAlaProLysLeuAsnLeuAlaGlyLeuLeuAspLeuArgIleLy	3535
667		667
667 3534	TTGGATGGTGGACCAACCGGTCAACCAGTT	638 3518
637 3518	TGTCCCGATGCCAGTATGCCGTTATGAAATT	607 3501
606 3501	AGTGCACAGATTGAAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAAT	557 3486
556 3485	CGTGCATATCGAĞTACAATGCTTTTACATGGAAGCTGATAAAACAGTT 	509 3469
3469	2 pHisValAspLeuGluTrpLysProProAlaAsnAspGlyGlyAlaProI	3452
508		508
3452		3441
508	GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG	
3440	l laLysAsnProPheAspGluProAspAla	3431

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Seq_Documentation_Dick:
swells Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
R; Scrota (domestic pig)
R; Scrota (domestic pig)
R; Status: Special pig)
A; Status
                                                                        alignment_block:
US-09-323-427-1 x T03099
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                                                                                                                                                                                     Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1140 CTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAA 1189
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                                                                                                                                                                                     104.00
0.654
39.259
from: 1
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Gaps: 20
Percent Identity: 21.975
to: 13288
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823 13136	ACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAA	774 13123	
773 13123	GGTTGTCCATTCCTGCTTTGTCGATGAT	742 13106	
741 13106	TGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGC	704 13090	
703 13089	CCGGTCAACCAGTTCAATTTGCTATCATTAGGTCAGCCAGTTTATCATAAA	654 13073	
653 13073	.ATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA :::	605 13062	Hill,
60 4 13062	TTTCAAACTCAA	593 13046	<u>-</u>
592 13045	ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCT :: ::::: ::: :: erLysGluIleThrAlaSerProLysValSerSerProGluThrThrAla	546 13029	seque
545 13029	CAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTG	499 13017	
498 13016	ATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTAC	449 13011	in in
448 13010	CATTTGATTCATGCAATGTTGCGCGGTACACGATCTCTGAATCCACGTGGT	. 399 12995	
398 12995	TAATGATGAAGGTGGACGTCAAGTTGCCGGGAATTTCACTTC	358 12982	chain
357 12981	TTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCG	308 12979	
307 12978	AATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCA 	261 12962	
260 12962	TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTG ::::::::::	223 12945	
222 12945	ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT	173 12936	
12935		12935	
172	CAATCTTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATG	123	
122 12935	AACAACAACAGCAATAATAACCCCATCAAGTGGAAGAAGAAGAAGACAGGAAG	73 12923	
12923	GISTCIMIAACACCGACIGCAGCAGCAACAACAACAACAACAACAACAACAACAACAA	12907	

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   Swissprot_38: PGS1_HUMAN +
Swissprot_38: YIIG_ECOLI +
Swissprot_38: XRD2_XENLA +
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Swissprot_38: YXS2_CAEEL +
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Swissprot_38: PXK1_SCHPO +
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Database sequences: 82229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search time (sec): 138.700000
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-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-YGAPEXT=0.000 -GAPOP=6.000 -FGAPOEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -FGAPOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS-human40.cdi'-LIST-45 -DOCALIGN=20
-THR_SCORE-pct -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
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Len i Documentation ...

116 424 i Q03755 caenorhabditis elegari

21 1024 i P21421 plasmodium falciparu

21 495 i Q09276 caenorhabditis elegari

21 495 i Q09276 caenorhabditis elegari

21 495 i Q09276 caenorhabditis elegari

21 369 i P21809 bos taurus (bovine).

25 742 i Q03656 saccharomyces cerevis

21 150 i P12021 sus scrofa (pig). apom

25 4 i P34855 apis mellifera llqust

26 i P17889 bacillus subtilis. tra

27 28 i Q08455 apis mellifera llqust

28 i P24198 dictyostelium discoid

29 10 10211 schizosaccharomyces geruginos

2136 i P09975 marchantia polymorph

2136 i P09975 marchantia polymorph

2136 i P09975 marchantia polymorph

2136 i P09863 mus musculus (mouse).

369 i P28653 mus musculus (mouse).

369 i P28653 mus musculus (mouse).

369 i P24855 apis malciparum

368 i P21810 homo sapiens (human).

441 i P75802 escherichia coli. hy

875 i P12890 xenopus laevis (afric

21427 i P25648 saccharomyces cerevi

2161 i P4719 saccharomyces cerevi

2189 i P41951 caenorhabditis elega

2244 i Q09794 schizosaccharomyces

4485 i Q39575 chlamydomonas reinha

2616 i P01027 mus musculus (mouse).

2715 i P25823 drosophila melanogast

553 i P01975 marcharomyces cerevi

2715 i P25823 drosophila melanogast

553 i P3837 paramecium primaurel

2715 i P13837 paramecium primaurel

2715 i P38692 saccharomyces cerevi

2715 i P13837 paramecium primaurel

2715 i P38692 saccharomyces cerevi

2715 i P13837 paramecium primaurel

2715 i P38692 saccharomyces cerevi

2715 i P13837 paramecium primaurel

2716 i P38692 saccharomyces cerevi

2717 i P38692 saccharomyces cerevi

2718 i P38692 saccharomyces cerevi

2719 i P3918 saccharomyces cerevi

2710 i P3918 saccharomyces cerevi

2711 i P38692 saccharomyces cerevi

2712 i P3938 rattus norvegicus (rat)

2713 i P3938 rattus norvegicus (rat)

2714 i Q09441 archaeoglobus fulgidu
                                                                        SwissProt_38:SYA_MYCPN +
                                                                     REPEAT
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SwissProt_38:RMAR_CANGA +
SwissProt_38:UL52_HSV7J +
SwissProt_38:AMD_HUMAN +
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01-FEB-1994 (Rel. 28, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                  EMBL; M55997; AAA27995.1;
EMBL; Z49125; CAA88934.1;
PIR; A49772; A49772.
                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "cut-1 a Caenorhabditis elegans gene coding for noncollagenous component of the cuticle."; Dev. Biol. 146:519-530(1991).
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MEDLINE; 91323673.
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            G -> P (IN REF. 1).
P -> G (IN REF. 1).
A -> G (IN REF. 1).
MISSING (IN REF. 1).
CL -> SS (IN REF. 1).
IG -> MR (IN REF. 1).
IG -> MR (IN REF. 1).
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! P21358 candida glabrata (
! P52468 herpes simplex vir
! P19021 homo sapiens (human
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|||||:::||||:::||||||:
| snProLysGlyValPheValSerThrThrValValIleSerPheHisPro 107
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ATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA
                                                                                                                                     TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA
                                                                                                                                                                                                                   ysAlaValValHisSerCysThrValAspAspGlyAsnGlyAspThrVal
                                                                                                                                                                                                                                                                      nGlnValTyrHisLysTrpThrCysAspSerGluThrThrAspThrPheC
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Ratio: 4.228
milarity: 80.769
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seq_name: SwissProt_38:RPOB_PLAFA
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                                                                                                                                                            GAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATT 1267
                                                                                                            GCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCA 1315
                                                                                                                                                                                                                                                                                                                                aLeuValSerGlu.....GluSerValArgArgArgAlaThrSerThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGC
                                                                              IleValAlaThrAlaLeuSerAlaThrIlePheTyrValAlaArgPro
                                                                                                                                            lyIleCysLeuThrProIleGlyPheAlaSerPheLeuGlyIleGlyThr 403
                                                                                                                                                                                                                                         ACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATG 1217
                                                                                                                                                                                                                                                                     AspIleMetGluGly.....AlaSerProSerAlaProGluAlaAlaAl
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STANDARD;
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1024
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ID. RPOB_PLAFA STANDARD; PRT; 1024 AA.

AC P21421;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 35, Last annotation update)
DT 01-OCT-1996 (Rel. 35, Last annotation update)
DT 01-OVV-1997 (Rel. 31, Last annotation update)
DT
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alignment_scores: Quality: Ratio: alignment_block: US-09-323-427-1 x RPOB_PLAFA Percent Similarity: Align seg 1/1 to: RPOB_PLAFA from: 1 EMBL; X75544; CAA53232.1; -.
EMBL; X52177; CAA36427.1; -.
EMBL; X52775; CAA64572.1; -.
PIR; S10438; RNZOBF.
PROSITE; PS01166; RNA_POL_BETA; 1.
PFAM; PF00562; RNA_POL_B; 1.
PFAM; PF00562; RNA_POL_B; DNA-directed RNA polymerase.
SEQUENCE 1024 AA; 122185 MW; 59EAF3E1 CRC32; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 372 322 TTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTG
:::: :::||| |||:::||| 197 ACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATG....... 522 TACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAG 571 191 euPheIleTyrAsnAsnIleIleAsnLysLysIleLeuIle..... 472 CATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAG 521 152 rgIle.....LeuAsnIle 135 nAsnAsnLysAsnIleIleTyrValTyrIleTyrIleSerLeuGlyLeuA 152 119 IleGlnLeuPheLysLysAsnAsnLysIlePheIleIleLysPheLysAs 102 roPheIleTyrAsnAsnIleIleIleLeuAsnGlyLeuTyrLysThrCys 118 147 AATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACT 196 422 CGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGT 471 163 AspCysTyrPheAsnAsnPheLysPheAsnPheLeuIleLeuLeuTy 179 86 eAsn...IleAsnLysIleIleLysPheAsnIleLeuIlePheIleLeuP 70 AsnIleAsnAsnLeuLeuLysIleIleLeuThrLeuLysLeuAsnPheIl 86 TyrAsnTyrIle.....LysPheIleTyrSerLysTyrAsnAsnIleAs ACAATCA.....ATTTTAATACACGTAATGCATTCGAAGGACATGT 321 ATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAAT 671 nAsnIleIleSerLeuLysLeuPheIleIleLysLeuAsnLysPheAsnA GTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGT 621 rLeuAsnAsn..................IleTyrIleAsnLysAsnIleSerL 191 GACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA 280 112.00 0.373 45.113 Length: 665
Gaps: 28
Percent Identity: 17.594 to: 1024 162 135

1376	1327 ATAAAAATGATAGAATCATCGAAGCAATAATAAAACTGCCATATATA ::::::::::::::::::::::::::::::	13
489	473 eIleGluAsnLeuIleProPheIleHisTyrAsnAspSerIleArgA	4
1326	CTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGG	12
473	467 PheAsnTyrLeuLeuSerPh	4
1276	CCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGA	12
466	::: ::: 57 snileThrGlnAsnileIleTyr	4.
1226	SACAACCTGTAATACT	11
57	: ::: ::: :::: :::::::::::::::::::::::	
1176	2 TTGCCAGTTGATTTACGTCACCGTGCACTTCTGC	11
440	::: ::::::::::::::::::::::::::::::::	4
1141	STACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGC	10
423	ä	4
1091	ACTCAAGAAAAGATCTGCAGAACCGGAGAATATC	10
407	<	ω
1052	1052	10
390	uValAsnTyrI	w
1052	AGCTGCGCAACTTC	10
373	:: :::::::::::::::::::::::::::::::::::	
1034	AGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGC	
357	ırGlyLeuAsnSerL	ω
984	AC.	
340	LeuSerGluIleAsnG	
974	ACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAA	
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932	ACAAATATGCGGATCGATCACAGCTTTTCT	8
310	295 gAsnIleTyrAsnAsnIleThrLeuLeuLeuAsnAsnLysLysT	N
882	TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACG	8
295	rLeuLysIlePheLysTyrGlnLeuLeuAsnIl	2
832	ATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGC	7
280	277 leLysSerLys	Ν
782	TTCTGCGCG	7
277	rAsnLysLysPheTyrSerIleIleAspAsnLeuI	Ν
732	GGACATGCGATTCTGAAACCGTTGATA	7
260	244 IleLeupheSerIleLysLeuAsnpheSerTyrTyrSerAspPheTyrIl	N o
	70 HEFOREX EDVERTED TO THE PROPERTY OF THE PRO	
243	236 snIleTyrIleAsnLeuLeuAsn	

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I Sequence of the sequence of 
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YOH3_CAEEL STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL C43C3.3.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 55.1 KD PROTEIN C43C3.3 IN CHROMOSOME
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                                        Hypothetical
                                                                                    EMBL; Z47067; CAA87330.1; -. WORMPEP; C43C3.3; CE01525.
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alignment_scores:
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                                                                                                                                      AsnGlyHisGluValIleAlaSerThrGlyGlyLysProLysPro....
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; mammarro,
Eukaryota; Metartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
MEDLINE: 89255324.

MEAME P.J., CHOI H.U., ROSENBERG L.C.;

"The primary structure of the core protein of the small, leucine-rich proteoglycan (PG I) from bovine articular cartilage.";

J. Biol. Chem. 264:8653-8661(1989).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (LEUCINE-RICH PG
                                                                                                                                                                                                                                                                                                                                                           XU J.H., RADHAKRISHNAMURTHY B., SRINIVASAN S.R., "Primary structure of bovine aorta biglycan core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGS1_
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                                                                                                                                                                                                                                                                                                                                  "Primary structure cloned CDNA.";
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use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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Glycoprotein; Connective tissue; Extracellular matrix;
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-!- SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of the dermatan sulfate DS-PGII, from bovine articular cartilage a sepharose chromatography.";
J. Biol. Chem. 264:2876-2884(1989).
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                                                                                                                                                       leThrLysValGlyValAsnAspPheCysProValGlyPheGlyVal 328
                                                                                                                                                                                                                                                                                                                                        ......ATTTTATTCTAACAGTTTATCATTTGTGATAATA 1650
                                                                                                                                                                                                                                                                                                                                                                                                    LeuArgGluLeuHisLeuAspAsnAsnLysLeuSerArgValProAlaGl 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt is AsnGlnIle Arg MetIle Glu AsnGly Ser Leu Ser Phe Leu Pro Thr}
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   STANDARD;
   PRT;
   742 AA
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alignment_block:
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE SERINE/THREONINE-PROTEIN KINASE YMR216C
YMR216C OR YM8261.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z49809; CAA89931.1; -.
HSSP; P24941; 1AQ1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00059; pkinase; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. SIMILAR TO S.POMBE DSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
293 AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGA 342
                                                                                                                                                                                                                                                                                                          419 SerGlyAsnArgAsnIleProSerSerIleAsnAsnAsnSerIleAsnAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                         93 CCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAA 142
                                                                                                                                   TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG
                                .....AsnAsnAspAsnSerLysAsnLysAsnAsnAsn.AsnAsn
                                                                ......AspAsnAsn.......
                                                                                                                                                                   isSerValThrArgMetPheIleAsnGluAspSerAsn......
                                                                                                                                                                                                         ATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTG
                                                                                                                                                                                                                                         \verb|nGlyIleGlyIleLysAsnSerAsnAsnSerPheLeuAsnSerValProH|\\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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20.462
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apomucin.";

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repeated,

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Seq ID AC AC DT DT DT DT DT DT DT DT RN RN RR RR RR RR RR RR RR RR RT
                                                                                                                                                                                                                                                                                seq_name: SwissProt_38:APMU_PIG
                                                                                                                                                                                                                                                    documentation_block:
                                                                                                          01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).
Sus scrofa (Pig).
Eukhryota; Metazoa; Chordata; Craniata; VerEutheria; Cetartiodactyla; Suina; Suidae; S
                                                                                                                                                                                                                      APMU_PIG
P12021;
591
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                                                                  TISSUE=SUBMAXILLARY
                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          791
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                                                MEDLINE;
                                                                                                                                                                                                                                                                                                              yLysTyr 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euSerThrPheAspIleSerAsnIleSerGlnSerSerAspThrAsn...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTT
                                                                                                                                                                                                                                                                                                                                               GGAATAT 847
                                                                                                                                                                                                                                                                                                                                                                          LeuLeuGly.....
                                                                                                                                                                                                                                                                                                                                                                                                       ATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       luGlyHisSerTyrThrLysAspAspAspHisIleAlaGlnIleIleGlu
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                                                                                                                                                                                                                                    STANDARD;
                                                                GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .TrpGlyCysGlyAlaAspIleTrpSerThrAl
                                                                                                                                                                                                                                                                                                                                                                          .GluLeuProSerTyrLeuLeuArgAsnGl
 contains addition
                              ABERNETHY J.L., ZHAO Y., HILL R.L.;
                                                                                                           Craniata; Vertebrata;
ina; Suidae; Sus.
                                                                                                                                                         otation update) (FRAGMENT).
                                                                                                                                                                                                                                    PRT;
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a cystine-rich
to a highly re
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 a highly repetitive,
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                                                                                                                            Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580
 GERKEN T.A., OWENS C.L., PASUMARTHY M.;

"Determination of the site-specific O-glycosylation pattern of the porcine submaxiliary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:galnac transferase peptide binding site.";

J. Biol. Chem. 272:9709-9719(1997).

-i- FUNCTION: ADOMUCIN IS DART OF MUCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
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                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOHNSON W.C. JR., HILL R.L.; "Structural properties of porcine submaxillary gland J. Biol. Chem. 262:11339-11344(1987).
                                                                                                                                                                       PROSITE; PS01208; VWFC; PFAM; PF00007; Cys_knot
                                                                                                                                                                                                                                                EMBL; M61883; AAA30998.1; -. EMBL; M21174; AAA30990.1; -.
                                                                                                                                                                                                                                                                                                or send an
                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYDRATE-BINDING SITES, AND SEQUENCE OF TISSUE-SUBMAXILLARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 87280230
ECKHARDT A.E., TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 45-80.
TISSUE-SUBMAXILLARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIMPTE C.S., ECKHARDT A.E., ABERNETHY J.L., HILL R.L.; "Porctine submaxillary gland apomucin contains tandemly identical sequences of 81 residues."; J. Biol. Chem. 263:1081-1088(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=SUBMAXILLARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-503 FROM N.A.
 DOMAIN
                                                                                                                          DOMAIN
                                                                                                                                            NON_TER
                                                                                                                                                                                                      PROSITE; PS01225; CTCK_2;
                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                    PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: EXTENSIVELY O-LINKED GLYCOSYLATED ON SER AND THR RESIDUES OF THE REPEAT UNITS. HIGHEST GLYCOSYLATION APPEARS TO OCCUR ON SER RESIDUES WHICH HAVE GLY AT POSITIONS AT +2 OR -2 FROM THE GLYCOSYLATION SITE OR, WHERE GLY IS THE PENULTIMATE RESIDUE. THE PRESENCE OF PROLINE (USUALLY AT POSITION +3 OR -3) APPEARS TO ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 CHERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.

DOMAIN: CONTAINS TANDEMLY REPEATED, IDENTICAL SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MULTIMERIC MUCIN STRUCTURE.
SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENVIRONMENT: INTERMOLECULAR DISULFIDE BONDS COULD HELP MAINTAIN
                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENHANCE GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                    A40009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.E.,
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                                                                                                                                                                                                                      PS01185;
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                                                                                                                                                                                                                                                                                                  email to license@isb-sib.ch).
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                                                                                                                                                         Repeat.
                                                                                                                                                                       Cys_knot;
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 CTCK
                 VWFC
                              6 (INCOMPLETE)
                                                                                                                          81
                                                                                                           (FRAGMENT)
                                                                                                                            AA TANDEM REPEATS
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                                                                                                                                                                                                                                                                                                                                                        There are no restrictions
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23 GTGTCTATAACA ::::: 769 ValThrValGly 73 AACAACAACAGC 1 785 rThrProThrG1 123 CAATCTTAGTTT 797	gnment_block -09-323-427- ign seg 1/1	nment_score Qua F cent Simila	DISULFID CARBOHYD CAR
TATAACACCG :::: IVAIGLYThr CCAACGCAAT : 'rOThrGluVa 'TTAGTTTTCCT 'TCTTATTGCT 'TCTTATTGCT 'TTGACAATGG ::::::::!	: 1 x API to: AI	s: lity: latio: rity:	10062 10085 10085 10089 46 46 50 51 50 51 50 66 66 67 77 67 77 67 77 81 77 81 77 81 77 91 94 94 94 95 94 94 95 94 94 95 95 96 97 97 97 97 97 97 97 97 97 97 97 97 97
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IGCAGCAACAACAACAACAACAACAACAACAAC 72 ::: ::: ::: ::: ::: ::: ::: :::	 from: 1 to: 1150	Length: 405 Gaps: 20 Percent Identity: 21.975	BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY

1035 1056	CAGGTGGTGCCGCAGCAAAACCTGCTGC.: ThrTrpCysAlaGluGluAspArgValTyrAspSerLysGlnCysCysT	1008
1007 1039	GGATTCGGAGCTGTTAA GlyPheThrAlaValVa	974 1024
973 1023	ACCATTAAAGAACCAAATAGCGAATGTGTTCGAC ::::: ::: ::: SerPheAspAspProAsnAsnProCysValThrT	924 1007
1007		1007
923	TCA	874
873 1006	. >	824 999
866	AspThrCysCysGluIleGlyHisCysGluLysArgTh	
823	TACTGTGGAAATTCTAAATGCTGATGGATGTGG	774
985	GGTTGTCCATTCCTGCTTTGTCGATGAT	968
4 70	GGACATGCGATTCTGAAACCGTTGATACTTTCT ::::::: ysThrCysThrGluAlaLysThrValAspCysLysProLysGluC	0 0
703 951	GTTCAATTTGCTATCATTGGTCAGCC ;;; ;LysSerProGlyAspValTrpThrAl	654 935
653 935	GAAATTTT	605 924
924	spGlnGluAsnGluAsnLysThrGlyCysProAlaP	908
604	CTCAA	593
592 907	II.	546 891
891	AlaThrGl	879
. 7	laSerGluThrThr	7
498	TTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTT	4
448 872	CATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGT	399 857
398 857	TAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTC	358 844
843	heLysGly	841
357	CGAAGG	308
840	ARIGIGGACCACCTICAAIIAACAAIICAATTTAAIIACACGIAAIGCA ARIGIGGACCTICAAIIAACAAIITTAAIIACACGIAAIGCA	824
N	Gly1leSerThrGlyProGluAsnSerThrProGlyThrThrGluThr	0

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alignment_scores:
Quality:
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US-09-323-427-1 x NU5M_APILI
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                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
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PFAM; PF00361; oxidored_q1; 1.
PFAM; PF00662; oxidored_q1_N; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
Oxidoreductase; AA; 65590 MW; 9E256E2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1073 TyrAsnGlyCysThr 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CROZIER R.H., CROZIER Y.C.;
"The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";
Genetics 133:97-117(1993).
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01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).
                                                                                                                                       515 TATC......GAGTACAATGCTTTTACATGGAAGCTGA 546
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                                                                                                                                                                                                                                     465 CTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
                                                                         547 TAAAA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoidea; Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                    27
                                                                                                                                                                                              11 LeuPheGluPheSerPheLeuMetMetLeuMetSerLeuTyrLeuLeuTy 27
                                    etLysPheAsnPheLeuLeuIleAspTyrLysSerLeuMetPheIle 60
                                                                                                                rLeuAsnLysGluPhePhePheGluTrpAsnIleTyrThrPheAsnSerM 44
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.....CAGTTAGTGCACAGATTGAGGTA 574
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Gaps: 34
Percent Identity: 21.480
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348	let.IleLeuIlePheSerIleLeuSerLeuCysGlyPheProPheL	332
J		د
122 331	ACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA ::::: ::: :!: snGlnAspIleArgMetTyrTyrGlyMetTyrTyrIleTyrProMetLys	1177 315
		0 1
300	GIULeuVaiPheLeuHisLeuPheIleHisAlaMetPheLysSerLe GaTaATCAAGCTTTGCCAGTTGATTTACGTCACCTGCACCTTTTTGCA	284 1127
112	AGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGC	1077
283	GlyPheMetMetSerMetLeuSerIleGlySer	268
107	CTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAAC	1027
268	:::: LeuLysLysValValAlaTyrSerT	251
102	AAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAA	987
251	eMetLeuIleAlaSerLeuThrMetLeuPheAlaGl	235
986	GAACCAC	975
234	:::::: LeuLeuAspPheAsn	220
974	ACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAAT	925
220	ProValSerSerLeuValHisSerSerThrLeuValThrAlaG	203
924	GTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCA	879
Ö	 	8
878	CAGATTTAATGGCTGGCCAAGAAGCTC	852
186	luPheMetMetIleTyrIleLeuLeuMetAlaPheThr	170
851		851
170	hrTyrTyrGlySerTrpAsnLeuSerPheT	153
851	AATATTTGCTAAATAATTTGGAATATCCAA	821
153		140
820	AACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGAT	771
139	<pre>fyrTyrMetLysMetLysSerPheThrSerGlyMet</pre>	123
770	ATG	768
123	H	106
767	TTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATG	725
106	<pre>lesermetTyrmetLeuIleLeuSerPr</pre>	96
724	CATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACC	675
95		91
674	TATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTG	625
	: ::: :::::: tAspLeuSerGluLeuLysMetAspArgPheLeuTyrL	7
624	CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG	575
77	PheLeuValSerMetIlePheSerMetIleIleIleTyrSerIleSerTy	61

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Sequence of the control of the contr
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01-NOV-1990 (Rel. 16, C
01-NOV-1990 (Rel. 16, I
15-DEC-1998 (Rel. 37, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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15-DEC-1998 (Rel. 37, Last annotation update)
TRANSLATION INITIATION FACTOR IF-2.
                                                                                         subtilis gene (infB)
                                                                                                                                        "Isolation and molecular genetic characterization of the Bacillus
                                                                                                                                                                                                                                      SPERLING-PETERSEN H.U.,
                                                                                                                                                                                                                                                                                 SHAZAND K.,
                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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              Bacteriol.
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TERSEN H.U., GRUNBERG-MANAGO M., RABINOWITZ J.C.,
172:2675-2687(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                         encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                         protein synthesis initiation factor
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Percent Similarity:
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMILTER (NOV-1997) to the EMBL/GenBank/DIBJ databases.

-I- FUNCTION: IF-2, ONE OF THE ESSENITAL COMPONENTS FOR THE INITIATION
OF PROTEIN SYNTHESIS IN VITRO, PROPECTS FORMYLMETHIONYL-TRNA FROM
SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDLING TO THE 30S
RIBOSOMAL SUBUNITS. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP
DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
-I- ALTERNATIVE PRODUCTS: IT IS PROBABLE THAT BY USING ALTERNATIVE
INITIATION CODONS IN THE SAME READING FRAME, THE GENE TRANSLATES
INTO TWO ISOZYMES: ALPHA AND BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01176; IF2; 1. PFAM; PF00009; GTP_EFTU; 1. Initiation factor; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A35269; A35269.
PIR; B35269; B35269.
PIR; S31994; S31994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M34836; AAA22673.1; -. EMBL; Z18631; CAA79234.1; -. EMBL; Z99112; CAB13536.1; -.
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SHAZAND K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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SUBTILIST; BG10268; INFB.
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SEQUENCE FROM N.A.
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                                                                                                                       99
nAsnAsnAsnLysAsnGlnHisGlnGlnLysProValLysProLysLysG
                                                    CAACAGCAATAATAAC............CCCATCAAGTGGAGGAAGA 112
                                                                                                                                                                           TATAACACCGACTGCAGCAACAACAACAACAACAACAACAACAACAA
                                                                                                                 PheAsnLysAsnLysLysAsnAsnAsnLysLysAsnLysArgAsnAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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                                                                                                                                                                                                                                                                                          x IF2_BACSU
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R -> A (IN REF. 3).
ACB9B730 CRC32;
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INITIATION FACTOR IF-2-BETA (PROBABLE).
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Identity: 18.
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818	6GGTGATACTGTGGAAATTCTAAATGCTGATGC	77
	3 AspLysGlyArgGlySerValAlaThrLeuLeuValGlnThrGlyThrL	40
775	7 TCCATTCCTGCTTTGTCGATGATGG	44
402	6 ysAlaAsnProAs	38
746	7 TCATAAATGGACA	69
386	7 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATT : ::: :::: 9 eAspGluLeuValGluMetIleLeuLeuValSerGl	36
369	3 lyGlyGluThril	Ü
646	7 AAACTCAAATTGT	59
353	::::::::::::::::::::::::::::::::::::	ω i
1 3 2 3 6	O ProfleffeValA	· N
546	0 TTTTACATGGAAG	ū
319	ProGlnTh	30
529	0 TTCATCCATTATT	48
303	8 TATTTTTGTAACA 	4 00
286	4 Pro	27
447	8 CCATTTGATTCAT	9
273	2 lu	6
397	8 AAGGTTGCCGTAA	34
262	8 uAlaGlyGlyIle	4 4
7	7	_
316 248	7 2 LysThrThrLeuL	23
231	5 euGluIleArgPr	-
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215	8 uGluGluThrGlu	9
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165	Section Sect	4
7	O AAAAATOCAATTTAAAATOTTAAAATOTTCATCAAATCATCATCATT	u
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419 HHISVARICIYASPPTOTIEVALVAIGLYASPTHTPhedlyArgVal 419 ATRAARATTTCCTAAACTAATTTT

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alignment_scores:
Quality:
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US-09-323-427-1 x MUCS_BOVIN
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DOMAIN 61 158
REPEAT 61 71
REPEAT 112 122
REPEAT 148 158
DOMAIN 338 404
DOMAIN 471 555
SIMILAR 1 282
DISULFID 471 518
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                                                     302 AATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGG
                                                                                                              252
                                                                                                                                          229
                                                                                                                                                                     202
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                                                                                                                                                                                                                            152
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                                                                                                                                                                                                                                                                                    102 GTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATCGAATTT 151
                                                                                                                                                                                                                                                                                                              190 rGlyIleGlnThrGlyIleThrGlyThrGlySerGlyThrThrSerSerP
                                                                                                                                                                                                                                                                                                                                                                     174 ThrAlaThrGluThrThrThrSerArgHisSerSerAspAlaThrGlySe
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PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
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                                                                                                                                                                                                                                                                                                                                       82 AGCAATA.....ATAACCCCATCAA 101
                                                                                                                                                                                                                                                                                                                                                                                                 roGlyGlyPheAsnAlaGluAlaThrThrPhe.....LysGluHis
TTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCAT 401
                      ThrAla.....valValSerGly.....
                                                                                 roGluSerSerAsnThrGlyThrSerThrGlyValGlyArgGlnThrSer
                                                                                                             CAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGT
                                                                                                                                                         TATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGC
                                                                                                                                                                                                 ValArgThrThrGluThrArgIle
                                                                                                                                       ....LeuSerGlyThrThrArgGlyArgSerGlyThrThrValIleP
                                                                                                                                                                                                                            ACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACTACACT 201
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42.931
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Gaps: 19
Percent Identity: 21.594
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                                                                                 259
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	documentation_block: AAC4_DICDI STANDARD; PRT; 317 AA. P14198; 01-JAN-1990 (Rel. 13, Created)	seq_docu ID AAC AC P14 DT 01-
	e: SwissProt_38:AAC4_DICDI	seq_name
	6 ATCATTGATGTACGAAC 1101 ::: alAsnvalThrValAsn 481	1085 476
108 476	CAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAAT	1035 464
464	GlnThrTrpCysAlaGluGluAspArgValTyrAspSerThrLysCysCy	1006 448
-4 0	AATGTTCAGAGCACAAGGATTCGGAGCTGTTAA	432
971 432	CCAGATCAGTATTACCATTAAAGAACCAAATAGCGATGTGTT :::::::::::::::::::::::::::::::	1 1 2
		· -
921	GAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG	872
871 415	/TTGCTAAATTAGGATATCCAACAGATTTAATGGCTGGCCAA ::: hrCysLeuPheAsnAsnAsnAspTyr	827 407
826 407	AATTCTAAATGCTGATGGATGTGCTCTT :::: ::: sPheLysAspAsnAspThrCysCysGlu	790 390
789 390) GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA :::	740 377
739 376	2 AATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC 	702 360
701 360	<pre>? AACCGGTCAACCAGTTCAATTTGCTATCATTAGTCAGTCA</pre>	652 343
651 343	CAAATTGTCCCGATGCCAGTATG::::::	602 333
601 332	2 CAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACT ::::::::::::::::::::::::::::	552 317
551 317	AGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAA :::	502 302
501 302	2 TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAA :::::::	452 290
451 289	TTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATT ::: ::: ::: :::	402 273
273	::: ::: ::: Supering State	266

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DICTYDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHAW D.R., RICHTER H., GIORDA R., OHMACHI T., ENNIS H.L.;

"Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters of asparagine, glutamine, or threonine.";

MOL. Gen. Genet. 218:453-459(1989).

-!- DEVELOPMENTAL STAGE: THE CONCENTRATION OF AAC-RICH MRNAS IS LOW IN DORMANT SPORES AND GROWING CELLS, BUT INCREASES DURING SPORE-GERMINATION AND MULTICELLULAR DEVELOPMENT.

-!- MISCELLANEOUS: SEVERAL PROTEINS DERIVE FROM AAC-RICH MRNA, WHICH, DUE TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Last sequence update) 01-FEB-1994 (Rel. 28, Last annotation update) AAC-RICH MRNA CLONE PLK330 PROTEIN (FRAGMENT). Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                     143 ATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                      193 TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat
                                                                                                                                                                                                                                                                                                         70 n.....AsnAsnAsnThrSerIleSerAsnA
                                                                                                                                                                                                                                                                                                                                           93 CCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTCTAAAA 142
                                                                                                                                                                                                                                                                                                                                                                           .....CysLeuAlaThrPheGluGln.ValGlnAsn.....
ACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S05356;
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317
                                .AsnCysPheGluThrCysAspPheLysAlaThrGluArgGl 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S05356.
                                                                                                                                                                                                                                       .....GlyAspIleAsnAsn.....
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ASN-RICH.
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18
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seq_documentation_block:
ID VGLH_HSVSA STANDA
AC P16492;
DT 01-AUG-1990 (Rel. 15,
DT 01-AUG-1990 (Rel. 15,
DT 01-OCT-1996 (Rel. 34,
DE GLYCOPROTEIN H PRECUR
GN GH OR 22.
OS Herpesvirus saimiri (
OC Viruses; dsDNA viruse
OC Gammaherpesvirinae.
RN [1]
                                                                                                                                                                                                                                                                           seq_name: SwissProt_38:VGLH_HSVSA
                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
GLYCOPROTEIN H PRECURSOR.
                                              Herpesvirus saimiri (strain
Viruses; dsDNA viruses, no F
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                                                                                                                                                                                                                    STANDARD;
                                              RNA stage; Herpesviridae;
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alignment_scores:
    Quality:
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                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE; 89036162.

GOMPELS U.A., CRAXTON M.A., HONESS R.W.;

"Conservation of glycoprotein H (gH) in herpesviruses: nucleotide sequence of the gH gene from herpesvirus salmiri.";

J. Gen. Virol. 69:2819-2829(1988).
                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
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CARBOHYD
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HONESS R.W., CRAXTON M.A., WILLIAMS L., GOMPELS U.A.;

"A comparative analysis of the sequence of the thymidine kinase gene of a gammaherpesvirus, herpesvirus saimiri.";

J. Gen. Virol. 70:3003-3013(1989).

-I- FUNCTION: GH AND GL FORM A COMPLEX THAT INDUCES NEUTRALIZING AND SYNCYTIA INHIBITING ANTIBODIES (BY SIMILARITY).

-I- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN H.
                                                                                                              182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D00400; BAA00302.1; EMBL; D00543; BAA00433.1; PIR; JQ0010; VGBE11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structure of the herpesvirus saimiri genome."; J. Virol. 66:5047-5058(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X64346; CAA45645.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALBRECHT J.-C., NICH NEWMAN C., WITTMANN HONESS R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 92333688.
                                                                                                                                         74
                                                                                                                                        ACAACAACAGCAATAATAACCCCCATCAAGTGGAGGAAGAAGACAGGAAGC
                           TTCGTCTTATTGCTTCTGTACTACACTTATTGCATTGTCTTATTCGATT
                                                                                AATCTTAGTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGA 173
                                                                                                           ThrIleSerCysHisIleThrProAsn..........
                                                      ....TyrLeuPheValSerValGluPheThrLysPheAspSerLeu
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0.358
42.121
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                                                                                                                                                                                                                                                                                                                                     16
717
43
59
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128
444
613
....ThrLeuLeuPheGlyHisSerHisTyrLeu
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Gaps: 39
Percent Identity: 20.000
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 214
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918	GATCGATCACAGCTTTTCTATCA	. 896
471	${\tt ValLeuSerSerMetCysThrSerLeuGluIleGlyAsnLeuLeu}$	455
895	CG	885
884 455		835 438
834 438	TGTGCTCTTGATAAATATTTGCTAAA	809 422
808 421		771 406
770 405	AACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATG	721 394
720 393	TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA ::: nMetLeuSerLeuPheArgLeuSerArgHis	671 383
670 383	AACCAGTTCAA 	660 367
659 366	AGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTC : : : : : : : : : : : : : : : : : : : : : : : :	618 350
617 350		584 335
583 334	GTATCTGAAATC ::: SerGluLeu	534 330
533 330	ATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTT::::::::::::::::::::::::::::	490 313
489 313	TTTCGTTTCATCCATT :: laHisPheLeuValIl	443 297
442 296		393 283
392 283	CAAGTTGCCGGAATTT ::::: GluMetPheThrIleG	343 277
342 277	TATGTGAAAGGTCTTTATGA ArgGluIleIleGluThrProProLeuThrPheIleLysAsnLeuGlnAs	323 261
322 260	 LysPheAspIleAlaLysValPhe	306 244
305 244	AATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATG : :::::	256 231
255 231		224 215

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1111 CACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTC 1160
                              1648 ATATCACAAATTATACCTTGTATTG
                                                                                                                                                                                                                                                                                   1552 TAAATGTTTCATCATT....AGGCCATGAATAGTTTCGTTTGTTATTATC
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                                                                                           IleMetVal......PheIleLeuPheLeuValGlyLeuTyrLe 708
                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAAAGCTT...ATTCATTATTCAGTAATCTTTTATATGCATACTATTG
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 0.554
Percent Similarity: 43.672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: YAY3_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-323-427-1 x YAY3_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME
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                                       289 TTTTAATACACGTAATGCATTC.....GAAGGAC
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                                                                                                                                                                                                                                                                                                                        47 nPheAspSerProSerIlePheAlaArgIleLeuAspAlaArgAlaGlyH
                                                                                                                                                                                                                                                                                                                                                                                                         36 LeuAspGlySerValGluMetMetCysTrpPro.....As
                                                                                                                      TGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTG 467
                                                                                                                                                                                                   GGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGT 417
euLeuAspPhePheHisArgProTrpGluAspTyrGluProLeuTyrPro 115
                                                                               eLeuHisThrLysPheTyrSerGluArgGlyValLeu.....ArgL
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                                                                        TATTACCATTAAAGAACCAAATAGCGAATGTGTT...CGACCACAATGTT
ATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGATCTGCAGAACCGGAG...AATATCATTGATGTACGAACTGATATC 1108
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                                                                                                                                                                                                                                                                                                           AACACCCTTGAAATTAGCGATGATAATCAAGCTTTG...CCAGTTGATTT 1155
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                                                                                                                                                                                                       ACGTCAC...CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTG
                                                                                                                                                                                                                                                        .....TyrSerIleHisGlyAspSerGlnAsnLeuGluGluValGluLe
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                                                .Gly.AsnAlaAlaValHisHisLeuGln.LeuAspIleT
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seq_documentation_block:
ID YCFZ_MARPO STANDARD;
AC P09975;
AC P09975;
DT 01-MAR-1989 (Rel. 10, Creat DT 01-MAR-1989 (Rel. 26, Last DT 01-JUL-1993 (Rel. 27, Last DT 01-JUL-1993 (Rel. 27, Last DE WARL)
OC Marchantia polymorpha (Livog Chloroplast.
OC Eukaryota; Viridiplantae; OC Marchantiales; Marchantiae; OC Marchantiales; Marchantiae; OC Marchantiae Polymorpha K.; FUKUZAWA H., KO OHYAMA K.; FUKUZAWA H., KO O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-323-427-1 x YCF2_MARPO
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiopsida;
Marchantiales; Marchantiaceae; Marchantia.
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01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation updat
HYPOTHETICAL 259 KD PROTEIN (ORF 2136).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 yrGly 389
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PFAM; PEO0004; AAA; 1.
Chloroplast: Hypothetical protein.
SEQUENCE 2136 AA; 259911 MW; A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OHYAMA K., FUKUZAWA H., KOHCHI T., SHIRAI H., SANO T., SANO S., UNESONO K., SHIKI Y., TAKEUCHI M., CHANG Z., AOTA S., INOKUCHI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                            78 CAACAGCAATAATAACCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 AACAACAAA.....AA
                                                                                                                                                                                                                                     TTAGTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG
                                                                               TCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGG 227
SerPheAsnIleIle.....ThrValIlePheAspLys.L 770
                                                                                                                                                          heSerPheSerLysAsnSerValLeuAspThrPhePhePheAsnLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.00
0.316
46.375
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Percent Identity: 18.
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228	TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 2	77
770	IleG1	98
278	AATACACGTAATGCATTCGAAGGACATGTTTATGT	27
	AAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGT	77
803	TyrPheIleAsnGlu	810
378	ATGTTGC	27
811	AsnLeuThrThrThr	815
428	CTCTGAATCCACGTGGTA	71
816	heAsnAspLysGluPheAsnIlePhe	826
472	CATCCATTATTTGTTACCAAAGTTGATCGTGCAT	21
827	8PheLeuGluLeuPheIleSerGluIleAsnAsnAspPheLeuM	141
522	ACAATGCTTTTACATGGAAGCTGATAA	59
841		157
560	TGAGGTATCTGAAATCACAACTGCTTTTCAAA	909
857	OD.	374
610	ATGCCAGTATGCCGTTATGAAATTTTGC	59
874	uLysThrLysIleLeuThrPheIleAspPheLeuGlnAspProGluLeu	990
660	ACCAGTTCAATTTGCTATCATTGGTCAGCCAG	03
891	TyrAsnAsnArgPheIlePheHisLeuGluLysLysThrIleLysAs	907
704	ACATGCGATTCTGAAACCGT	41
907	AsnAsnLeuLeuTyrLeuArgLeuLeuL	24
742	GGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAA 7	91
924	rg	124
792	GTGCTCTTGATAAATATTTGCTAAATAATTTG	841
925	uLeuIleAs	30
842	ATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC	391
931	GluIleLysSerPheIleGluLysLysAsnAsnL 9	142
892	GCTTTTCTATCAATGCCAGATCAGTATTACCA	41
942	nLeuSerAsnValLe	954
942	AACCAAATAGCGAATGTGTTCGA	71
955	sAsnSerTyrLysPhePheAspAsnIleP	71
972	AATGTTCAGAACCACAAGG 9	990
971	snAsnGlnAsnTy	88
991	ATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTG	040
)

ASATTYLLYSTHEPHOGINTEPILESER. AARCAAGCTTTGCCAGTTGATTTACGTCAGTTTGCTTGCTGCTGCTGCTGTAATTTTGCTTGC	1747 TCATTTGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1697 CTATTCTGTAAACAATTC. ::: 1219 luIleIle	1681	1639 TTTGTGATAATATCACAA ::: ::: 1186 TrpValllePheSerLeu	1613 TCCTATTŤTATTCT ::::::: 1169 snPheLeuTrpSerAspP	1585 1152 pAsnLeuArgPhePheAs	1548ATTGTAAATGTTTCAT	1499 AGCTTCTGAAAAGCTTAT" : ::::: ::: 1119 eLysLysLysLysIleIl	1452 AATACAATAAGTGATATTT ::: :::::: 1103 GlnileileGlnGluThrP	1408 AATTTTAGCTAACAAATAT ::: :: 1086 erTrpPhePheThrLeuG1	1358 AATAAAACTGCCATATATA:	1308 TTCGTCCAAATCAGAAGGG::: 1060LysAsnIleSerTyr	1059	1258 TTTAAGCATTGCATTGAT	1214 AATGGAATCTGC: ::: ::: 1050 sIleGluLysAsnAsnTy	1164 GTGCACTTCTGCAACATA	1114 CCTTGAAATTAGCGATGAT	1064 AGATCTGCAGAACCGGAGA	1041 CGCAAC
12 12 13 14 15 17 17 17 17 17 17 17 17 17 17 17 17 17	177 124	TATTGCAATTAAAAAGTATT ::: ::: ::: hraspargSerargSerLeu	TraTGGGCATCATTTC ySerAspCysPheHisLeuTrpLysAsnPheG	TATTGCCCAATTT ;;; ePheLeuTyrTyrGlnLysIl	AACAGTTTATCA ::: AsnLeuIleAsnAsnCysAsnAsnLeuTyr	GTTTGTTATTATCATCATTATCAACTTG ::: ::: !lulleasnTyrLysLysAsnTyrLeuLeuA	AATAGTTTC ::::: HisasnPheLysLeuLysTr	TAATCTTTTATATGCATACT. :: ::::: ::: euLysPhePheLeuLysSerL	TTCATCAAAACTTCTTCTATCGCTTTTAT ::::: ::: ::: :::: PhePheGlnIleThrAspValLeuGluTyrPh	ATAGTATGTAGGAAATAATTACTGT ::: ::: JT:pTrpGluTyrAsnThrTyrIleLeuLeu	TTCGTTTCTTATCATCCTTCTAATAACT :::::: ::::::::::	CATAAAAATAATGTTAGAATCATCGAAGCAAT :::::::::::::::::::::::::::::::::		TATTACCATTTCGTTTAAAT	GCTTCTCAATGTTTATGGG	GTAATACTTGCTGCAGTACAA ::: uAsnTyrLysIleGlnAsnLy	AATCAAGCTTTGCCAGTTGATTTACGTCACC ::: :: :::GluLeuIlePheTyrSer	ACAC	PheSerTyrLysIlePheIlePheGlnLeuLe

seq_name: SwissProt_38:GALU_PSEAE

TTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACAT

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alignment_block:
US-09-323-427-1 x GALU_PSEAE
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Quality:
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Percent Similarity:
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                                                                                                                                                                                 397
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                                                                                                                                                                                                                                                                                                                                                                                                                           300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHANG H., LEE C., PENG H.;
Submitted (DEC-1993) to the EM
-!- FUNCTION: MAY PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (
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Q59633;
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                                                     GTATT.....TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS
lyLeuGlyHisAlaIleLeuThrGlyArgProLeuIleGlyAspGluPro
                                                                                                                   sLeuLeuAspGluCysSerPheSerTyrThrArgGlnThrGlnMetLysG
                                                                                                                                                                           TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTG 446
                                                                                                                                                                                                                                                                                                     GGT...TGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACT
                                                                                                                                                                                                                                                                                                                                                          ysArgAlaLeuGluAspHisPheAspIleSer....TyrGluLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uAlaLeuAspAlaGlyLeuAsnGluIleSerIleValThrGlyArgGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAATTGAATGTGGACCAACTTCAATAACAATC...AATTTTAATACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: UTP + ALPHA-D-GLUCOSE 1-PHOSPHATE
                                                                                                                                                                                                                                      AsnGlnIleLysGlyThrAspLysGluLysTyrLeuValGlyIleArgLy
                                                                                                                                                                                                                                                                                                                                                                                                                     GTAATGCATTCGAAGGACATGTTATGTGAAAGGTCTTTATGATCAAGAA
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SIMILARITY: BELONGS TO THE PROKARYOTIC UDPGP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
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Kinase; Nucleotidyltransferase
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0.807
50.424
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NY A ROLE IN STATIONARY PHASE SURVIVAL
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12
20.763
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92233467.

PITT G.S., MILONA N., BORLEIS J., LIN K.C., REED R.R., DEVI
"Structurally distinct and stage-specific adenylyl cyclase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADENYLATE CYCLASE, AGGREGATION SPECIFIC (EC 4
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                              different roles in Dictyostelium development. Cell 69:305-315(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q03100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAA OR ACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYAA_DICDI
                                                                                                                                                                                                                                                                                                      -!- FUNCTION: COORDINATES CELL AGGREGATION BY SYNTHESIZING THE THAT INFLUENCES DIFFERENTIATION AND MORPHOGENESIS OF CELLS
                                                                                                  DEVELOPMENTAL STAGE: CELL AGGREGATION AND LATER DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                   ENZYME REGULATION: REGULATED BY A SURFACE RECEPTOR THROUGH A GUANINE NUCLEOTIDE BINDING PROTEIN. BOTH POSITIVELY AND NEGATIVELY REGULATED BY EXTRACELLULAR CAMP; THIS REGULATION
                                                                                                                                                                                                                                                              WITHIN A DEVELOPING MULTICELLULAR STRUCTURE. CATALYTIC ACTIVITY: ATP \sim 3^{\circ}, 5^{\circ}-CYCLIC AMP + PYROPHOSPHATE
                                                                                SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                             DURING AGGREGATION
                                                                                                                                                                                  PART OF THE MECHANISM THAT ESTABLISHES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ysvalile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspIlePheLysLeuIleGluGluThr.....GluProGlyLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leIleGlyArgTyrIleLeu.....ThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gAspMetValGluLysProAlaProGluAspAlaProSerAsnLeuAlaI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATGAAATTTTGGATGGT............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rgCysThrIleValAlaValMetGluValAsnProThrGluThrAsnLys
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EMBL

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    Ratio:
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US-09-323-427-1 x CYAA_DICDI
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EMBL; L05496; AAA33163.1; JOINED.
EMBL; L05497; AAA33163.1; JOINED.
EMBL; L05498; AAA33163.1; JOINED.
PIR; B42239; B42239.
HSSP; P26769; 1ABB.
DICTYDB; DD02024; ACAA.
PROSITE; PS00452; GUANYLATE_CYCLASES; 1.
PFAM; PF00211; quanylate_cyc; 2.
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                                                                                                                                                                                                                    841 IleLeuAspThrThrValAsnAsnAsnAsnAsnAsnAsnAsnThrAsnAs
903 rgValMetGlyIleLeuHisHisValLysIleSerAsnAspLysIleAsp 919
                                                                                                     148
                                                                                                                           874 luAspPheLysIleLysSerLysSerAsnSerSer.Phe...GluIleG1 889
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                        TCAAGTGGAGGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAAATCGA 147
                                                       CACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGT
                                                                                                     ATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACTA 197
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1169	рмет	1167
1104	AACTG	1055
16	:::::: ::: :::	1154
05	TGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTT	1005
1004 1153	CGAATGTGTTCGACCACAATGTTCAGAACCACACAGATTCGGACCTGTTA ::::::::::::::::::::::::::::::::::	955 1145
14	ThrIleSerValAsnLys	w
954	SCTTTTCTATCAATGCCAGATCAGTATTACCATTA	905
1138	<pre>LysLeuAlaMetArgLysAlaTrpValValAsnCysLysIleAsnPheLy</pre>	1122
904	ACGTATACAAATATGCGGATCGA	858
~ (alLeuLeuIleGlnIleCysSerSerTyrG	1110
1109	IeG1yPheVall1e	1104
07	TTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGAT	758
1104	SerProThrLeuThrA	1088
757	TCTGAAACCGTTGATACTTTCTGCGCGGTTGT	708
0	:::: erValLeuPheLeuAsnLeuPheIlePheSerPhePheIleIleCy	1071
707	AATTTGCTATCATTGGTCAGCCAGT	667
666 1071	CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGT	617 1056
1056	TATUTGAAATUACAACTGUTTTUAAACTCAAATTGTUCCGATG ::::::: ::: :: ::	1040
, ,	reneurenc Aswieser Akarc Asilit karrener	1020 1020
572	CATGGAAGCTGATAAAACAGTTAG :::: cTouTouCysaladhaClyValCy	523
522 1023	ATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGT ::: ::: :: :::: :: :::: :: :::: :: :::: :: ::::: :: :::: :: ::::: :: ::::: :: ::::: :: ::::: :: ::::: ::::::	473 1009
0	LeuValmetGlyIleAlaPheLeuValTyrIleC	996
472	TGAATCCACGTGGTATTTTTGTAACAACAACI	423
996		979
422	TCACTTCCATTTGATTCATGC	392
979	::: LeuValIleGlyLeuIleLeuHisLeuMetPheTyrL	967
391	CCGGAATT	365
966	ysTyrValIleIleAsnAsnValValGluThrLysPhePhe	953
364	ACATGTTTATGTGAAAGGTCTTTATGATCAAG <i>P</i>	315
LTI.	leTyrPhePheGluAsnLeuThrThrGluLysPhePheH	936
314	AATTTAATACACG	287
936	Lys GluIleIleGlnIleAspGluAspPheValLysValThrLysLeuAr	920

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Sequence

sp_invertebrate:093115 + 1653 50 2798.35

sp_invertebrate:018479 + 1313 50 2218.16

sp_invertebrate:098YWM7 + 725 50 1218.10

sp_invertebrate:0921808 + 654 50 1019.11

sp_invertebrate:021808 + 654 50 1019.11

sp_invertebrate:021808 + 655 00 1119.11

sp_invertebrate:021808 + 654 50 1099.14

sp_invertebrate:021503 + 595 00 993.33 4

sp_invertebrate:021504 + 546 50 912.73

sp_invertebrate:022164 + 546 50 912.73

sp_invertebrate:023097 + 477 50 794.02 6

sp_invertebrate:023097 + 477 50 794.02 6

sp_invertebrate:093937 + 479 50 780.30 1

sp_invertebrate:09586 + 453 50 750.30 1

sp_invertebrate:09586 + 453 50 750.30 1

sp_invertebrate:09586 + 401 50 667.08 1

sp_invertebrate:094677 + 361 00 687.08 1

sp_invertebrate:018314 + 344 00 687.08 1

sp_invertebrate:024328 + 357 50 589.67 1

sp_invertebrate:01834 + 357 50 589.67 1

sp_invertebrate:01834 + 158 00 248.44 1

sp_invertebrate:01834 + 158 00 248.44 1

sp_invertebrate:018117 + 139 50 209.10 8

sp_invertebrate:018117 + 139 50 209.10 8

sp_invertebrate:01828 + 139 50 209.10 8

sp_invertebrate:01828 + 139 50 188.07 0

sp_invertebrate:01828 + 139 50 188.07 0

sp_invertebrate:025802 + 119 50 178.71 0

sp_invertebrate:025802 + 119 50 178.71 0

sp_invertebrate:025802 + 119 50 169.65 0

sp_invertebrate:097286 + 119 50 178.75 0

sp_invertebrate:09736 + 118 00 162.47 0

sp_invertebrate:09736 + 118 00 175.56 0

sp_invertebrate:096468 + 119.50 179.55 0
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-MODEL=frame+.n2p.model -DEV=xlp
-O-/cgn2_/USEPT0_spool/USE9323427/runat_14042000_170514_19920/app_query.fasta.
-O-/cgn2_/USE9T0_spool/USE9323427/runat_14042000_170514_19920/app_query.fasta.
-DB-SPTREMBL_12 -QFMT=fastan -SUFFIX=backtrans.tspt
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPECL=0.000
-LOOPEXT=0.000 -GAPEXT=4.500 -VGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXX=7.000 -YGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXX=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELEOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=D10SUM02 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN-0 -MAXLEN-1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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Database length: 693
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           ! Documentation
                                                                                                                                                                   03115 ascaris lumbricoides (1019707 caenorhabditis elegans 1018479 meloidogyne artiellia (2018707 caenorhabditis elegans 1027575 brugia malayi. cuticli (2018705 brugia malayi. cuticli (2018705 brugia malayi. cuticli (2018705 brugia malayi. cuticli (2018705 caenorhabditis elegans (2019705 brugia pahangi. cut-1 (2019705 caenorhabditis elegans (2019705 brugia pahangi. cut-1 (2019706 caenorhabditis elegans (2019706 brugia pahangi. cut-1 (2019706 caenorhabditis elegans (2019706 caenorhabditis elegans (2019706 brugia pahangi. cut-1 (2019706 caenorhabditis elegans (2019706 brugia pahangi. cut-1 (2019706 caenorhabditis elegans (2019706 caenorhabditis elegans (2019707 caenorhabditis elegans (2019707 caenorhabditis elegans (2019707 caenorhabditis elegans (2018117 caenorhabditis elegans (201817) ca
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sp_invertebrate:077372
sp_invertebrate:097230
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SEQUENCE
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seq_name: sp_invertebrate:Q93115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-323-427-1 x Q93115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ascaris lumbricoides (common roundworm).
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-NOV-1998 (TrEMBLrel. 08, CUT-1-LIKE CUTICLIN PROTEIN
                                                                                                                                                                                                                                                                             320 GTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG
                                                                                                                                                                                                                                                                                                                           270 CAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACAT
                                                                                                                                                                                                                                                                                                                                                                                         220 GATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "cut-1-like genes of Ascaris lumbricoides.";
Gene 193:81-87(1997).
                                                                                                                                                                                                                                                                                                                                                                        16 alleProValAspAsnGlyValGluGlyGluProGluIleGluCysGlyP
                                                                                                                     gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG
                                                          GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                    MetCysArgAlaValSerPhe...LeuAlaLeuPheGlyLeuAlaAlaAl
                AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
                                                                                                                                                                                    yGlyArgGlnValAlaGlyIleSerLeuProPheAspSerCysAsnValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTC
                                                                                                                                                                                                                   TGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTG
                                                                                                                                                                                                                                              AlaTyrValLysGlyLeuTyrAspGlnGluGlyCysArgSerAspGluGl
                                                                                                                                                                                                                                                                roThrSerIleThrValAsnPheAsnThrArgAsnProPheGluGlyHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U73005; AAB66646.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1653.50
Ratio: 4.593
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92.784
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CUT-1-LIKE
BDEB1169
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Last annotation update)
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1 097272 plasmodium falcipar
1 077372 plasmodium falcipa
1 097230 plasmodium falcipa
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Q19707 PRELIMINARY;
Q19707 PRELIMINARY;
Q19707;
01-NOV-1996 (TrEMBLrel. 0:
01-NOV-1996 (TrEMBLrel. 0:
01-JAN-1999 (TrEMBLrel. 0:
F22B5.3 PROTEIN.
                                                                                                                                                                                                                                                                                        1214 AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAG 126:
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                                                                                                                                                                                  CAAATCAGAAGGCA 1327
                                                                                                                                                                                                              aValAlaLeuAlaAlaAlaValValValValSerPheLysLeuArgP
                                                                                                                                                                                                                                                                                                                                                              CACTTCTGCAACAT...AATGGACAACCTGTAATACTTGCTGCAGTACAA 121:
                                                                                                                                                                                                                                                                                                                                                                                                          TGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTG 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCT 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nPheAlaThrIleGlyGlnGlnValTyrHisLysTrpThrCysAspSerG
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                                                                                                                                                                                                                                                                        GluGlyIleCysMetSerProPheGlyPheSerIlePheMetGlyLeuAl
                                                                                                                                                                                                                                                                                                                                  GlyGlyAspTyrAspAsnThrLeuAspValArgThrAspPheSerAlaLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leAlaProLysLysGlnArgArgCysGlnLeuArgLeuIleLysLysSer 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA
                                                                                                                                                    roGlnGlnLysAla
                                                                                                                                                                                                                                                                                                                                                                                           uAspIleSerAspArgAspGluAlaLeuProMetAspLeuArgHisArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA
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                                                                                                                     sp_invertebrate:Q19707
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100,
               Last sequence update)
Last annotation update)
                                              Created)
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alignment_block:
US-09-323-427-1 x Q19707
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Ratio: 4.177
Percent Similarity: 85.974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: Q19707
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BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SULCTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANGHAN K., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
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SIMS M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
EMBL; 250044; CAA90355.1;
SEQUENCE 389 AA; 42983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
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                                                                                                                                                                                                                                                                                     79
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                                                                                                                                                                                                                                                                                                                                                        63 GluCysArgAsnAspGluGlyGlyArgGlnValAlaGlyIleGluLeuPr
                                  CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGA 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGA
                                                                                                                                        AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
                                                                                                                                                                                                                                  TTTTTGTAACAACTGTTGTTGTCATTTCGTTTCATCATTTTGTTACC 499
                                                                                                                                                                                                                                                                                                                                                                                                                        hrGlnValValProMetProIleCysLysTyrGluIleLeuAsnGlyGly
                                                                                       AACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAA 599
                                                                                                                                                                                                                                                                                                    ATTTGATTCATGCAATGTTGCGCGGTACACGATCTCTGAATCCACGTGGTA 449
                                                                                                                                                                                                                                                                                                                                                                         GGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCCGGAATTTCACTTCC
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                                                                     sThrValSerThrGlnIleGluValSerAspLeuThrThrAlaPheGlnT
                                                                                                                                                                                                                 alPheValThrThrThrValValValSerPheHisProGlnPheValThr
                                                                                                                                                                                                                                                                                   oPheAspThrCysAsnValAlaArgThrArgSerLeuAsnProLysGlyV
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94150718.
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Gaps: 8
Percent Identity: 69.610
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seq_documentation_block:
ID 018479;
AC 018479;
DT 01-JAN-1998 (TrEMBLre
DT 01-JON-1998 (TrEMBLre
DT 01-NOV-1998 (TrEMBLre
DT 01-MOV-1998 (TREMBLR)
CUTICLIN-1.
GN MTCUT-1.
OS Meloidogyne artiellia
OC Eukaryota; Metazoa; N
                                                                                                                                                                                          seq_name: sp_invertebrate:018479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTGATTTACGTCACCGTGCACTTCTG.....CAACATAATGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAlaGluLeuThrThrLeuGluValLeuGluGlyAsn....LeuPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTACTCAAGAAAAGATCTGCAGAA...CCGGAGAATATCATTGATGTA 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aValLysGlnAlaAsnGlnThrAlaGln........PhePheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATC
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                                                                                                                                                                                                                                                               AGAAG 1324
                                                                                                                                                                                                                                                                                                lAlaIlePheIleThrTyrMetIleValSerArgMetMetValProSerA
                                                                                                                                                                                                                                                                                                                                                                                                    AACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rgValLeuLysLysArgSerAlaProValMetGluAsnIleLeuAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt AsnGluGluCysAlaArgProThrCysSerGluProGlnGlyPheGlyAlangluc}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oThrAspLeuMetAlaGlyGlnGluAlaHisValTyrLysTyrAlaAspA
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   e artiellia.
Metazoa; Nematoda;
                                                                    3 (TrEMBLrel.
3 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                                         PRELIMINARY;
                                                                      05,
                                                                 Created)
Last sequence update)
Last annotation update)
   Secernentea; Diplogasteria;
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 Tylenchida;
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alignment_block:
US-09-323-427-1 x O18479
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MEDLINE; 97218031.

DE GIORGI C., DE LUCA F., DI VITO M., LAMBERTI F.;

PMODULATION OF expression at the level of splicing of cut-1 RNA infective second-stage juvenile of the plant parasitic nematode Meloidogyne artiellia.";

Mol. Genet. 253:589-598(1997).

EMBL; X96677; CAA65452.1; -.
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[1]
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                                                                                                                                                         TTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAA
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                              lyThrCysAspSerGluThrIleAspThrPheCysAlaValValHisSer
                                           GGACATGCGATTCTGAAACCGTTGATACTTTTCTGCGCGGGTTGTCCCATTCC
                                                                                                               CGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAAT
                                                                                                                                           ValValProMetProValCysLysTyrGluIleLeuGluGlyAlaAlaLe
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TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGA
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: 4.042
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                                                                                                                                                                                                                                  documentation_block:
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SEQUENCE FROM N.A. MEDLINE; 94150718.
BURTON J.;
"2.2 Mb of contiguous
                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
                                                                                                                            F53F1.1.
                                                                                                                                                                                                       Q9XVM7;
                                                                              Rhabditina; Rhabditoidea;
                                                                                                                                         F53F1.1 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAAAGATCTGCAGAACCG...GAGAATATCATTGATGTACGAACTGAT 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eArgHisHisHisLeuMetGluAsnLeuSerAlaGluProGlnArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGTCACCGTGCACTTCTGCAACATAAT.....GGACAACCTGTAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTT 1155
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                                                                                                                                                                                                                                                                                                 1His 417
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                                                                                                                                                                                                                      PRELIMINARY;
   nucleotide
                                                                            pda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                      PRT;
 sequence
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   from
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   chromosome
                                                                              Caenorhabditis.
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   of.
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alignment_block:
US-09-323-427-1 x Q9XVM7
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMOR B., O'CALLAGHAN M.,
PARSONS J., PECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATENSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
EMBL; Z81088; CABO3124.1;
SEQUENCE 364 AA; 40843
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACC
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                                                                                                  uArgGlnArgValLeuAsnProLysGlyLeuAlaValArgThrThrIleT
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PheGlyLeuTleGlyGlnGlnValTyrHisGlnTrpLysCysAspAsnAs
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LeuLeuCysLeuTyrArgGluSerGlnValThrValAlaAsnAsnIleSe
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                                    TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
                                                                                                                                                   TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA
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alignment_block:
US-09-323-427-1 x Q9XYU9
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Percent Similarity:
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01-NOV-1999 (
01-NOV-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.; "Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wuchereria bancrofti.
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Wuchereria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, CUTICULIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. RAMZY R., HELMY H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282
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                  872
                                                                                                                            772 TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA 821
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF125580; AAD28743.1; -.
NON_TER 1 1
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                                                                                                                                                                         1 ThrValAspThrPheCysAlaValValHisSerCysPheValAspAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGÄTGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCC
::::::||||||::::|||||||
SerAsnGlyCysSerIleAspLysPheLeuLeuSerAsnLeuGluTyrPr
                                                               ACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTTGTCGATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yAsnGlyAspLysValGluLeuLeuAsnAlaAspGlyCysAlaLeuAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTAAAACAGGT 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspGlnGluCysValArgProIleCysGluAspValGluGlyGlyGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oGlyAsnLeuLeuAlaGlyGlnGluAlaHisValTyrLysPheAlaAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isThrCysSerValAspAspGlyArgGlyGluThrSerPheLeuIleAsp
                  GAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG
                                                ysPheLeuLeuAsnAsnLeuGluTyrProThrAspLeuMetAlaGlyGln
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                     206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    695.00
4.064
86.364
                                                                                                                                                                                                                                                                                                                                                                                                                      22602 MW;
                                                                                                                                                                                                                                                                                                               Length: 198
Gaps: 4
Percent Identity: 69.192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     4DEE20D0 CRC32;
                                                                                                                                                                                                                                          206
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                  921
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alignment_block:
US-09-323-427-1 x 096775
                                                                                                                    alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: sp_invertebrate:096775
                              Align seg 1/1 to: 096775
                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1213
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, CUTICLIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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                                                                                                                                                                                                                                                                        "cut-1-like genes are present in the filarial nematodes Brugia pahangi and Brugia malayi and, as in other nematodes, code for components of the cuticle.";
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                                              Brugia malayi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096775
470 GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                                                                                                                                                         Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ012617; CAA10074.1; -.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
LEWIS E.K., HUNTER S.J., TETLEY L.,
                                                                                                                                                                                                                                                                                                                       DEVANEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACTTCTGCAACAT...AATGGACAACCTGTAATACTTGCTGCAGTACA 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGT... 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTG 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAlaHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerLeuLeuAlaHisGluAsnGlyHisProValIleValAlaThrMetTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sGlnIleSerIleThrIleLysGluProAsnSerLysCysGlnArgProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..TTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rGlnGlyIleCysMetSerIleThrGlyPheThrLeuAlaGlyMetLeuI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pValArgAspGluAsnIleValAspValArgThrAspLeuAsnAlaLeuA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spIleAsnGluGluPheThrSerLeuProAsnAlaLeuArgHisArgSer
                                                                                                                                                                                                127
127 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                AA;
                                                                                                      662.00
5.296
98.425
                                                                                                                                                                                                14119 MW;
                               from:
                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                3F738071 CRC32;
                              to:
                               127
                                                                                                                                                                                                                                                                                                                                    PAVIA NUNES C.,
                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
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570 AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCA 619

 ${\tt gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG}$

34

569

520

۲

VallleSerPheHisProLeuSerValThrLysValAspArgAlaTyrAr AGTACAATGCTTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG

17

US-09-323-427-1 x Q21808

17

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SOO
                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block:
Q21808 PRELIMINARY;
                                                                                                                                                  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SWITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATTERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              021808;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
                                                                                              Nature 368:32-38(1994).
EMBL; Z49207; CAA89068.1;
SEQUENCE 290 AA; 33215
                                                                                                                                            "2.2 Mb of contiguous nucleotide
elegans.";
                                                                                                                                                                                                                                                                                                                                MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                 Quality:
Ratio:
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    654.50
3.306
69.965
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                                                                                              MW;
Length: 283
Gaps: 8
Percent Identity: 45.230
                                                                                                                                                                                                                                                                                                                                                                                                                                        oda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                               441587FE CRC32;
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Align seg 1/1 to: Q21808 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 AATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCC
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                                                                                                               GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATTAAAGAACCAAATAGCGAA...TGTGTTCGACCACAATGTTCAGAAC 983
                                                                                                                                                                                                                                                                                                       {\tt ThrAlaIleAlaAlaHisIleGluTyrGlu.AspSerGluIleIleSerA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
snAlaPheLeuPheIleIleSerLeuValSerIleValHisValCys
                                   GCCAGTTGATTTACGTC.....ACCGTGCACTTCTGC 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnPhe.....AspMetArgIleSer....
                                                                                                                                                                                         AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 1093
                                                                                                                                                                                                                           {\tt spTyrIleIleProAsnAspAspIleIleSerLeuAsnTrpLeuGlnArg}
                                                                                                                                                                                                                                                            CysMetLeuValHisSerCysPheValAspAspGlyAsnGlyGlnArgVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTC
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                                                                                                                                                                                                                                                                                                                                          roProArgArgArgSerAsnThrLeuProAlaProAspAspAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt rValLysGluProGlyLeuAspTyrCysAspValProSerCysProAspP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnMetValTyrHisLysTrpThrCysAspThrGluHisGluAsnThrPhe
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seq_name: sp_invertebrate:Q21540

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I Sequence of the control of the con
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Quality:
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US-09-323-427-1 x Q21540
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Q21540;
Q1-NOV-1996
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BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.
BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LOVD C., MCMURAKY A., MORFIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SONNHAMMER E., STADUR R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VADUSIN M., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R142.2.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea;
Pelrina: Rhabditoidea; Rhabditidae; Pelr
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EMBL; Z73428; CAA97806.1; -.
PFAM; PF00092; vwa; 1.
PRINTS; PR00453; VWEFADOMAIN.
SEQUENCE 550 AA; 61445 MW;
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eans.":
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                                                                                                                                   GTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGT
                                                                                                                                                                                                     sTyrHisAspGluGluCysArgAlaGlyProGluLysPheProAspSerA
                                                                                                                                                                                                                                                                       TTATGATCAAGAAGGTTGCCGT.....AATGATGAAGGTGGAC
                                                                                                                                                                                                                                                                                                                                  LysAlaSerThrLysGlnProPheGluGlyAsnValPheValMetAspHi
                                                                                                                                                                                                                                                                                                                                                                                                       AATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCT
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ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT
                                                                 rgSerIle...GlyLeuThrValProPheSerAlaCysAsnValHisArg
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: Identity:
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seq_documentation_block:
ID Q19053
AC Q19053;
DT 01-ONV-1996 (TrEMBLrel 01)
DT 01-JAN-1998 (TrEMBLrel 05)
DE E04D5.3 PROTEIN.
GN E04D5.3 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemato
OC Rhabditina; Rhabditoidea;
RN [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: sp_invertebrate:Q19053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1010
                                                                                                                                                                                                                                                  Q19053;
01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1999 (TrEMBLrel. 09,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nPheGlnCysGlnIleThrLeuCysLeuLysTyrAspGlyGlyCysGluG
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oidea; Rhabditidae;
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                                                                                      Secernentea; Rhabditia; Rhabditida;
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                                                     Peloderinae;
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alignment_scores:
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Nature 368:32-38(1994).
EMBL; Z66496; CAA91280.1;
SEOUENCE 484 AA; 53325
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                                                          TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT
                                                                                                                         luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
TyrHisLysTrpThrCysValAlaGluLeuGluAsnValTyrCysMetLy 177
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                                                                                                                                                                                                                                                                                                                TCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                            GATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTT
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ID Q93532 PRELIMINARY;
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                                                                                                Align seg 1/1 to: Q93532
                                                                                                                                                                    US-09-323-427-1 \times Q93532
                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., AINSCOUGH R., AONDERL M., COPSEY T., COOPER J., COULSON A BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LICHTNING J., LLOYD C., MCMURRAY A., MORTLMORE B., O'CALLAGHAN M., PARSONS J., PECKY C., RITKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THORAS K., VAUDIN M., VANDEN M., VAUTEN M., VAUDIN M., VARTENSTON R., WILKINSON-SPROAT J., WOHLDMAN P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. Belegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
EMBL; 278542; CAB01742.1;
SEQUENCE 315 AA; 35785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-JAN-1999 (TrEMBLrel. 09,
                                   158 TCTTCTGAAATGATGATTCGTCTTATTGCTTTC.
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                                                                                                                                                                                                                                                                               Percent Identity:
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Last sequence update)
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                                                                                                                                                                                                                CTCACGTATACAAATATGCGGATCGA 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrSerProPheCysValThrValHisSerCysAsnValLysAspGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValLeuThrGluSerLysThr...GluGluValAlaPheAlaThrValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCACAACTGCTTTTCAAACTCAAATT...........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCCGGAATTT 392
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                                                                                                        erGlnValCysSerTrpThrValArg
sp_invertebrate:Q22164
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seq_documentation_block

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alignment_block:
US-09-323-427-1 x Q22164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMOR B., O'CALLAGHAN M.,
PARSONS J., PECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q22164
Q22164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
EMBL; 266565; CAA91480.1;
SEQUENCE 384 AA; 43964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Rhabditina; Rhabditoidea; Rhal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                            279 TAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                  229 TGACAATGGTGTCGAAGGTGAGCCAGAATTGAATGTGGACCAACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENNARD
                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LeuValGluPheThrTyrPheValLeuGlyPheSerAlaAlaIleGlnAs
                                                                                                                                                                                                                                                                                                                                                                  pAspAsnGluLeuIleGlyGlnProGluIleGlnCysAsnAlaAspThrI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTATTGCTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGT
                                                                                                                                                                                                                                                     AAAGGTCTTTATGATCAAGAAGGTTGCCGT.....AATGA
                                                                     snMetAspArgGlnArgMetIleAlaProGluGlyMetMetPheSerThr
                                                                                                                                                                  TGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCA 413
                pGlnPheGlyArgProValGlyGlyIleLySLeuAsnHisGlyAlaCysA
ValLeuIleIleSerPheHisProLeuPheLeuThrArgMetAspLysAl
                                                                                                         ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA 463
                                                                                                                                                                                                                   LysGlySerTyrAsnArgProGluCysArgValAspTyrSerThrLysAs
                                                                                                                                                                                                                                                                                        leAspMetGlnPheArgThrArgLysGlnPheAsnGlyLysValTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546.50
2.240
61.929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 394
Gaps: 9
Percent Identity: 31.218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9FFEFF44 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                       109
                                                                                                                                               93
                                                                                                                                                                                                                     76
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seq_documentation_block:
ID O2VVN2 PRELIMINARY;
AC Q9XVN2;
DT 01-NOV-1999 (TrEMBLrel.)
                                                                                                                                                                  seq_name: sp_invertebrate:Q9XVN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1102
Q9XVN2;
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                          1290 TTACCATTTCGTTTAAATTTCGTCCAAATCAG 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1002 TTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGT 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 heLysAspAlaAsnSerAsnGluLysGlnIleValLysArgAsnAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614 ATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 laIleAspValSerAsnLeuProThrGluSerValGlnSerAspLeuPro 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||:::::::|||:::||| ||||||| :::||||||:::|||
| aTyrHisIleArgCysMetTyrLysGluAlaAlaArgThrValThrAlaA 143
                                                                                                                                                                                                                            alValValTyrHisArgTyrCysLysAsnGlu 375
                                                                                                                                                                                                                                                                                                                                                    aValThrPhePheThrPheIlePheValLeuPheValThrThrIleLeuV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTT 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTG 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrPheLysProLysAspAlaAsp.....MetPheSerGlnThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAAC 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgPheGlnCysGluIleArgLeuCysLeuLysAsp...AspGlyGlyCy 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sThrAspArgLeuLeuGlyAspProThrTyrValGluAlaLeuAsnM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluAspGlyGlnGlyGluLysGlnMetIleIleAspGluArgGlyCysHi 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTA 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...LeuAspProGlnThrIleCysLeuAlaProLysLeuLeuValValAl 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGCAGTACAAAATGGAATCTGCATGTCACCA......TTTGG 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           luIleArgGlu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lTyrValMetAspLysGluAsnGlyAspSerThrSerAlaGlnAlaAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sAspGlyIleThrProProMetCysSer......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T.....GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etAlaTyrArgGluSerPheValPheLysPheAlaAspArgIleAlaVal 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTA...A 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spSerGlu.....AspTyrGlyLeuLeuValHisSerCysTyrVal 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eLeuLysTyrAlaLysValGlyAspGlnValValHisArgTrpGlnCysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetProThrCysSerTyrThrIleArgArgAspGlnLeuAspGlyProIl 176
         Created)
                                                                       610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312
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alignment_block:
US-09-323-427-1 x Q9XVN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU ZONNELL M., COPERY T., COOPER J., CULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., MCMURRAY A., MORTIMORE B., SUNDERS D., SHOWNKEEN I.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                       304 TGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTT 353
                                                                                                                                                                                                                                                                                                                         254 GAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 TTAGTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z81086; CAB03116.1; SEQUENCE. 610 AA; 68585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, F53B6.6 PROTEIN.
448 TATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 TCTTATT.....GCTTTCTGTACTACACTTATTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F53B6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "2.2 Mb of contiguous nucleotide sequence from
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 LeuArgPheGluSerValGlnPhe...LysAsnProProIleLeuLeuLe
                                                                                                                                                                                                              {\tt sProPheAsnGlyArgIleTyrValAspGlyGluSerAspLysGlnHisC}
                                                                                                                                                                                                                                                                                            GluValPheCysGlyIleAspThrIleArgValLysValAsnThrGluHi
                                        ProIleGlyAlaCysAsnMetArgArgGlnArgThrLeuHisProArgGl
                                                                                CCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGG 447
                                                                                                                            ysValGlnHisSerAlaAspAlaHisSerSerProGlnGluPheThrIle 132
                                                                                                                                                                      GC.....CGTAATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTT 397
                                                                                                                                                                                                                                                                                                                                                                                     euSerThrSerSerCysPheGluIleGlnAsnGlyValValGlyLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                           TGTCTTATTCG.....ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uLeuIleTyrAsnArgIlePheLeuGlnSerIleThrIleLeuIleLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513.50
2.593
66.443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 35.906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D793181D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610
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Sequence of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
Q23097 PRELIMINARY;
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SUNDERS D., SHOWNKEEN
SNALDON N., SMITH A., SONNIAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATESONS A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TIEMBLIEL 01, 01-NOV-1996 (TIEMBLIEL 01, 01-JAN-1999 (TIEMBLIEL 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1996)
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alignment_block:
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EMBL; Z71267; CAA95850.1;
SEQUENCE 387 AA; 43212
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aAspSerAsnGlnLeuTyrPheThrCysGlnIleArgLeuCysGlnLysG
                                   GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG
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                                                                                 AspAlaSerLeuMetArgAlaHisAlaSerSerGlnValPheLysTyrAl
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                                                                                                                                                                                                          ATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATAT
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                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPEY J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
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THIERRY-MIEG J., THOMAS K., VADUIN M., VAUGHAN K., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1171
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01-FEB-1997 (TrEMBLrel. 02,
01-NOV-1998 (TrEMBLrel. 08,
01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1071 CAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAA 1120
Submitted
                                                                                                                                                                                                          "2.2 Mb of contiguous nucleotide
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZK265.8 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307
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                                              LENNARD N
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCC 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA 1220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCATGTCACCATTTGGCTTCTCAATGTTTATG......GGTTTAAGC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ys \texttt{ArgGluAlaAspArgSerAspTyrGluIleAspValAlaThrSerGlu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lnMetGlyMetCysGlnGluValThrProProAsnCysGlyValLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCAAAT.....AGCGAATGTGTTCGACCACAATGT......
(JUL-1996) to
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the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AsnArgThrL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COULSON A.,
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alignment_block:
US-09-323-427-1 x Q93967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR
DR
SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 281143; CAB03520.1; EMBL; 275713; CAB03570.1; JEMBL; 275713; CAB00057.1; EMBL; 281143; CAB00057.1; SEQUENCE 440 AA; 49299 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAA 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LeuLysIleLeuIleIleAlaTrpThrGlyTrpArgValAlaAsnAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pValIleAspAspLysGlyCysProIleAspProIleLeuIleThrGlyI
                                                                                                         GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                      ATGCCAGTATGCCGTTATGAAATT......TTGGA 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                                          AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT
                                                                                     ValLeuIleAsnAsnCysTyrValThrAspGlyPheGlyLysLysAlaAs
                                                                                                                                                                     rgValLeuHisGlnTrpHisCysAsnAspGln.....MetTyrGly
                                                                                                                                                                                                                CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC
                                                                                                                                                                                                                                                             pAlaGlyArgProAlaGlyAsnValIleGlnPheAlaArgValGlyGluA
                                                                                                                                                                                                                                                                                                TGGTGGA....CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC
                                                                                                                                                                                                                                                                                                                                             IleProGlyCysThrTyrSerIleHisArgSerThrIleAspGluLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                  luLeuGlyValSerMetIleProThrThrGluLeuGluAlaArgHisGly 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aTyrHisValLysCysPhePheGluGluAlaAsnLysGlyLeuThrAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eSerIleAspAsnGluIleIleGlyGluProAspIleGluCysLeuGluA
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2.296
65.000
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MW; 3F2BBBA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 33.438
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  234
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                                                                                     217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613
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alignment_block:
US-09-323-427-1 x Q22680
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                                      Align seg 1/1
                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  documentation_block:
Q22680 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., EAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMUBRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
MATSON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1069 TGCAGAACCG 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               977
                                                                                                                                                                                                                                                    EMBL; Z49071; CAA88879.1; -. HSSP; P03000; lTIF. SEQUENCE 609 AA; 68882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T22C8.7 PROTEIN.
T22C8.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 GluGluGluLysAlaProSerSerArgArg.....LysThrTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sMetLysLys...HisGlyMetCysAspGlyIleThrProProSerCysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leArgTyrSerSerAspLeuGlnArgAlaTyrAlaGluSerSerValPhe
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GATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATT
                                                                                                                                                                           Quality:
                                                                                                                                                       Ratio:
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                                        022680
                                                                                                                                     453.50
2.399
65.854
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                                              snGlyCysGluGlyIleSerProProIleCysArgProMetAspLeuGly
                                                                                        ATAGC...GAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGA
                                                                                                                                       nValMetValHisPheSerCysGlnIleThrThrCysGlnLysGlnGluA
                                                                                                                                                                                        ATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAA
                                                                                                                                                                                                                                  AspLeuLysSerAlaPheThrAlaValArgAlaPheArgTyrAlaAspGl
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285 ProIleLys

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Minimum DB seq length: 0
Maximum DB seq length: 1000000
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1: gb_bal:*
2: gb_ba:*
2: gb_ba:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
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-1115.753 Million cell updates/sec
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gb_pr2: *
gb_pr3: *
gb_ro: *
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em_vi:*
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gb_in1:*
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45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1
CEF22B5/c
LOCUS
DEFINITION
ACCESSION
VERSION

CEF22B5 25823 bp DNA INV 02-SEP-1999 Caenorhabditis elegans cosmid F22B5, complete sequence. 250044 250044.1 GI:899234 E10ngation factor; GTP-binding ADP-ribosylation

ALIGNMENTS

KEYWORDS

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REFERENCE
AUTHORS
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The true left end of clone M05D6 is at 25723 in this sequence. The true right end of clone F14E5 is at 4610 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unambiguously on both strands, or on a single strand with both a dive primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IT INFORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small content of the specified clone. It may be shorter because we arrange for a small content of the specified clone. It may be shorter because we arrange for a small content of the specified clone.
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Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
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Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Miley, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Crulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Conner, R., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is not the entire insert of clone F22B5. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-JUL-1995) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94150718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R., Ainscough, R., Anderson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor; Phenylalanyl-tRNA synthetase; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end of this sequence (25723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         true
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            right end of clone F22B5 is at 16002 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              left end of clone F22B5 is at 24607
                                                                                                                                                                                                                                                   /note="similar to RNA binding protein; cDNA EST yk390d8. comes from this gene; cDNA EST yk499d6.3 comes from this
                                                                                                                                                                                                                                                         comes from this
                                     /protein_id="CAA90354.1"
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                                                                                                                                                                                                                                                                                                                                                     join(411. .462,584. .663,745. .1127,1216. .1471)
/gene="F22B5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F22B5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
/db_xref="SWISS-PROT:Q19706"
                                                                                                                                                  /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="F22B5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secernentea; Rhabditia; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .25823) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baynes, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mortimore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  small
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:Q19708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MSLSKAPRKTMFRFVLSRNASTSNVPSPARIQLKKPAEAGHFQY"
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                                /gene="F22B5
                                                                                                                                                                                                                                                                                                                                                             Joın(1870. .2158,2209. .2387,2534.
∕gene≖"F22B5.1"
                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                       /note="similar to GTP-binding
                                                                                                                                                                                                                                                                                                                                       ADP-ribosylation factor"
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from this gene; cDNA EST CEESX90RB comes from this gene; cDNA EST EMBL:T00412 comes from this gene; cDNA EST yk386c7.3 comes from this gene; cDNA EST yk504b12.3 comes from this gene; cDNA EST yk504b12.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk652b8.3 comes from this gene /gene="F22B5 note="similar to cuticulin; cDNA EST EMBL:T01970 comes .4393)) ; cDNA EST

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/translation="MaryStGLGICLLVASVSAIPVDNNVEGEPEVECGPTSITVNEN
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GGPTGEPVQFATIGQQVYHKWTCDSETVDTFCAVVHSCTVDDGNGDTVOILDENGCAL
DKFLLNNLEYPTDLMAGQEAHYYKYADRSQLFYQCQISITVKEPNEECARPTCSEPQG REIGEDSFRQELCISSFHISVVTVFLGLTVFVAIFITYMIVSRMMVPSDKMQSAC" /protein_id="CAA90355.1" /db_xref="GI:3876227" 'codon_start=1

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/note="cDNA EST yk304c8.3 comes yk304c8.5 comes from this gene; from this gene" /protein_id="CAA90356.1" /db_xref="GI:3876228" codon_start= comes from this gene; cDNA EST gene; cDNA EST yk594h3.3 comes

SRNWSRDPREVKVAIQKGDTPYQFLVRRLGHAYEVYPLFVLTAAWFVLFCSASYWSFG KAEIWLDRSNSKAPWDWERLRDTYWKMPTVAFDLDGRTRKRCELMEQLQDEMLEAAKK complement(10849. .12154)

complement(join(10849. .10984,11033. .11343,11397. .11521,
11578. .11832,11917. .12154)) /gene="F22B5 /gene="F22B5

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Matches 633;
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                                                                                                                                                                                                                              402
                                                                                                                                                                                                                                                                                                                                                                     CAGTAAACTTCAACACACGTAATGCCTTCGAGGGACACGTCTACGTTAAGGGACTTTTCG
                                                                                                                                                                                                                                                                                                                                                                                             caatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtctttatg
                                                                                                                                                                                                                                                                          ATCAACAAGAATGTAGAAATGACGAAGGAGGTCGTCAAGTCGCTGGAATCGAACTTCCAT
                                                                                                                                                                                                                                                                                                    atcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcacttccat 401
                                                                                        CAACTGTCGTCGTCTCTTTCCATCCCCAATTTGTCACCAAGGTTGATCGGTAAGACTATG
                                                                                                                TCGATACTTGCAACGTTGCTCGTACCAGATCTCTGAATCCAAAGGGAGTCTTCGTTACCA
                                                                                                                                                                                                      ttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtatttttgtaacaa
AAACTTCTGTAATTTTTAAGGAATGCTTCTTGAAGGTTTTAGGATACCGAAATTATAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Note-"limited similarity with the elongation factor EF-3 (Swiss Prot accession number P25997); CDNA EST EMBL:C12588 comes from this gene; cDNA EST yk49D7.5 comes from this gene; cDNA EST yk49D7.5 comes from this gene; cDNA EST yk420b2.5 comes from this gene; cDNA EST EMBL:M89075 comes from this gene; cDNA EST EMBL:D36040 comes from this gene; cDNA EST yk421d3.3 comes from this gene; cDNA EST yk421d3.5 comes from this gene; cDNA EST yk39b3.3 comes from this gene; cDNA EST yk39b3.5 comes from this gene; cDNA EST yk39b3.5 comes from this gene; cDNA EST yk39b3.5 comes from this gene; cDNA EST yk3595.5 comes from this gene; cDNA EST yk351a5.3 comes from this gene; cDNA EST yk351a5.3 comes from this gene; cDNA EST yk351a5.3 comes from this gene; cDNA EST yk3548b2.3 comes from this gene; cDNA EST yk348b2.3 comes from this gene; cDNA EST yk348b2.5 comes from this gene; cDNA EST yk351h3.3 comes from this gene; cDNA EST yk351h3.3 comes from this gene; cDNA EST yk351h3.5 comes from this gene; cDNA EST yk251h3.5 comes
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/gene="F22B5.6"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSNWDYLDEVDIIPKLPPNFDELRESKKWQERKEALEALLKVLI
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RQLDLVPAKQPKGFIKAVVPVFGKLTGDADQDVREASLQGLGAVQRIIGDKNVKNLL
GDASSDEGKMKKIGEYAEKSTASFAEEQAKNAPVAFTSSTESASASGDFSGGTATA
VVSSGAPVABADPWDELDAFDYLSKWDDGFDTNIESKKWQERKEALEGLLGLLTTANBE
LDPKANYGALVERLQKVLEKDANINVAALAANCITGIANGLRTKFQPFAVSVTPIIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15384. .21812

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join(15384. .15575,15622. .16479,16527. .17105,18608. .18694,

18794. .18946,18996. .19449,19497. .19843,20042. .20554,

20672. .21600,21677. .21812)

/gene="F2185.7"

/note="limited similarity with the elongation factor EF-3
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FKTHFTFTYYVYMNIAVYAGGLFYGYLLGHIVEIWFAKWSTIYSCROLGIOTYLTS
KSTGEEVRKLESAGCETAISSEFKNVFFDLLIQAVFIPLHILLTAFSWTFSGLYRPRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFKEKKPTLRDPLVACIDAVVATTNLEAVGEIVLAALGKPNPSIKTQTDLFLQRCFMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA90359.1"
/db_xref="GI:3876232"
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Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                     Cuticulin; Fork head
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3103 AGTTTTGGAAGGAAATGTAAGTTGTCAAAATGGTGTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3511 CAAATGGACCTGTGATTCTGAAACCGTTGATACTTTCTGCGCTGTCGTTCACTCTTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3571 TAACGGAGGACCAACTGGAGAACCAGTTCAATTCGCAACTATTGGACAACAAGTCTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agtacaatgcttttacatggaagctgataaaacagttagtgcacagattgaggtatctga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTGATGATGGAAATGGTGATACCGTGCAAATTTTTGGATGAGAACGGTTGTTGCTCTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aatcacaactgcttttcaaactcaaattgtcccgatgccagtatgccgttatgaaatttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGATCCGCTCCAGTAATGGAGAATATTCTTGATGTCCGTGCTGAGCTCACAACTTTGGA
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Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M., Bonfield,J., Burton,J., Conneall,M., Copsey,T., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Riiken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Maing,J., Thomas,K., Vaudin,M., Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Secernentea;
Rhabditina; Rhabditoidea; Rhabditidae; Pelo
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oderinae; Caenorhabditis.
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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections.
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IMPORTANT: This sequence is not the entire insert of clone C47G2.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-APR-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustfl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The true left end of clone T24F1 is at 34731 in this sequence. The true right end of clone T05B9 is at 12750 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neighbouring submissions. The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 34831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end of this sequence (34731. .34831) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to cuticulin; cDNA EST EMBL:C10444 comes from this gene; cDNA EST EMBL:C12078 comes from this gene; cDNA EST Yk262c12.3 comes from this gene; cDNA EST Yk265h3.5 comes from this gene; cDNA EST Yk265h3.5 comes from this gene; cDNA EST Yk278g8.3 comes from this gene; cDNA EST Yk278g8.5 comes from this gene; cDNA EST Yk278g8.5 comes from this gene; cDNA EST Yk439e8.5 comes from this gene; cDNA EST Yk439e8.5 comes from this gene; cDNA EST Yk439e8.5 comes from this gene; cDNA EST Yk583c11.3 comes from this gene; cDNA EST Yk580x11.5 comes from this gene; cDNA ES
                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT: Q03755"
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/translation="MTWKPIICLAALVLSASAIPVDNNVEGEPEVECGPNSITVNENT
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ISEHPQFVTKVDRAYRIQQCFYMESDKTVSTQIEVSDLTAFQTQVVPMPVCKYEILDG
GPSGQPIQFATIGQQVYHKWTCDSSDKTVSTQIEVSDLTAFQTQVVPMPVCKYEILDG
KFLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKDPGSECARPTCSEPQGF
GAVKQAGAGGAHAAAAPQAGVEEVQAAPVAAAAAPVAAAAAPAVPRATLAQLRL
                                                                                                         LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGICLTP
IGFASFLGIGTIVATALSATIFYVARPTSHKH"
15433 ...17108
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/gene="cut-1"
join(2562. .2679,2992. .3217,3898. .4636,4687. .4878)
/gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA88934.1"
/db_xref="GI:3875030"
                                                    /gene="C47G2.2"
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.15770,16205.
.16531,16772.
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/note-"similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:C13631 comes from this gene; cDNA EST SWIBL:C13631 comes from this gene; cDNA EST Yk358b10.3 comes from this gene; cDNA EST Yk30164.3 comes from this gene; cDNA EST Yk30164.5 comes from this gene; cDNA EST Yk30164.3 comes from this gene."
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/note="similar to fork head domain protein; cDNA EST
EMBL:T01618 comes from this gene; cDNA EST EMBL:D6805 comes from this
gene; from this gene; cDNA EST yk288f8.3 comes from this gene; cDNA EST
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yk288f8.5 comes from this gene; cDNA EST
yk288f8.5 comes from this gene; cDNA EST yk670a12.3 comes from this gene;
cDNA EST yk670a12.3 comes from this gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENSILFSAILLCRLTPPICLNFLGMIHMDSHISMAKSFGIETQFTKLMGHLDVIPILA
KGINIYLPICIILLCAIHYYRVGAYVLHNIGFDQFVEADEMTNDMINSGRSLVQIERN
SIKRSNDRSQRTQNWTNSFGSSNAGNGSTTSKFKRSNKNDEERPMLEDDDEEVEESST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIEKLASEKSEAEENVKDIYKKVRVLFNSMKNDSNGQRRKVRTILSKFSDDVIDNLFP
SRQVIDNAHLDESGPCSEAKLISLHKKTIYAVGTLNNATAQMKVLVDRALFLEBNLAFS
ESNGVIDNAHLDESGPCSEAKLISLHKKTIYAVGTTUNNATAQMKVLVDRALFLEBNLAFS
ESNGVNLELSRNTCVPIGVRREWYTRALOFPFCRILGIYVPMTFEVLLFSECTTFFVVS
TLSPAAFVTEYASTRFHYKYTQFVAFGIIVYLITSAYFTIFRLQIYKYYHLDPNGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(24417. .24975,25043. .25176,25237. .2552
25668. .25907,25967. .26054,26106. .26227,26277. .26608,
26681. .26785,26846. .26914))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(24417. .26914)
/gene="C47G2.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(30076. .30134,30184. .30492,31050. .31274,31321. .3
31534. .31653,31701. .31835,31889. .32104,32160. .32570,
32639. .32935,32998. .33215,33263. .33651,33802. .34049)
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RVVYWSAQLLTWLILPLLQSYVTAGNFTILGKIRAAVINNALYYAIYSLCFLAILIYA
MFKGVSINIENLKVIVVSASNTWGLFLLVVLLGHGLVELPRSLWHHGNRHYRLRKTYF
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MPAFFIPQNIDSQKLLSMMASRIMPMDAPVSSGQKRTSSSSSPNENGSSAVSDKLSA"
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                                                      TDLPMKQQYRLSFIASEILTIRGTDVFQKQIVTTEETRKCLVDFLNDKTPLNHLVAGF
                                                                                                            ENSLMRLLKTONFTLEDVLLNEFVVQESRYGKAELVQYITSRENMKALLELSLNPKIN
                                                                                                                                                             IAQESASEAVTDGRSSDEDSHTARRSLCYHRSRKSMPAKKLSKMFTSIFQMFWAKEEE
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FEYYKEKFPAWQNSIRHNLSLNDCFVKVARGPGNPGKGNYWALDPNCEDMFDNGSFLR
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PSTSASVLEHDLKFGESRKRSRSLGDEPTEDEDGVPVRKANKRNHSTSSAADSSSDDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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SOURCE
ORGANISM
                                                                                                                     ACCESSION
VERSION
REFERENCE
AUTHORS
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Best Local Similarity 74.2
Conservative
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                                                                                                                                                                                                                                                                                                                                                           ttcagaaccacaaggattcggagctgttaaaacaggtggtgccgcagcaaaacctgctgc 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCATCGGACAACAAGTCTATCACAAATGGACTTGCGATTCTGAGACCACCTGACACCTT 4122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCACACAGATCGAAGTCTCGGATCTCACCACTGCCTTCCAGACCCAGGTCGTACCAAT 4002
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                                                                                                                                                                                                                                                                    CGCTGCTCCAC 4433
                                                                                                                                                                                                                                                                                                                                                                                                                              tcaatgccagatcagtattaccattaaaggaaccaaaatagcgaatgtgttcgaccacaatg
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                                                                                                                                                                                                                                                                                                                                      CTCAGAGCCACAAGGATTCGGAGCCGTCAAACAAGCTGGTGCCGGAGGAGCTCATGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                             TCAATGCCAAATCTCCATCACCATCAAGGACCCAGGAAGCGAATGTGCCCGTCCAACTTG
                                                                                                                                       CELCUT1
C.elegan
M55997
                             cuticle protein; cuticlin 1.
C.elegans DNA.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Ca
                                                                                                                      M55997.1 GI:156271
                                                                                                                                                        elegans cuticlin
(bases 1 to 2310)
bastano,M., Lassar
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MDETLLAKIADNLIVEEGCPARELVKKSALISASAKILEAFIKUTVSNAPAQQLEEI
ERNLIEERHYSYGLMRPCMDNDPYEHSYQDPERIVEGILANRLPNILQTVLRDIEAN
GSVWQPLLRLIIELGWINCMSTHEKIAVAFRSLPFINLIKAAKMLPRASVLHCLLVKV
VILLLHSSFPCDELSPAAEYLLTEGGILONIYDTATSPNPGSSVACSGLRSFNONLGD
AINRAKKAGIPNQKLLAILSADNTWTELEDIIHLYNLKHRPQWDDFNDSSVYSSIRN
DSHGFNDSEWTDASTKPAEMJATSSAKQAFEGFSSPFEPMQRFSDFEGDEDDFDE
DEFRKLCSERANSSSCAGISFETSPIKWPGEAEKTSEKASEPBSVAASTYPQQTNGNQ
AFLEQEEGDGEWWPTVPPLGFTEVVTQTGHRPENNWVDETAPDFSHLDMAPPKEDDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WADFSSFPTISPTAAANSASSSSSDAWPGSDIHLQGEASDWPLNNSHESKASDPVMVG
LAASISHPGDSSEA"
, 6786 c 6432 g 11024 t
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74.2%;
Lassandro, F.
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1
                                                                                                                                                        (cut-1)
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Pred. No. 2.1e-46;
0; Mismatches 142
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                                               GGAGGACCATCCGGACAACCAATCCAGTTCGCCACCATCGGACAACAAGTCTATCACAAA
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/protein_id="AAA27995.1"
/protein_id="AAA27995.1"
/db_xref="G1:156272"
/translation="RLPYPCFYMESDKTVSTQIEVSDLTTAFQTQVVPMPVCKYEILD
GPSGQPIQFXTIGQQVYHKMTCDSETDTFCAVVHSCTVDDGNGDTYQILNEEGCAL
DKFLLNNLEYPTDLMAGQEAHVYKYADRSDTDTFCAVVPGQQISTTIKDPGSECARPTCSEPQG
EGAVKQAGAGGAHAAAAPQAGVEEVQAAPVGAAPVAAPAVAAAAPAVPRATLAQLLL
LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGISSTP
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 ccgcagcaaaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaac 1076
                                                                                                                                                                                                                                                aaaccgttgatactttctgcgcggttgtccattcctgcttgttcgatgatggtaacggtg 779
                                           gtgttcgaccacaatgttcagaaccacaaggattcggagctgttaaaaccagg---tggtg 1016
                                                                                           gatcacagcttttctatcaatgccagatcagtattaccattaaagaaccaaaatagcgaat 959
                                                                                                                               TAGAATATCCAACAGATTTAATGGCTGGACAAGAAGCACGTATACAAATACGCTGATC 180
                                                                                                                                              tggaatatccaacagatttaatggctggccaagaagctcacgtatacaaatatgcggatc 899
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Submitted (03-FEB-1999) Research & Training Center on Viseases, Ain Shams University, Abassia Square, Cairo,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Filarioidea; Onchocercidae; W 1 (bases 1 to 724) Ramzy,R., Helmy,H., Adely,M.,
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
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Wuchereria bancrofti
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Ramzy,R., Helmy,H., Adely,M., Curtis,K. and
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AF125580.1
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ASRQAAAFRVLKKDVBDENIVDVRTDLNALDINBEFTSLPNALRHRSSLLAHENGHP
VIVARMTQGIOMSITGETLAGKLIFUTVSVATIVAITLLRSHSTKV"
112 c 128 g 236 t
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/db_xref="taxon:6293"
/dev_stage="L3 larvae"
                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cuticulin-1"
/protein_id="AAD28743.1"
/db_xref="GI:4741875"
/translation="TVDTFCAVVHSCFVDDGNGDKVELLNADGCALDKFLLNNLEYPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to Ascaris
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Pred. No. 6.4e-36;
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Timinouni,M. and Bazzicalupo,P.
cut-1-like genes of Ascaris lumbricoides
Gene 193 (1), 81-87 (1997)
97390131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U73005
U73005.1
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Timinouni, M. and Bazzicalupo, P.
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Ascaris lumbricoides CUT-1-like
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                                                                                                                                                                                                                                    /product="CUT-1-like
766. .5081
                                    /gene="ascut-1"
/note="cuticlin gene; ASCUT-1;
proteins of other nematodes"
                                                                                                                                        882. .929
                                                                                                                                                                                               /gene="ascut-1"
766
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                  /codon_start=]
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                                                                                                                  /gene="ascut-1"
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                                                                                                                                                                                                                                                                                                             /gene="ascut-1"
                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:6252"
                                                                                                                                                                                                                                                                                                                                                                            /variety="suum"
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Ascaris lumbricoides'
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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cuticlin
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precursor"
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Best Local Sim
Matches 352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACTATCACCATAAAAGAGCCAAACAGCGAATGCCCCCAGACCCCACTTGCAGTGAGCCGCA 3935
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                                                                                                                                                                                                                                                                             tatcaacacccttgaaattagcgat 1129
                                                                                                                                                                                                                                                                                                                                                       aggatteggagetgttaaaacaggtggtgee---gcagcaaaacetgetgeagetgegea 1044
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                                                                                                                                                                                                                                                              CTTCAGCGCCCTCGACATTAGTGAT 4080
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                                                                                                                                                                                                                                                                                                                                  ACTCCGCCTGATCAAAAAGAGTGGGGGTGACTATGACAACACCCTTGATGTACGCACCGA 4055
M.artiellia Mtcut-1 gene.

M.artiellia Mtcut-1 gene.

M.96677

X96677.1 GI:2648040

cuticle protein; cuticlin 1; Mtcut-1 gene.

Meloidogyne artiellia.

Meloidogyne artiellia.

Meloidogyne artiellia.

Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria;

Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;

Meloidogyninae; Meloidogyne.
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5064. .5070
/gene="ascut-1"
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FFEGHAYVKGLYDQEGCRSDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVIS
FHPLFITKVDRAVRVQCFYMEADKTVSTG1EVSEITTAACTQTYMPVCRYEELLDGGP
TGQPIQFATIGQQVYHKWTCDSETVDTFCAVVHSCFVDDGSGDTIQILNEEGGALDKY
LLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQITITIKEPNSECPREFCSEPQGFGA
VRPGGSIAPKKQRRCQLRLIKKSGGDYDNTLDVRTDFSALDISDRDEALPMDLRHRAR
HARGQQYILSPANEGICMSPFGFSIFMCLAVALAAAVVVVVSEKLRPQQKA"
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/gene="ascut-1"
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69.7%;
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                           ttatgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcact 396
                                                                                                                                                 aataacaatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtct 336
                                                                                                                                                                                                                                       TGCAATTCCAGTGGACAACGGTGTGGAAGGCCAGAGCCAGAGATTGAATGTGGCCCAACCTC 588
                                                                                                                                                                                                                                                                      ttcgattccggttgacaatggtgtcgaaggtgagccagaaattgaatgtggaccaacttc 276
CTTTGACCAGGCCGGATGCCGTTCGGATGAGCACGGCCGACAAGTGGCGGGAATTGAGCT
                                                                                                                     AATCACCGTCAATTTCAACACACGCAACCCTTTCGAGGGGCACGTCTATGTGAAAGGCCT 648
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De Giorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
Modulation of expression at the level of splicing of cut-1 RNA in
the infective second-stage juvenile of the plant parasitic nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2584)
De Giorgi,C.
Direct Submission
Submitted (15-MAR-1996) C. De Gio
Biologia Molecolare, Via Orabona
2 (bases 1 to 2584)
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join(<467. .943,1139.
jene="Mtcut-1"
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/db_xref="taxon:42426"
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Brugia malayi cut-1 gen
AJ012617
AJ012617.1 GI:3858954
cut-1 gene; cuticlin.
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Brugia malayi
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Filarioidea; Onchocercidae; Brugia.
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Submitted (06-NOV-1998)
University of Glasgow, F
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/translation="Visyhpleytkvdrayrvocfymeadktvstgievseittafgt
QIVPMPVCRYEILDGGPTGQPIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
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/db_xref="GI:3858955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cut-1-like genes are present in the filarial nematodes,
pahangi and Brugia malayi, and, as in other nematodes,
components of the cuticle
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-NOV-1998) Devancy E., Veterinary Parasitology, University of Glasgow, Bearsden Road, Glasgow, G61 1QH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Filarioidea; Onchocercidae; Brugia.

1 (bases 1 to 358)
Lewis, E., Hunter, S.J., Tetley, L., Nunes, C.P., Bazzicalupo, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brugia pahangi cut-1 go
AJ012618
AJ012618.1 GI:3858956
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18
                                                                                                                 /gene="cut-1"
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a 64 c
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350. .356
                                                                                                                                                                               /gene="cut-1"
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/db_xref="GI:3970656"
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/gene="cut-1"
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/gene="cut-1"
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                                                                                                                                                                                                                     translation="PIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEI"
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87.7%;
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                                                  Score 156.6; DB 3 Pred. No. 1.1e-17;
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                                                                                                                                                          sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone F53F1. The true right end of clone M04G12 is at 21759 in this sequence. The start of this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-007-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wust1.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For a graphical representation of this sequence and its analysis
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                                                                                                           uence (1..101) overlaps with the end of sequence 281103. end of this sequence (39379..39478) overlaps with the start of
                                                                                         AL021448
/organism="Caenorhabditis
                                                        Location/Qualifiers
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/db_xref="taxon:6239" /chromosome="V"

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                                                                            /Note="predicted using Genefinder; similar to cuticlin; cDNA EST EMBL:D72018 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C12451 comes from this gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST EMBL:C10682 comes from this gene; cDNA EST yk306b3.3 comes from this gene; cDNA EST yk319-5 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h5 Comes from this gene; cDNA EST yk311h5 Comes from this gene; cDNA EST yk300g2.3 comes from this gene; cDNA EST yk3016-3 comes from this gene; cDNA EST yk30103-3 comes from this gene; cDNA EST yk30103-5 comes from this gene; cDNA EST yk10103-5 comes from this gene; cDNA EST yk10
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MYLIHYPKSFDYGDQDPMNKTLRIATWNDLWECKNAGKIRSVGVSSFEIRHLEELKDL
GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEIITRLAEK
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18339. 18524)
18339. 18524)
/gene="F53F1.2"
/note="similar to aldehyde reductase; cDNA EST yk473d8.3
/note="mailto aldehyde reductase; cDNA EST yk473d8.5
comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKNSFLTFFKSPYMYVVGITNYHNKAIQKL"
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/db_xref="GI:3877456"
/db_xref="GI:3877456"
/translation="MonKEIRRTLEDYFPKGFLISESSKYDCHLEDMHLVLQLLLATL
AVNPVPIQNSLYGDVQVECDSRTISVQIKTEKPFVGVIFVKDFASEEVCTSRGTGRLS
AFLEIEIGLCGALRQRVLNPKGLAVRTITISSHPYFITKVDRFYNLLCLYRESQVTV
AFLEIEIGLCGALRQRVLNPKGLAVRTITISSHPYFITKVDRFYNLLCLYRESQVTV
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16033. .16271,16318. .16486))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="cAB03128.1"
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/db_xref="SPTREMBL:P91998"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(18714. .18887,18935. .19056,19113. .19302,19353.
19919. .20008,20072. .20251)
/gene="F53F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F53F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKFADRDALFFQCQISITVKEPDQECVRPICEDVEGGGAPVVGPPPYGMISKNLVNIW
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/protein_id="CAB03125.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(21582. .21670,21781. .22009)
/gene="F53F1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHVPKTTVLLSWATSQKVGIIPKSTNPERLAQNLKTVLLEEEEVKKICNLNLDKHYVR
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/db_xref="GI:3877459"
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                                                  codon_start=]
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GRK*
25572...25660,25850...26408)

//gene="FSSF1.5"

//form this gene: chan seri semilar to cutticlin:
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comes from this gene: chan seri semilar to cutticlin:
comes from this gene: chan seri semilar to cutticlin:
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                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both dye primer and dye terminator reaction, from distinct subclones. Bxceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (25-OCT-1995) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
                                               IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                             predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                       bin/display?db=wormace&class=Sequence &object=E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McMurray,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; Cuticlin-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266496.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEE04D5
                                                                                                                                                                                                                                                                                     http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 31536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 31536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                  graphical representation of this sequence and its analysis
                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:1041307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31536 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.7%;
neighbouring submissions. sequence is not the entir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.5e-09;
0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmid E04D5, complete sequence.
  entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis.
  clone E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15231
                                                                                                                                                                               ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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sequence Z48585.

The true left end of clone ZK673 is at 31437 in this sequence. The true right end of clone T09F3 is at 11412 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions. The true left end of clone {\tt EO4D5} is right end of clone {\tt EO4D5} is at 2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It may be shorter because we only sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: Cl11194 comes from this gene; cDNA EST pkBL:Cl1213:

comes from this gene; cDNA EST EMBL:Cl1811:

gene; cDNA EST yk412d7.3 comes from this gene; cDNA EST yk49b6.3 comes from this gene; cDNA EST yk454b6.3 comes from this gene; cDNA EST yk454b6.3 comes from this gene; cDNA EST yk454b1.3 comes from this gene; cDNA EST yk454b1.3 comes from this gene; cDNA EST yk45b1.1 comes from this gene; cDNA EST yk413f5.5 comes from this gene; cDNA EST yk402d12.5 comes from this gene; cDNA EST yk402d12.5 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk374f8.3 comes from this gene; cDNA EST yk374f8.3 comes from this gene; cDNA EST yk356e8.3 comes from this gene; cDNA EST yk365e8.5 comes from this gene; cDNA EST yk365e8.5 comes from this gene; cDNA EST yk356f12.3 comes from this gene; cDNA EST yk358f12.3 comes from this gene; cDNA EST yk558f12.3 comes from this gene; cDNA EST yk558f12.3 comes from this gene; cDNA EST yk558f12.3 comes from this gene; cDNA EST yk656f12.3 comes f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or longer because we arrange for a small overlap
                                                                                                                                                                                                                                                                             /db_xref="Sptrembl:Q19052"
/tianslation="mpapnttpsrdsnefvisssfsnefllpekfktesferlsqtli/translation="mpapnttpsrdsnefvisssfsnefuldekcekfktesferlsqtli
QINKMGDNLVYAVRSSGESFYLKRGLGKDAVTVEQNKTSRDVACNVFAYSNNGQLFAY
CDNQVTRVFELATNKEILCVELKRTRKILFSPKDNFLLTFEPMAVYGPKTAENQKPEP
NVRVYSLADGKHVSTFSAPKEASWEPQFSDDESLAARMVGSEVFFYTMNSFDKTDHKL
VEKGATNFALSPGPAPNHVAVYVPAVGSTPARVRHVRVSEPVGNTFFFKDKAVM
TWNQRGQSLLILASVEVDKTNQSYYGEQSLYLINIQSGESVVVPLEKKGPIYAAKWNP
NGREFAVCYGYMPAKVTFYNPRGVPIFDTIEGPRNDVFYNAFGNIVLICGFGNIAKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z48585
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complement(8619. .11718)
/gene="E04D5.2"
                                                                                        EQERKAFQLKKKVEETKVLKQRVANGDQLQPNQMEKIQRENEYLSELSKLTI"
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ETHFESPKELWEVRWRPMTGYNKFAIKELTKTDKMAAGLPIRKKDASHPLNNVPAGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA91279.1"
/db_xref="GI:3875451"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                         RQAGAYIPPHLRKPLGGGSAGPPSAAAPTPGNQNQRPAQPRANGNGNAPQPFRPQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="E04D5.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'clone="E04D5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence (31437. .31536) overlaps with the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at 1 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence. The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sections
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complement(join(8619: .8761,8813. .8988,9895. .10028,
10089. .10283,10330. .10614,10730. .10935,11582. .11629,
11691. .11718))

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tggaccaaccggtcaaccagttcaatttgctatcattggtcagccagtttatcataaatg 705
agaaccaaatagcgaatgt
                                                    CTTCAAATTTGCTGACAAAGCTGGGCTTTATTTCAATTGTCAAATTCAATTAACAATCAA
                                                                                                 atacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccattaa 942
                                                                                                                                                                                        tgatggtaacggtgatactgtggaaattctaa---atgctgatggatgtgctcttgataa 822
                                                                                                                                                                                                                                                                                                                                                               GACTTGCGTTGCTGAACTTGAGAATGTGTACTGTATGAAAGTTCACTCATGTACGGTTTA 27902
                                                                                                                                                                                                                                                                                                                                                                                                         gacatgcgattctgaaaccgttgatactttctgcgcggttgtccattcctgctttgtcga 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAAGCCGGTGGATCACCTATTAAGTACGCTCGAATCGGAGATCAAGTCTATCACAAATG 27842
                                                                                                                                                                                                                                                          TGATGGACAAGGTGGACCACCAGTAACTGTCATTGATGCCAATGGATGTTCTGTAGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHKWTCVAELENVYCMKVHSCTVYDGQGGPPVTVIDANGCSVDGVILQNLEYTSDLTA
GKLAPVFKFADKAGLYFNCQIQLTIKDVNYGCSNTQPQCPTSQYVVEPAQKTTETAEP
YPYDSHESGYPTRPANYPVASSRYPIPTTQAPASYPSSPAPPPBGADIDNGYPEPQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mmsinltvhiillvtfsvshvvttavtkatgettvrgagqdlgdvsssefyetttastcaddpntdctqytflcsnakytpllqqfcaktcgfcgsgstaap
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vsepscmtvgdgktghrfevrhdscgvrgreingvvisatviisfhsifitkidray
RVSCfyvegtkkvhnhvdisalttqllesetqlpvcrveilneaggspikyarigdqv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VACVDTSTQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA91281.1"
/db_xref="GI:3875453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LILLCLLFATTVVVFIVIVQKQRQILAQTAFFKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIAETPENAYDGIVGFNDTEQPFTTSAAYTEDGVYSRLİKRNVVESTEQINASNKKRP
VTVGDIDLPERGILVFGLEEMEDGETTNAGDHGATRALREARNSQEKTCFSTSRMYFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA91280.1"
/db_xref="GI:3875452"
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join(25834. .25873,27277. .27512,27582. .27721,27768. .28110,
28158. .28410,28491. .28811,29092. .29213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDFHVITAIQMMFPFVVLLLLNLTIIKRLVAEKRENMYPILRGAGTTTEVKKASFVQG
NLPENYVLLQVAADVIKESLIHRSSRSKRSQLRNAIYTMLAIVTSYLVCNGVHLFLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MEGENLFYADIHSTIPFKCEKLKIRVFLSENAQKHLFGFFLKYPINFQLLMAVERSLPSSIFLATLATCOMLICLTYTLLFGVDAGLWAKKNTTLFFLYHRYIVFLKYPLTLLSFLXHRYITLFFLYHRYINFLKYBGITFQVLTLSLSFRKAFSAL
YIVPVFF1AKVVQPA1PFILILITFBRYLMYGTPFRKRBGITFQVLTLSLSFRKAFSAL
FNERGRIVTVIFVCFFSVAIRIPVLYAMKVKTFPLCDDYFRSESLDGTPFAATEAYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA91282.1"
/db_xref="GI:3875454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="E04D5.4".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q19053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="E04D5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKREKSIETNSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LERFDPSYLYESTDRMQSSTFYIVLSDTVSICYMASSAIRTFIYAKCNPKLRQEITDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="E04D5.2"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oin(29675. .29840,31127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="similar to cuticlin like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q19055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="SPTREMBL:Q19054"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="E04D5.4"
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56.1%;
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TITLE
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BASE COUNT ORIGIN

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bin/display?db=wormacesclass=Sequence &object=F53B6 Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence Z81523.

The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F53B6.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small content of the second section.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu computer analysis, Coding sequences below are predicted from computer analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M., Johnston,L., Jones,M., Kershav,J., Kirsten,J., Laister,N., Mortimore,B., O'Callaghan,M., Parsons,J., Lloyd,C., Rikken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry,Mieg,J., Thomas,K., Vaudin,M., Vandan,R., Sulston,J., Thierry,Mieg,J., Thierry,Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neighbouring submissions.
The true left end of clone F53B6 is right end of clone F53B6 is at 5116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368 (6466), 32-38 (1994) 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chron
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence Z81523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; Cuticulin; Human platelet tetraspan antigen like; Initiation factor associated protein; Thrombospondin like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end of this sequence (32306.
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                                           /chromosome="I"
/clone="F53B6"
1480.
                                                                                                                                                                             /db_xref="taxon:6239"
                                                                                                                                                                                                                                     /organism≖"Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:1627952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .32412) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at 1 in this sequence. The true in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome III of C.
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CDS

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complement(join(4270. .4339,4493. .4547,5071. .5295,
5368. .5662,5891. .6148.6204. .6752,6818. .7287,7546. .7676,
8104. .1844,12576. .12775,13246. .13384,13931. .14132,
14183. .14294,14341. .14457,14994. .15155,15198. .15311))
//gene="F5386.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKFIKKVSEYTACASNCDDIYDMSGARSIASTSQFIVVCVNAITGRVVPEKLCADK
LRPKVEARPCPHLICPSRWAAADWIECVBCCGCFIRKEVYCCYGAHNVTVHVPDTFC
ENGTRPAAEENCVSTSGGRWEAAKWSKCTASGGGVRRRHVACVGGSDCDEGGRPQ
ETCYAGIFCSIATNSLDWNDRAYLDGNTFGSMDNHNDWQAPRLVAGEWSTCSSTCGTG
VMSRTVECVAVWPISSAPIKLEMSECQDOEQFKLFESCEVRSCCPLQEDSKLSEDEAPY
OWRYGDWTQCSASCLGGKOKAALKCIQVSTGKSVOWSQCDARRRPPEKSRPCNOHPC
PFWLTSKYSDCSMSGGSGTARRSVKCAQTVSKTDGADAHIVLRDDRCHFKKPQETETC
NVVACPATWVSSLNKRHKIKIKNKKITKAQWTECSRCOSGERRACVWCCIRDSGKSTCGT
RYDACPATWVSSLNKRHKIKIKNKKITKADAHIKVSANGNLRVFHARMEDAGVYECFTDR
SIKIKCPAKKFDKKITYWKKNOKKITKNDAHIKVSANGNLRVFHARMEDAGVYECFTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="predicted using Genefinder; similar to thrombospondin like; cDNA EST EMBL:Z14404 comes from this gene; cDNA EST EMBL:C12571 comes from this gene; cDNA EST yk1950-3 comes from this gene; cDNA EST yk1950-3 comes from this gene; cDNA EST yk28697.3 comes from this gene; cDNA EST yk28697.3 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk353hl.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4270. .15311)
/gene="F53B6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKSAIGEEGRKKNQLLKRDFSKLANPLSEFSLYREQPDTQFLKNRKIKNVDQQDSRLFSLLEKYIFHSLSINLTIYLKALHFQTRVFPFKSFPHFNTLKFTFQKMGALGDSAYGARGRLIKFSYIVTALISILFSISCICYGIWLLARBSQYAELVSPS
                                                                                                                                                            /note="predicted using Genefinder; cDNA EST yk193h3.3 comes from this gene; cDNA EST yk193h3.5 comes from tis gene; cDNA EST yk411f5.3 comes from this gene; cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(19892. .20022,20241.
/gene="F53B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEIRNUDNSICESLASYRPPERPCHREDCPRWEASQWSECSSORCVSSMLAOKRRNV
TCRFTNGTSVDIQHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRLL
SCVWIESGRPAGRNCEQMRRPHSARACVADEPLPPCMFTASALYQRDASCQDQSRFCD
IIKLFHSCDSLEYRQKCCSTCTFYERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQLRRCLTSKCSGESVRFKVCAQKTCESKSRLARDTICGGEEIVSRGQCEVVCRSRLTGANFLWRVDDGTPCQAATSRAVCSKGSCQIVGCDGLISSSFRFDACGVCGGRGDTCDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKWYMHQRAPKLLIPESCCIPSEIERCRSNPFDQDAPPPYYTSTCYEPLQNDLLHVMN
VASWLCITNAIVQVIFVSLKTIKLLNFILLKT"
                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(20516. .20602,20648. .20953,20999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(20516. .21818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGYYQSNYWGKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(19892. .20283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQGNVTLNFKYRDFPASRVDLAPKPQIPSTKNRQRVQVSKEDVLREQASVLHKMNVSL
IEALLTAPNDEKAREQLRKYGNELVARWDIGHWSECRQKTCHVAGYQARGISCKVTFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB03121.1"
/db_xref="GI:4008366"
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/db_xref="GI:3877452"
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/db_xref="GI:5824510"
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                                                                                                            yk411f5.5 comes from this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F53B6.4"
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latelet-endothelial tetraspan antigen (SWLPET3_HUMAN)"
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                                                                                                                                                                                                                                                                                                                    CANTICCANTIGGAGCATGCAATATGCGGAGGCAACGAACACTGCATCCACGTGGAATAT 29772
                                                                                                            CATTTTCCTTCACAATGATCACCTCGTTTCATCCATTCTTTGTGACGGGAATGGATCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                cacttccatttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtattt 452
catatcgagtacaatgcttttacatggaagctgataaaacagttagtgcacagattgagg 572
                                                                                                                                                                                                             ttgtaacaacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtg 512
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gene

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Mismatches

Indels

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Gaps

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/protein_id="CAB03118.1"
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/db_xref="GI:3877450"
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EVPCSSPDMKSYQTAAFLIKGLGLSYT"INIDPALLSYRQMLPPNFQEMLLSPRAFFNM
GYPINIQYLPSQGFIRAENIEDYNLRIQAFFKKNIAKIEQKQYVVISDNYMYDLTRNE
HVETYDDILQCIKKPTCQMNFISLKKGEAQIMDSPILPLTKSLYLYKPFYWTDVPLQL
SVPNIPPELNQN"
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vpltalyvtslemvaalafcakurktvuakunknsksksaksskstrgasksoksrr
sskahiskrssksskkgtsgksgksgksgkssksskskkvktattsgsoystvsa-
gvsdkosnsskssrksskssksrkureldsdaorkmeksgksgkvalipktqoytgs
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HPFFVTGMDRAPSIRCFLESIKGLANAEIDVGTLAPOHVODKSLPVCAYHLKOGIEG
HVLRFAQVGQKVTHVWRCDQDASHVYGILIHSCYADDGHGNKFELVDDRGCSTDPFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(27666. .27862,27919. 28905. .29001,29330. .29417,29467. ... 30107. ... 30301,30478. .30589))
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GQSIAQCRIHTEKTVPIVKGGEQARMEENEIYAIETFGSTGKGVFHDDMETSHYMKNF
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23555. .24160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(27666. .30589)
/gene="F53B6.6"
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/note="r=
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LMLI LTLFTDRWMAMVGACI LQSFAGKI I GKRANLLLNLI I "
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/db_xref="GI:3877451"
/db_xref="SPTREMBL:P90883"
                                                                                             PQIEYEHGAISAYTNAHVFKYADKVQLYFTCTVQLCYKHDGGCEGITPPQCSGHSHGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="TTT Lys K-tRNA; predicted using tRNAscan-SE-1.11;
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                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F53B6.6"
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4.2%;
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Score 74.8; DB 34
Pred. No. 0.00056,
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                             DB 34;
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                         Length 32412;
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.29606,29648. .29915,
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CEY111B2_1
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ttcgtttgttattatcatcattatcaacttgtcctattttattctaacagtttatcattt 1641
                                                                                                                           attcagtaatcttttatatgcatactattgtaaatgtttcatcattaggccatgaatagt 1581
                                                                                                                                                       gtgatattttcatcaaaacttcttctatcgcttttatagcttctgaaaagcttattcatt 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGGGTATGTTAACTCTGAAGTATTAAATCAATT 29618
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                                                                                                                                                                                              164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (27-0CT-1999) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,
Hinxton University, St. Louis, MO 63110, USA. E-mail:
Jes@sanger.ac.uk or rw@nematode.wustl.edu
On Oct 19, 1999 this sequence version replaced gi:6016917.
Order of segments is not known: 800 n's separate segments.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1. (bases 1 to 614429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans chromosome III clone Y111B2,
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/db_xref="taxon:6239"
/chromosome="III"
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                                                                                                                                                                                         Score 71.6; DB Pred. No. 0.001 0; Mismatches
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                                                                                                                                                                                                             .0017;
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                                                                                                                                                                                                                                                                                                                                                                    elegans
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                                                                                                                                                                                             Indels
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CEY18D10A/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctgtaaacaattcacttatttgcattattgcaattaaaaagtatttcatttgtgaaaaaa 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Staden, R., Sulston, J., Watson, A., Weinstock, L.,
                                                            neighbouring submissions.

The true left end of clone F08A8 is at 152766 in this sequence. The true right end of clone B0019 is at 105 in this sequence. The stoff this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone Y18D10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-DEC-1998) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 152878)
Harris, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bin/display?db=wormace&class=Sequence &object=Y18D10A Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368 (6466), 32-38 (1994)
94150718
The end of this sequence (152766. .152878) overlaps with the start
                                                                                                                                                                                                            It may be shorter because we only sequence overlapping once, or longer because we arrange for a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For a graphical representation of this sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predictions from Genefinder (P. Green, U. Washington),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL034393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 152878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152878 bp
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between
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FEATURES
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VPEDEADDEVDREIROLENELLQRVKEKTVRRDDFTAKMIELKAKSRAPRIVETKFVK

KWPEGIHKPTEKDSFGLLNSTKIHRNQPTSDFTIAQATAEKKALLGAQGAAGASE

PGSSSSIHKKGKTVRELQTEMKGESVKEKAARMRAEASAGRSQAPGPAPAPASEL

QDPQDDFGLSMSDPGSDSETEEEIQKQEKHIPAAVTRRSARLSALPVTEKKASSSSKM

PPPSSPSTFGRRRRRTLSTMSMEPAAAATTPAPRGRPRSRSAAKVSENTEPLSEA

PSAPVKKGRGRRRRTLSTMSMEPAAAATTPAPRGRPRSRSAAKVSENTEPLSEA

PSAPVKKGRGRRRSRSTMSITEDSEPSTSSTAAKRSEDEEQDLKLTNKSPEK

PKKRSKTTEETVGDLIKKRLRDTAKTTATVHTFGPDLKTRKMERMRAPTAVTSSKKE

KPKNAGSADSSINEEEHBDETMILEEQTILDLPQOTSQOEPRISGGSELLDEQFDASEE

RFGTVPSAPELTKNPAPPVPBASEASABEPKLDIFGOATPILALALPTVSSTALEF

RFGTVPSAPELTKNPAPPVPBASEASABEPKLDIFGOATPILALALPTVSTALEF
                                                                       /Translation="MOGSGEKAIGFLIQFSLNARFWIDKOLLATDEPFSSENYOMVRR
FRIISEKRPKSVDKLYKTGEIPARGRGNKVGGRVFSKMPISKSMELSLVKLKQTPIIQ
OFYMKNGKKSTMVHIISKKTVSFIGOKLAAQIDEQLFTKYGFKVEQLMELAGLAAAQA
IAAHYPKSNVAVLCGPGNNGGDGFVCARHLQQFGFTPSIVYPKESRNELMKSLVVQCE
                                                                                                                                                                                                                                                                                                                                                                 complement(join(29879. .30346,31220. .31296,31346. .31522,
34557. .34852,35323. .35351))
/gene="Y18D10A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(26502. .29006)
/gene="Y18010A.2"
complement(join(26502. .26573,27346. 27624. .27788.28732. .29006))
/gene="Y18010A.2"
/note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYQNVEKGGKKVNKIKTHLROALDLKIPFEELKRPMEEKGIKLGDSIPLTPSDAYDVM
MEFLRETSAADMWAYLNRQRIDANLKPLMKEEENFLOYSVTLMEHDQOLLEVFISRI
IFELCARESIGSNEGGRLIRLECHAVERSESAENPDDYTSPVYOKKSTWIRRLFOILL
LNHPNGIGKSTCYILMSDVAKYCRFLYVEEMDKDHMGSEFHLAFRVLMHKDSEQASAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKAQENPTAELPTISEISGRAPQALPTSSOTPPTSGÄAAPPVDDLLSEILSGAKTTKT
RKAAPPAVQKSISSTTQQAPPTSVQAPPTSCSAAPPVDDLLSEILISGAKTTKTTKT
MPPVDOKKISSBAPISDSAPTSVHQOTPKSPKOILNSKYGLDISDSEDEEEEEEER
METVEBEEEAPPISDSAPTSVHQOTPKSPKOILNSKYGLDISDSEDDEEEEEEER
MEIVEBEEEAPPISDSLQASEDSSTATVKPEKVVAVVKIFSPEIDSTSVEAPPEASVP
PKAPAATKIDNQLADQASEPEPFKARKLPIARKIPPKINTIDHOKASSTTSDDLMS
DILAGARTTKTTKKAPPTRVAQTTRTKNLAOKRKASSPPTPACTTAPKROYIKKSDDLMS
VLPPSSSSSSTEPPSADDSASTTSSMKKGGGAIMIEAVPCRFGGKAIKREOKPIGMKEM
VLPPSSSSSSTEPPSADDSASTTSSMKKGGGAIMIEAVPCRFGGKAIKREOKPIGMKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(29879. .35351)
/gene="Y18D10A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MQMNPNKSPPISINFPLFTMSKFLLFISISAVATASDLVEVFGI
SRCPDTSKFIHNQLVPFYQNYKGNLSDGLKLDFHAVPTGGHQVDGKYVNRCLHGALEC
ALNKLQMCSKKHIKQDWLVTAGCIQGKTAYSAGLKCLPDTEEGKIVQNCAESEEGEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNVLRVMIDNPFSSHSHAIFAALKQISPQVSQLREIIESSEINQYVEMTGEDAIRDAV
QNLVDLISIYTNFPLKPTTLPPSS"
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NVAFDFLRQKMDLIEEQFLKPKEMEKEPKRITAFSVPTVVTKMTKSEAEMLKKESKWQ
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ECEVLRMKLVSTDAAYRESVQREAEAINAKEIAEASLKQGQYDSEFYKKKSASLQEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTTLKAAKIENSSKTKKLDKYLKSVIQVVDALSSTSNLSKQSKSIKDLVTVFRRDDVR
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                                          TSSIPITATLPTNLQAFPLIVDALFGFSFHPPTREPFTEMLKTVRASGIHVFSIDVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNDENSYRYNVAPHSAWLPWIQVNGERNRNAEFKLKDFSSVFRLFFEVFLQKCLKRSI
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/db_xref="GI:3979929"
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EYPILTFAIGTTISAMVIGAGLYILGA IGLIFEFFFFECFARAMISAVDPVOTLAI
EQAVKVESLLYMLVFGESMLNDAVS IVLAAFALRHAKPSFNSLPASEIITSAFVFFE
MFFFSACLGVGIGLLSALLFKHVDLRKTPSLEFALLLIFSYIPYGFAEALDLSGIMAI
LFCGISMSQFTRHNVSPTAQITFRHTFGTISFVAETSTFAYIGMAFFTIKLNFAPWLI
EWSVULCLLGRACNVFPTEAYLNVGCKDVQISMKNQIIMMFSGMRGAVCFALVLYMDL
DKEKKSILLTTVLFLILFTTIFLGGSALPFISFINRCYPNERGRKRRTTPRNKESTGN
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GEAIDANATSLEQHGAAIVGNVSEEKKRSLAIFFILFVIMLATLVVHMLIVSKIHWMP
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'gene="YIBD10A.6"

join(47525...47593,48112...48208,48610...48751,49616...5

50501...50818,51553...51971,52106...52364,52847...53224)

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DIKPQNLLIDPESGVLKLCDFGSAKYLVRNEPNVSYICSRYYRAPELIEGATNYTNSI
DVWSAGTVMAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIQSMNENYKEEKFPQI
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                                                                                                                     FYPGKDILRRQGIYLIVNAKDGGNVLRQEYAQDFLKILDWILNVKLLSSAGRIFTYKD
VCLHFQNDCFSNPHAKLLANIYSKNHQNSMFNITYPIYRSTYATEPIDISKVLGNVSL
                                                                                                                                                                                                     /translation="mSQNHIILLPDSFKNSMIISKIRAAPLEQPWANIVAKYCLFVAKYPDFFIIIPLIITICLSMGIILNFKIVRGVNYLYAPLNATWKTEEAVFGENWAKDDDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAHPWNKVFRVHTPAEAIDLISKIIEYTPTSRPTPQAACQHAFFDELRNPDARLPSGR
PLPTLEMDGPMGTGEVSTTSGDVAGPSA"
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HIDGSIGYHFFSLDCLSLSLTLSTAAVVATATSSSSSPKAFGVSVSLFLWSLLVAWYV
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/note="~~~
                                                                               DYDGHVENASAWLILYQLKNEKWQLSRDFEDGLAEKIQSGEAPSELLNLYYFHSATFD
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join(39072. .39164,40245. .40513,41360. .41936,44226. .44375)
/gene="%18D10A.5"
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/gene="Y18D10A.4"
                                                                                                                                                                                                                                                                                     /protein_id="CAA22312.1"
/db_xref="GI:3979933"
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/codon_start=1
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Length 247332;

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RESULT 14
CEY18D10/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-SEP-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu On Nov 21, 1998 this sequence version replaced gi:3873430. On Nov 21, 1998 this sequence version replaced gi:3873430. On Nov 21, 1998 this sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                      segments
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                                                                                                                                                                   NOTE:
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                                                                                                                        This is a 'working draft' sequence. record will be updated with the finished record with a coession as it is available and the accession
   /chromosome="I"
/clone="Y18D10"
                                       /organism="Caenorhabditis
/db_xref="taxon:6239"
                                                                                          Location/Qualifiers
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0; Mismatches 227;
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                                                                                                                                     Wilson, R., Albscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
Direct Submission
Submitted (12-NOV-1999) Louis, MO
jes@sanger.ac.uk or rw@nematode.wu
                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans. Caenorhabditis elegans
                                                        Sulston, J
                                                                                                             Nature 368
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 rw@nematode.wustl.edu
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12-NOV-1999

Caenorhabditis

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FEATURES
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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone Y111B2D. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions
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ERIILIDDNAPAAKOPESAQKOSTTVINSAKKITATTSALEPAEKKKKDDSSSS

EEIILIDDNAPAAKOPESAQKOSTTVINSAKKIKOROELIAKOKPSSSSVTPSKPAA

PTASTPOKEEICTLETFILKNIF ANLDAKGKIYGEKKIKTPDTETLKBITTFIDVMKHI

KTEKVNMEPLIYSLAKSFGMTTQEVMKQVEQEISSKKATTPKPSTNAVLSTISQKSL

EKNAADWKLTOTDLPTMGEKDIQMLTTIVRSWKSKKEISNSWTGKVGUKKDVNQLKMNAD

QARKKLKTLLTKLGFPLKIGKFTRKSNSFTQFAPKIGRKSVGKVQTGKQTGANSRE

IFKFRVKKWTTYWTKSRNSESGGNLDPDIINTLPDSSEKNGGGGQDDANDLICEKSRU

FHFSSIYIKINRKTLFLQFADLPEIFNSGTSPVCREFSISEICRFAVKFTSKIYAGLP

EILNSDNLFVCRNFLLYPICLEDGIFHSGTLPIKHERSRKARMFHQWVYLISRKFILE

EILNSDNLFVCRNFLLYPICLEDGIFHSGTLPIKHERSRKARMFHQWVYLISRKFILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Y111B2D.b"

/gene="Y111B2D.b"

join(12998. 13081,13735. .14229,15626. .15715,16386. .16511,

16940. .17225,17597. .17869,21574. .21764,21915. .22057,

22109. .22243,23083. .23146)

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LVQAKKPRHFEIFWWKLVKNGLISTKFCVKNHKSKKITIFTPRPISDSPRPLFNQSNE
ITPRFISDSLRPLFNQSDEVGGARRWFTRENICSRPAIQ"
                                        QNPRQQPQNQIVQNFQSAPQRHPHQNPQIATSSSSGGVNQFYNNGGAAPPVVEQQAAN
RRSSFTMSHSVQQHQSPLQQQFPINSYQSPSHHNNSSSMSNSSLMQTPHSNSSMIARS
                                                                                                                                                                                            KDRIEAKKFEERMKKEQEKQEEKERKEREKEEKERKEREIREIMERKKREEDDRIAA
KLQIAQQLENDRKMREAEESARKETERRAKMETEAANALQGLEEDLLMDDIDFMTQQQ
TKVDEERKVAEARRAVERENQIKMMRAQQLQRRQEEAPPPQQAPAPHTQKIQVKNEPV
                                                                                                                                                                                                                                                                                                          /translation="mnddillimvtavyscgiplunomnmlknvlcqyggirmaqtla
TQKTQNKQCLTQNDYQLLFDYFGKFEKALEQRKAKKEEAERLKKLEEKLKKEKEKQAE
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                                                                                                                  EMPNVTQQYQAEQNHLAQSSNNSQYNAPSTSSQPQHFPTEPS1RQPPPQQSYNSNQML
                                                                                                                                                           DHSFDILKEAEKDAHIIPTKSIKAEPLDVQKPLSAFEKLASLRGRTQSADMRRGGDST
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/db_xref="GI:6434387"
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/db_xref="GI:6434388"
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.6844,6997. .7159,7260. .7390,7463. .7668,7725.
.9723,10796. .11001,11112. .11276,11362. .11438</pre>
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                                                                                                                                                                                SRSRSASRSPSRSPSPQ"
                                                                                                                                                                                                                         SHEGETAYIRVREDNSSGGGSGGGGRDRSRSRSPRAERRASPKYSPRRSRSRSRSRSRSR
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join(60241. .60280,60336.
64312. .64455,65697. .662
                                                                                                                                                                                                                                                                  ETSEEDVVVVVEDLKDHMRDAGDVCYADVARDGTGVVEFTRYEDVKYAVRKLDDTKFR
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Best Local Similarity 52.3%;
Matches 150; Conservative
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DEDGINLEEDACTIKFDSIRRKNDDNSVENGONAADLSDETDEWDVQRPDSGDDDP"
1 12141 c 12530 g 23596 t
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	ence allian ence ence ence ence ence ence ence en	Delcuve 6, WPI; 96-309587/31. WePI; 96-309587/31. Recombinant DNA molecule expressing mammalian ery useful to transform cell lines, and for gene ther anaemia and other red blood cell disorders Claim 7; Page 59-60; 84pp; English. Human apolipoprotein B (apoB) scaffold attachment element clones Rh32 (T31530) and Rh10 (T31531) rethe 3' human apoB SAR element and the distal 1212 SAR element and 1317 bp proximal sequence. These co-map with the boundaries of the human apoB gene domain. A novel recombinant DNA molecule adapted of a host cell comprises an erythropoietin (EPO) genomic clone (T31532) operably linked to an expression of the comprise of the human apoB gene genomic clone (T31532) operably linked to an expression of the comprise of th	IT 1 30 30 31 31 31 31 31 31 31 31 31 31 31 31 31	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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AATTAAAATATTT tactgtaatacaa	A; A; A; B; B; Catcot	ecule express cell lines, cell lines, ed blood cell ; 84pp; Engli, n B (apoB) sc. (T31530) and aR element and 7 bp proximal ndaries of th combinant DNA rises an eryt 32) operably	91 72 0	1 054656 1 758840 1 758840 1 V22750 1 V22733 1 Q53480 1 X52266 1 X52266 1 Q12515 1 Q12517 1 Q151710
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PS Claim 20; Fig lA-E; 69pp; French.

CC This sequence corresponds to the genomic sequence encoding a Plasmodium

CC falciparum strain K1 pre-erythrocytic liver stage antigen-3 (LSA-3)

CC protein (W24790). The gene sequence was isolated by screening a

CC protein was strain T9-96 library with the serum from a missionary

CC treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones

CC isolated, clone 7295 was used to screen a library generated from Thai

CC strain K1. One clone contained a 6.85 kb insert including the sequence

CC presented here. The gene organisation comprises a first exon, a short

C1 8b bp intron and a 5 kb second exon containing a 1.8 kb region encoding

CC 10 locks of 4 amino acid repeats and a 3' hydrophobic region

CC corresponding to a glycosyl-phosphatidylinositol membrane anchoring

CC sequence. The invention relates to new polypeptides of at least 10

CC amino acids derived from the LSA-3 polypeptide with the exception of

CC peptides W24791-4. The LSA-3 peptides can be used to raise antibodies

CC according to a glycosyl-phosphatidylinositor raise antibodies

CC sequence. The invention relates to new polypeptides of at least 10

CC amino acids derived from the LSA-3 polypeptide with the exception of

CC peptides W24791-4. The LSA-3 peptides can be used to raise antibodies
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Best Local
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12-JUN-1996;
13-JUN-1995;
1430 gtatgtaggaaataattactgtaatacaataagtgatattttcatcaaaacttcttctat 1489
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                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum poly:peptide(s) and related nucleic acids - derived from the liver stage antigen-3, useful for malaria vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daubersies P, Dru
WPI; 97-065464/06
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vaccine; immunotherapy; malaria; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T78867;
08-OCT-1997
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                                                                                                                                                                                                                                                                                                                                      as vaccines for immunotherapy of malaria.
uence 6152 BP; 2725 A; 463 C; 1
                                                                 ATATATATGTATCTTTTACAAAATTTTAAAATTTTAAAATTTATATATATATATATTTA
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                                                                                                                                                                                            197;
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m liver stage antigen-3 genomic sequence.
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275. .442
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77. .274
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Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                                                                     58.2; DB
No. 0.003;
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                                                                                                                                                                                                                                                                                                                                         1215 G;
                                                                                                                                                                                                                                                 Length 6152;
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       This sequence represents the var-7 gene of plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and siallic acid binding protein (SABP) conserved regions (see T7288) and T72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention.
                                                                                                                                                                                                                                                                           Wellems
WPI; 97-
                                                                                                                                                                                                                                                                                                       (USSH )
Chitnis
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Plasmodium var-7 gene.
DBL gene family. SABP; sialic acid binding protein; vaccine; therapy;
DUTY binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response
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comprise either a nucleotide sequence or encoded polypeptide
                                                                                                                                                                                Claim 4; Page 56-61; 96pp;
This sequence represents the
                                                                                                                                                                                                                 binding
                                                                                                                                                                                                                             New malaria vaccines - contains cysteine-rich DBL family pubinding domains homologous domains of the Duffy and sialic
                                                                                                                                                                                                                                                             P-PSDB; W22475
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07-JUN-1995;
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19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attgcccaatttttatgggcatcatttcctattctgtaaacaattcacttatttgcatta 1728
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) US DEPT HEALTH & S.C., Miller
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15140. .
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Peterson DS, Sim
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var-7; immune response;
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Best Local Similarity
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                                                                             WO9641877-A2.
27-DEC-1996.
12-JUN-1996; 1
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p. falciparum liver stage antigen-3 genomic sequence.

P. falciparum pre-erythrocyte; liver stage antigen; serum;

plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum;

prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob

glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. I are also used in the preparation of vaccines for inducing a protecti immune response in a mammal to plasmodium merozoites (especially plasmodium falciparum or Plasmodium vivax).

Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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                         Daubersies
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PS Claim 20; Fig 1A-E; 69pp; French.

CC Inlim 20; Fig 1A-E; 69pp; French.

CC This sequence corresponds to the genomic sequence encoding a Plasmodium CC falciparum strain K1 pre-erythrocytic liver stage antigen-3 (LSA-3)

CC protein (W24790). The gene sequence was isolated by screening a CC protein (W24790). The gene sequence was isolated by screening a CC protein (W24790). The gene sequence was isolated by screening a CC isolated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones CC isolated, clone 729S was used to screen a library generated from Thai CC strain K1. One clone contained a 6.85 kb insert including the sequence CC presented here. The gene organisation comprises a first exon, a short CC 168 bp intron and a 5 kb second exon containing a 1.8 kb region encoding CC plocks of 4 amino acid repeats and a 3 hydrophobic region corresponding to a glycosyl-phosphatidylinositol membrane anchoring Sequence. The invention relates to new polypeptides of at least 10 cm and as derived from the LSA-3 polypeptide with the exception of peptides W24791-4. The LSA-3 polypeptide with the exception of Sequence 6152 BP; 2725 A; 463 C; 1215 G; 1749 T;
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16-MAY-1991
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Claim 15; Fig 1; 90pp; English.

Claim 15; Fig 1; 90pp; English.

Creading frame indicated in the Features Table. The possible ORF is creading frame indicated in the Features Table. The possible ORF is creading frame indicated in the Features Table. The possible ORF is creading frame indicated in the Features Table. The possible ORF is creading frame indicated in the Features The RNA and polypeptide product of the Rep gene have not, however, been detected. It is creative that the product is produced in low amounts to positively cregulate initiation of plasmid replication. The polypeptide may also contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions that act as negative regulators of plasmid copy contain regions 
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91-164194/22.
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                                                                                1226.
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/EC_number= 6.3.5.
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                               cDNA;
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0.021;
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                                                                                                                                                            psCPSII gene;
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Best Local
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03-DEC-1992; AU-006206.
16-DEC-1992; AU-006380.
(UNIX) UNISEARCH LTD.
Flores MV, Osullivan WPI; 94-200271/24.
                                        (BEHW) Behringwerke.
Knapp B, Hundt E, Enc
WPI; 89-194071/27.
P-PSDB; P90417.
                                                                                              EP-322712-A.
05-JUL-1989.
20-DEC-1988;
30-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The cDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSII) of Plasmodium falciparum was determined. The cDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminese subdomain of the glutamine-amidotransferase subunit of CPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSa and CPSb.

Sequence 8920 BP; 3836 A; 774 C; 1232 G; 3078 T;
 acid sequences and
Claim 1; Table 17;
                                                                                                                                                                  Malaria-specific DNA insending DNA; malaria; clone 41-2;
                                                                                                                                                                                                             N90224 standard; DNA; N90224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding carbamoyl phosphate synthetase isolated from Plasmodium falciparum, used to develop the treatment of malaria. Disclosure; Page 6-16; 31pp; English.
                            New antigenic proteins from Plasmodium falciparum - new encoding nucleic
                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                1-NOV-1989 (first entry)
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P-PSDB; R55694.
Nucleic acid encoding
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195; Conser
                                                                                                121299.
DE-831351.
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                                                                      Enders
derived antibodies,
25pp; German.
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                                                                                                                                                                  insert of clone 41-2.
41-2; Plasmodium falciparum;
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              vaccines,
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               diagnosis
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Best Local Similarity
Matches 214; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The DNA is of a malaria-specific DNA insert of clone 41-2. The encoded peptide (see P90417) is useful in a protective vaccine, esp. against malaria. Produced antibodies are useful for passive immunisation, and antibodies, the protein and the DNA sequence are useful as diagnostic reagents. See also N90211-25 and P90403-19.

Sequence 1052 BP; 394 A; 93 C; 88 G; 477 T;
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                                                      misc_feature
                                                                                      misc_feature
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                                                                                                                                                                                                         Plasmodium falciparum MC type
                                                                                                                                                                                                                       detection;
                                                                                                                                                                                                                               cDNA encoding Plasmodium Plasmodium falciparum; en
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                                                                                                                                                                                                                  identification; treatment;
                                                                                                                                                                                                                                falciparum; erythrocyte membrane
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                                                                                                                                                     /product= Erythrocyte membrane 518. .520
                     /transl_except=
5546. .5548
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656. .658
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3461. .3463
transl_except=
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2909. .2911
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Pred. No. 0.04
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prevention; pa:
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Arginine
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                                                                                                                                Tyrosine
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                                                                                                                                                       1348
                                                                                                                                                                                                                                                                                                                                  primers used to generate characteristic amplification pattern different P. falciparum strains. Antibodies specifically immunoreactive with the PfEMP1 polypeptide or its fragments mused in diagnosis of malaria infection. This sequence encodes PfEMP1 protein of the MC type of Plasmodium falciparum. An
                                                                                                                                                                                                                                                                                                                                                                                                                                    A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte membrane protein 1 (PfEMP1) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or
                                                                                                                                                                                                                                                                                                          alternative, truncated version of the coding sequence is given in \mathbf{T41853}.
                                                                                                                                                                                                                                                                                                                                                                                      malaria. Nucleic acids derived from the PfEMPI gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from
                                                                                                                                                                                                                                                                                                                                                                                                                           malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malaria parasite infections
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                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Figure 12; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Plasmodium falciparum erythrocyte membrane proteins develop products for the diagnosis, treatment or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-1995, US-430908.
(AFFY-) AFFYMAX TECHNOLOGIES
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26-APR-1996;
                                                                                                                                                                                                                                 Local Similarity
nes 217; Conserv
                                                                             aattttagctaacaaatatatagtatgtaggaaataattactgtaatacaataagtgata
                                                                                                                                                                                                      tattaccatttcgtttaaatttcgtccaaatcagaaggcataaaaataatgttagaatca 1347
taatcttttatatgcatactattgtaaatgtttcatcattaggccatgaatagtttcgtt
                         ttttcatcaaaacttcttctatcgcttttatagcttctgaaaagcttattcattattcag
                                                                                                                              togaagcaataataaaactgccatatatattogtttettettateateettetaataact 1407
                                                                                                                                                                                 Conservative
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/transl_except=
6257. .6259
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7754. .8478
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5269. .6271
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/transl_except=
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5272. .6274
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275. .6277
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Pred. No. 0.
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Human apolipoprotein B (apoB) scaffold attachment region (SAR) element clones Rh32 (T31530) and Rh10 (T31531) respectively carry the 3' human apoB SAR element and the distal 1212 bp 5' human apoB SAR element and the distal 1212 bp 5' human apoB SAR elements of the human apoB gene chromatin domain. A novel recombinant DNA molecule adapted for transfection of a host cell comprises an erythropoletin (EPO) cDNA (T31529) or genomic clone (T31532) operably linked to an expression control sequence and to the 5' and 3' SAR elements. The SAR elements increase expression of the recombinant EPO in stable, long-term mammalian cell cultures.
1564 cattaggccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttat
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Delcuve G;
WPI; 96-309587/31.
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19-DEC-1994; US-358918.
(CANG-) CANGENE CORP.
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                                                                                                                                                                                                                                                                                            tactgtaatacaataagtgatattttcatcaaaacttcttctatcgcttttatagcttct 1505
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BP; 278 A;
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48.9%;
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SAR element; apolipoprotein
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Pred. No.
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07-JUN-1996; UO9508.
07-JUN-1995; US-487826.
(USSH) US DEPT HEALTH &
Chitnis C, Miller LH,
Wellems TE;
WPI; 97-052231/05.
comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to Plasmodium merozoites (especially Plasmodium falciparum or Plasmodium vivax).

Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
                                                                                                                                                                                                                                                                claim 4; Page 56-61; 96pp; English.

Claim 4; Page 56-61; 96pp; English.

This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see T72889 and T72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding
                                                                                                                                                   protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABF mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium var-7 gene.

DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;

Duffy binding like gene; Duffy antigen binding protein; erythrocyte;

DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response
                                                                                                                                                                                                                                                                                                                                                                                                                   New malaria vaccines - cont
binding domains homologous
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15140. .16205
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Peterson DS, Sim
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Query Match Best Local S Matches 180

Similarity

45.6%;

Score 51; I Pred. No. 0. Mismatches

DΒ

1; 215;

Length 19124;

0;

Gaps

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180;

Conservative

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RESULT 11

X20248_075
Continuation (3 of 10) o
WP Sequence split into 1
WP Fragment Name
WP X20248_00
WP X20248_01
WP X20248_03
WP X20248_03
WP X20248_05
WP X20248_05
WP X20248_05
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Best Local Similarity
Matches 242; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      catcatttcctattctgtaaacaattcacttattt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acagtttatcatttgtgataatatcacaaaattataccttgtattgcccaatttttatggg
                                                                                    aataactaattttagctaacaaatatatagtatgtaggaaataattactgtaatacaata
                                                                                                               CTGATGTTGCAAAAATCAAATTAAAAAGAGCCGTTATTTCCTCTTTTTCAGTATTCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agtgatattttcatcaaaacttcttctatcgcttttatagcttctgaaaaagcttattcat
                                                                        GTTCATAGTATTCATTAATAAATTCATATTATC----ATAATTTATCTTAGAGTTGA
                                                                                                                               agaatcatcgaagcaataataaaactgccatatatattcgtttcttcttatcatccttct 1400
                                                                                                                                                   TTGATGTATTAATTTCTGGGCTTAAGTTGTCTTGAAAGGAGCAGTAAAGATAAAATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttattcta 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctgtaatacaataagtgatattttcatcaaaacttcttctatcgcttttatagcttctga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttatcatccttctaataactaattttagctaacaaatatatagtatgtaggaaataatta
                tattcagtaatcttttatatgcatactattgtaaatgtttcatcattaggccatgaatag
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nilarity 44.8%;
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Pred. No. 0.16;
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Query Match
Best Local S
Matches 203
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11-SEP-1984; AU-007066.

11-SEP-1984; AU-007066.

10-SEP-1985; AU-047326.

(HALL-) HALL INST MED RES.

Kemp DJ, Anders R, Coppel R

WPI; 86-094055/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 1; 55pp; English.
The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp, to all or a portion of the base sequence coding RESA (N60472) or FIRA (N60473). RESA and FIRA lantigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.

Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
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DNA coding for Plasmodium
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27-MAR-1986.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             poly:peptide(s) having
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les 203; Conserv
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agtttcgtttgttattatcatcattatcaacttgtcctattttattctaacagtttatca 1638
                                                                                                                                                                                                                 ctaataactaattttagctaacaaatatatagtatgtaggaaataattactgtaatacaa 1458
                                                                                                                                                                                                                                                                  TTTGTAAATATTCATCGGTTGTATTAAAATCTTCAAGATCAATATATTTTTGAATAAAAA
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                                                                                                                                            taagtgatattttcatcaaaacttcttctatcgcttttatagcttctgaaaagcttattc
                                                                                                                                                                                              ttagaatcatcgaagcaataataaaactgccatatatattcgtttcttcttatcatcctt 1398
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                                                  AGTTTTTGTAAAGATTGTCATTTAAATCTTTGGGGAAATTTTTAAAGGATTTTATCTTAT
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1199. 4225
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RESULT 1

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ID 472/c

ID 472/c

ID 24-A

AC N604

AC M604

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (M60472) or FIRA (M60473). RESA and FIRA have antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.

Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N60472;
24-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               poly:peptide(s) having antigenicity of RESA or F falciparum
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11-SEP-1985; 006960.
11-SEP-1984; AU-007067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malaria vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N60472 standard;
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10-SEP-1985; AU-04726.
14ALL-) HALL INST MED RES.
Kemp DJ, Anders R, Coppel RL,
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  269
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                                             taatcttttatatgcatactattgtaaatgtttcatcattaggccatgaatagtttcgtt
                                                                                                                                                                                                                                                                                                         tcgaagcaataataatactgcatatattcgtttcttcttatcatccttctaataact 1407
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  GAATAAGGAAGCTTTTAATTTATTTATTTTTTTTTTTTAATAATTCAACCACAGTAA
                                                                                                  TTTTATTATTTTTTTTTTTTGTATTTTATCAAAATAAAAAAGAACAAATATATAACAACCAA
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1199. .4225
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Best Local Similarity
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WO9845328-A2.
15-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                          V68800 to V68998 represent nucleotide sequences which encode human breast tumour specific polypeptides. Detection or measurement of human breast tumour specific polypeptides and nucleotide sequences, or the corresponding RNA in a sample, is used for diagnosis and monitoring of breast cancer. Human breast tumour specific polypeptides and nucleotide sequences, and the vectors containing the DNAs, are a useful in vaccines for inhibiting development (for prevention or therapy) of breast cancer. The polypeptides may also be used to raise monoclonal antibodies, used as immunoassay reagents. Sequence 715 BP; 183 A; 131 C; 86 G; 294 T;
                                                                                                                                                                                      1406
                                                                                                                                                                                                                                       New DNA sequences isolated from endogenous human retroviral element and related vectors, transformed cells, proteins and antibodies, useful for diagnosis, treatment and prevention of breast cancer Claim 1; Page 127: 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP. Frudakis TN, Reed SG, WPI; 98-557473/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1998; U06939.
11-DEC-1997; US-991789.
09-APR-1997; US-838762.
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Human; breast cancer; breast tumour tissue; diagnosis; treatment
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22-JAN-1999
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48.8%;
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3568/c Q03568 standard; DNA; 6124 Q03568; Q2-AUG-1990 (first entry)

ВP

of Plasmodium.

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22-FEB-1990.
10-AUG-1989;
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3406.
                                                                                               /label=Complementary to /note="Alelle II, skips 485. .2526
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3082. .3151
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121. .128
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Best Local Similarity 47.8%;
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding SERA antigen of Plasmodium falciparum - also DNA encoding signal and regulatory sequences of SERA gene, for diagnosis, prevention and treatment of malaria. Disclosure; p; English.

Sequence allows for production of antigenic malarial proteins, useful diagnosis, prevention and treatment of the disease. The sequence may bused in an expression vector, and signal and regulatory sequences may used to stimulate production of other products.

Sequence 6124 BP; 2567 A; 602 C; 801 G; 2137 T; 17 Others;
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Inselburg JW, Bzik DJ;
WPI; 90-083508/11.
P-PSDB; R05526.
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Search completed: April 16, Job time: 9747 sec 2000, 04:40:48

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Title:
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1779
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                  US-08-883-795A-36
US-09-056-075-1
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US-07-867-106-2
US-08-488-3795A-36
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US-08-488-38-36B-13
US-08-48-18-31-1
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1285.535 Million cell updates/sec
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Patent No. 5985607
Query Match
Best Local Similarity
Matches 217; Conserv
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Result No.

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Conservative

0; Mismatches 235; Score 64; DB 4; Pred. No. 4.5e-06;

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Sequence 32, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 41, Appl	Sequence 41, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Patent No. 5340934	

ALIGNMENTS

Minimum Maximum

Searched:

Sequence:

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CLONE: Rh
US-08-883-795A-36
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION: 1950
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 361-1398
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APPLICANT: Delcuve, Geneval APPLICANT: Awang, Gregor
                                                                                                                                                                                             TELEFAX: (416) 361-139
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 base pairs
                IMMEDIATE SOURCE:
CLONE: Rh 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 40 King CITY: Toronto STATE: Ontario COUNTRY: Canad
                                                                 ORGANISM:
                                                                                                                                TOPOLOGY:
                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ontario
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                                           TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                    REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 273
                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449
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                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 53701-2113
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STRANDEDNESS:
                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                ENGTH:
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            nucleic acid
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                               6243 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quarles & Brady
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1221
                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                              SOFTWARE: PatentIn Rel
                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1411 tttagctaacaaatatatagtatgtaggaaataattactgtaatacaataagtgatattt 1470
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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LOCATION:
                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               APPLICATION NUMBER: FILING DATE: 10-SE
                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                CITY: Newport Beach
                                                                                                                                                                                                                                                                               STREET:
REFERENCE/DOCKET NUMBER:
                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                              Israelsen, Ned
                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                            620 Newport
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Wellems, Thom
                                                                                                                               PatentIn Release #1.0,
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O Newport Center Drive
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                29,655
NIH121.001CP1
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Pred. No. 0.00022;
0; Mismatches 187;
                                                                                                                               Version
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16th
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US-07-867-106-2
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                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/07867106 Patent No. 5389526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1479
              COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1531
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                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Washburn Core Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                       APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
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                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                     CITY:
STATE:
                                                                                                                     ZIP: 19103
                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 19124 base pairs TYPE: nucleic acid
APPLICATION NUMBER:
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47.1%;
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US/07/867,106
                                                                                                                                                                                                        Washburn Kurtz Mackiewicz & No.
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Sequence 1, Application US/08446855A
Patent No. 5849573
GENERAL INFORMATION:
APPLICANT: Stewart, Thomas S
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Best Local Similarity
Matches 214; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                     1632 tttatcatttgtgataatatcac-----aaattataccttgtattgcccaattttt 1682
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                                                                                                                                  2003 TTTTACTTTGAAAAAAAAAAAAAAAAAAAAAAAAA
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TOPOLOGY: li
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APPLICANT:

Flores, Maria V

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US-08-883-795A-36/c; Sequence 36, Application US/08883795A
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Best Local Similarity 47.6%;
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SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1370 atatatattcgtttcttcttatcatccttctaataactaattttagctaacaaatatata 1429
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NG-DOS
OPERATING SYSTEM: PC-DOS/NG-DOS
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TITLE OF INVENTION: phosphate synthetase
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CURRENT APPLICATION DATA:
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                                                                                                      600
                                                                                                                                                                                                                                                                480 CCATCCTATATTATACACAATATATAATACTCCCCAATATTGTGGGTTCCTATAATTTT 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 222;
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APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recomb
TITLE OF INVENTION: Vector
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
                                                                                                                                               1564 cattaggccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttat 1623
                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: Rh 32
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ORIGINAL SOURCE:
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                                                                      1624 tctaacagtttatcatttgtgataatatcacaaatta-----taccttgtattgccc 1675
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1676 aatttttatgggcatcatttcctattctgtaaacaattcacttatttgcattattgcaat 1735
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OTTY: Toronto

OTTY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                              463 TATAAAATATGTAATTATAAAATATGTAATTATAAACATTTTAATTATAAAAATATGTAAT 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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M5H 3Y2
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                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 235-01
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                1736 taaaaagtatttcatttgtgaaaaaaaa 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                        Local Similarity
nes 180; Conserv
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19124 base pairs TYPE: nucleic acid
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ctgtaatacaataagtgatattttcatcaaaaacttcttctatcgcttttatagcttctga 1507
                                                           ttatcatccttctaataactaattttagctaacaaatatatagtatgtaggaaataatta 1447
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Miller, Louis H.
Peterson, David S.
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Wellems, Thomas E.
                                                                                                                                                                                      Conservative
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Pred. No. 0.01;
0; Mismatches 215; Indels
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US-08-232-463-14
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                                                                                        US-08-232-463-14
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 Best Local Similarity 4.3%; Matches 16; Conservative ?
                                 Query Match
                                                                                                                                                                                                                      TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G
TITLE OF INVENTION: RECO
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                                                                                                                    IMMEDIATE SOURCE:
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                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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Conservative 204; Mismatches
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                   Score 49.6; DB Pred. No. 0.016;
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Query Match
Best Local Similarity
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                                                                                                                                               TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEPAX: 703-816-4100
                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.00
                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855
FILING DATE: 06-Jul-1995
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                                                                             MOLECULE TYPE:
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                                                                                               TOPOLOGY:
                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
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Flores, Maria
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2.7%;
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Maria V
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 Score 48.6;
Pred. No. 0
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US-07-638-431-1
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TELEFAX: (301) 295-4033
INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 4673 base pairs
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ADDRESSEE: A. David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1645 ataatatcacaaattataccttgtattgcccaatttttatgggcatcatttcctattctg 1704
                                                                                       ORGANISM: Piacon ORGANI
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                                      TISSUE TYPE:
                                                                    DEVELOPMENTAL STAGE: erythrocytic stage
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                            Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                   linear
erythrocytic stage
                                      Blood
                                                                                                                                                                                                                                                                                             DNA (genomic)
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; OTHER INFORMATION:
US-07-638-431-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US92-00018-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application GENERAL INFORMATION:
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Best Local Similarity 48.1%;
Matches 165; Conservative
                                                                                                                                                                                           ZIP: 20814 .... COMPUTER READABLE FORM: TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hoffman, Stephen L.
APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
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              NAME: Spevack, Avram D. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759
                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: Py-lambdagt11-2-7 kb CLONE: Py10.1111
                                                                                               APPLICATION NUMBER: POFILING DATE: 19920103
                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
TOTATTON: 718..3195
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                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                       Bethesda
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                                                                                                                                                                                                                                                                                                       Medical Center
                                                                                                                                                                                                                                                         USA
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295-4033
                                                                                                                                                                                                                                                                                                                                                                                      immunogen and
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                                                                                                                  PCT/US92/00018
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                                                                                                                                                                                                                                                                                                                       T-12 National Naval
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RESULT 12
US-08-484-105-15/c
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; OTHER INFORMATION:
PCT-US92-00018-1
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Matches 165; Conservation
                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                          Sequence 15, Applipatent No. 558934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4673 base pairs
                                                                                                                                                                                                                                        GENERAL INFORMATION:
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NAME/KEY: CDS

718..3195
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MOLECULE TYPE: DN
HYPOTHETICAL: N
ANTI-SENSE: N
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                                 TITLE OF INVENTION: ORIGIN OF NUMBER OF SEQUENCES: 24
                                                                                  APPLICANT:
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                 CORRESPONDENCE ADDRESS
                                                                    APPLICANT:
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ADDRESSEE:
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                                                                                                                                                                                                                                                                        Application US/08484105
                                                                             LAURENSON, Patricia
HERSKOWITZ, Ira
LI, Joachim J
                                                                                                                                                    RINE, Jasper
FOSS, Margit
                                                                   GAVIN, Kimberly
                                                                                                                                    MCNALLY, Francis J
                                                                                                                                                                                    KOBAYASHI, Ryuji
                                                                                                                                                                                                                       STILLMAN,
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FLEHR, HOHBACH, TEST,
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                                                   REPLICATION COMPLEX GENES
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 ALBRITTON & HERBERT
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                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08484106 Patent No. 5614618
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Best Local S
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                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
                                      APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1511 gcttattcattattcagtaatcttttatatgcatactattgtaaatgtttcatcattagg 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2398 TAATAGAAGTAGTATCKKWWTWWWYWYKYKTTTWYWKYTTYKTTWTCATGGGCAAA 2339
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LENGTH: 2504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1631 gtttatcatttgtgataatatcacaaatt 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1571 ccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttattctaaca 1630
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NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                             APPLICANT:
                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8700
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                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       GTATAGCTTTTATGCTATCCCAGCAAGTT 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGGTAAGGAAAGTTTTTATACTTTGTTCAATCGGTAAATTGCCTATTTCATCCAAAAA
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Similarity 45.5%;
95; Conservative 1:
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4 Embarcadero Center, Suite
                                                                                                                                                                       MCNALLY, Francis J
                                                                                                                                                                                      RINE, Jasper
FOSS, Margit
                                                                                                                                                                                                                           KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                BELL, Stephen P
                                                                                                                                                                                                                                                                  STILLMAN, Bruce
                                                                                                              LI, Joachim J
                                                                                                                                  HERSKOWITZ, Ira
                                                                                                                                               LAURENSON, Patricia
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                     FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
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Pred. No. 0.044;
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US-08-323-170B-1/c
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                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08323170B Patent No. 5733772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1631 gtttatcatttgtgataatatcacaaatt 1659
                                                                                                                                                                                                                                                                                 APPLICANT: Williamson, Kim C. APPLICANT: Kaslow, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2218 GTATAGCTTTTATGCTATCCCAGCAAGTT 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2278 TAAGGTAAGGAAAGTTTTTATACTTTGTTCAATCGGTAAATTGCCTATTTCATCCAAAAA 2219
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ATTORNEY/AGENT INFI
NAME: Osman Ph.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 494-8700
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                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                    ZIP: 94111-3834
                                                                                                    COUNTRY:
                                                                                                                            STATE:
                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAAAAGATAATTTAAGTCGTAATTTATAATTAGAAGTAAACATTTTAAAAATTCAAGAGG 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttattctaaca 1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAATAGAAGTAGTAGTATCKKWWTWWWYWYKYKTTTWYWKYTTYKTTWTCATGGGCAAA 2339
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45.5%;
                                                                                                                                                                                                                                         Cloning and Expression of Plasmodium faliciparum Transmission-Blocking Target Antigen,
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US-08-323-170B-1
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6483 GGTTTTAATGAAAA 6470
                                                                                                                       1690
                                                                                                                                                             6603 TTATCAAAAGTAAAATTCGATTTCCATAAACCCCTTTCAAAGCTAAACTAATAGATACT
                                                                                                                                                                                                        1630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 9636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
EILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
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mes 257; Conserv
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                                                                                                                                                                                                                                                                                                                                                     cttattcattattcagtaatctttta--tatgcatactattgtaaatgtttcatcattag 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                    tttgtgaaaaaaaa 1763
                                                                                                                                                                                                                                                                                   gccatgaatagtttcgtttgttattatcatcattatcaacttgtcctattttattctaac 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGAAATCA--CATAATTTAAATGAATTTTCTGATACATTTTTCCTAACAAAATATAT 6724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAGTGCACTTTTTTTCTTTTACTTGACTATTTAATTCCATTAATGAAGTCGAACCTGT 6782
                                                                              TCATTTTTTTCTTTTCCTATAACTTTAATATCATTATTGTTATCATCAAAAACTAATGAT 6484
                                                                                                                                                                                                                                            TCTGTATCTTGTTTATTGGAGGTATAAAAAAACTAATTCCTTCTCCTTTTTTTCCATTT
                                                                                                                                                                                                                                                                                                                             TGGAAATATAGCAAAACCTTTAGGACATTTCAATCCAAAAATATCTCCTTTTTTAATTTT 6842
                                                                                                                 tcatttcctattctgtaaacaattcacttatttgcattattgcaattaaaaagtatttca 1749
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                                                                                                                                                                                                                                                               Query Match 2.6%;
Best Local Similarity 52.3%;
Matches 102; Conservative
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5181 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,5
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: | FILING DATE: 18-MAR-| PRIOR APPLICATION DATA: APPLICATION NUMBER: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 1
FILING DATE: 11-JUN-
PRIOR APPLICATION DATA:
                 1756 aaaaaaaaaaaaaa 1770
                                                                                                                                                  1636 tcatttgtgataatatcacaaattatacccttgtattgcccaatttttatgggcatcattt 1695
                                                                                                                                                                                                  3046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
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3226 AATAAGAAAAAGAA 3240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: SI
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TELEX: 425066 CURTMS
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                                                              AATGATACCTATTTTAATGATGATATCAAACAATTCGTAAAATCTAATTCAAAAGTAATT
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de Taisne, Charles
Tine, John A.
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11-JUN-1993
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Search completed: April 16, 2000, 04:35:02 Job time: 9676 sec

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Title:
Perfect score:
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4538634 segs, 1887831982 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21	Result
391.8 22.0 373.8 21.0	sult Query No. Score Match Length DB ID
22.0 21.0	% Query Match
665 628	Length
42 37	DB
AI111196 AA701731	SUMMAR
AI111196 SWOv3MCA1 AA701731 SWOv3MCA1	Description

369.4 365.8 355.8 337.2 314

L3 larva

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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                         Williams,S.A., Lizotte-Waniewski,M., Genes expressed in molting L3 larvae Unpublished (1997) on Sep 12, 1996 this sequence versio Contact: Steven A. Williams
                                                                                                                                                                                                                                                       Onchocerca volvulus.
Onchocerca volvulus
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AII11196
AII11196.1 GI:3510080
EST.
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AI313768
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AI438781
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AV201949
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AA841200 MB3DGAA46
AA61895 SWOV3MCA3
AA625010 SWOV3MCA3
AA625022 SWOV3MCA7
A1322078 SWOV3MCAM
C71078 C71078 YUji
AV203892 AV203892
C67783 C67783 YUji
C70345 C70345 YUji
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70 WEST02691
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SWOV3MCA6
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MB3D6AA4G
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/db_xref="taxon:6282"
/clone="SWOv3MCA1232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Onchocerca volvulus molting
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Pred. No. 1.1e-
0; Mismatches
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SOURCE ORGANISM

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                                                                                                                                                                                                                                             453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 19, 1997 this sequence version replaced gi:1517220 Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AA701731
AA701731.1 GI:2704931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                 slustigm@nybc.org).
1 121 c 125 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="SWOv3MCA1144"
/clone_lib="Onchocerca volvulus molting L3 larva
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 TATTCCGGTTGATAACGGTGTAGAAGGTGAACCAGAAATTGAATGTGGTCCAACATCAAT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ggatggtggaccaaccggtcaaccagttcaatttgctatcattggtcagcc--agtttat 697
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                                                                                                                                                                                                                                                                                                                                                              Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigme Genes expressed in molting L3 larvae of Onchocerca volvulu Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797212.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI322117 639 bp mRNA 5MOV3MCAM12G08SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM12G08 5',
                                                                                                                                                                                                                                                                                      Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
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                                                                                                                                                                                                                               genome@smith.edu
                                                                                           /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM12G08"
               /dev_stage="molting L3"
/lab_host="XL1-Blue MRF
                                                       (SL96MLW-OvmL3)"
                                                                           /clone_lib="Onchocerca volvulus
/note="Vector: Lambda Uni-ZAP
                                                                                                                                                     /organism="Onchocerca volvulus"
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                                                                                                                                                                                                                                                                                                                                                                                          acatggaagctgataaaacagttagtgcacagattgaggtatctgaaatcacaactgctt 593
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                                                                                                                                                                                                      ccggtcaaccagttcaatttgctatcattggtcagccag 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gacaggaagcaatcttagtttttctaaaaatcgaatttactaaatcttctgaaatgatga 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAACAAGTACATCAACAACAACAACAACAACAACAACAACAACAGCAACAGCAACAGGAT 60
                                                                                                                                                                                                                                                             TTGCAACACAAATTGTACCGATGCCTGTATGCCGATATGAGATTCTTGATGGTGGACCAT
                                                                                                                                                                                                                                                                                                                                                                  ACATGGAAGCTGATAAGACAGTTAGCGCTCAACTTGAAGTTTCCGAAATGACAACTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCATTCCATTCTTTGTGACAAAAGTTGATCGAGCATATCGAATACAATGCTTTT
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AA618895 672 bp mRNA EST 12-NOV SWOV3WCA1879SK Onchocerca volvulus molting L3 larva cDNA
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tgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcacttcc 399

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                                                                                               163
                                                                                                                    220 gattccggttgacaatggtgtcgaaggtgagccagaaattgaatgtggaccaacttcaat
                                                                                                                                                                                             103
TACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCTTATA
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                                                                                                                                                                                             TACTGATATTATCATGCTTCGGTTAATAAGCGTATTTGCTATTTATCACTGCTGTAAATGC 162
                      aacaatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtcttta
                                                                                                                                                                                                                                          ttctgaaatgatgattcgtcttattgctttctgtactacacttattgcattgtcttattc 219
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439; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science Center, College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes expressed in molting L3 larvae of Onchocerca volvulumpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405188 Contact: Steven A. Williams
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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Email: genome@si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Filarioidea; Onchocercidae; Onchocerca.
1 (bases 1 to 672)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmenybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. I3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
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EST.
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SWOV3MCAM02C01SK Onchocerca
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Molecular Parasitology
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(bases 1 to 610)
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primer: pBluescript
                                                                                                                                                                            /clone="SWOv3MCAM02C01"
/clone_lib="Onchocerca volvulus
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Brugia malayi.
Brugia malayi analayi bukaryota; Metazoa; Nematoda; Secernentea;
Filarioidea; Onchocercidae; Brugia.
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a 106 c 138 g 178 t 1 others
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                                                                                        atatcattgatgtacgaactgatatcaacacccttgaaattagcgatgataatcaagctt 1142
                                                                                                                                                                                                                                                                                                                                                                                                        caaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaaccggaga 1082
                        gcattgcattgattgctgccgtcattattaccattttcgtttaaattttcgtccaaatcaga 1322
                                                                                                                                                                                       TACCAGTTGACTTACGTCATCGTGCACGTTTGCATCTCGGTGGACAACCAGTGGTACTCG
GCATTGCATTGATTGCTGCCGTCATTGTCACCATTTCCTTGAAATTTCGTCCAATGCAAA
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Molecular Parasitology
Smith College Department of Biological Sciences
Smith College Department of Biological Science Center, Smith
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On May 5, 1995 this sequence version replaced gi:797827
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biological Sciences, C College, Northampton, MA, 01063, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="third stage larvae, nine days after infection"
/lab host="E. coli XLI-Blue MRF'"
/note="Vector: LambdaZap II (UniZAP XR); Site_1: Eco RI
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi
isolated from the peritoneal cavity of jirds nine days
after infection. The mRNA was converted to double
stranded cDNA using reverse transcriptase and oligo (dT)
followed by Rnase H and DNApol I. The library was
constructed by Michelle Lizotte-Waniewski. The library is
available from the Filarial Genome Project Resource
Center: contact Dr. S.A. Williams, Clark Schence Center,
Smith College, Northampton, MA 01063 USA phone +1 413
585-3826 fax +1 413 585-3786 email genome@smith.edu"

174 c 139 g 243 t 13 others
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(SAW97MLW-BmL3d9)"
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Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  College, Northampton, MA, 01063, USA Tel: 4135853826
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Contact: Steven A. Williams
Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome@smith.edu
Seq primer: pBluescript SK
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   157
                                                                                          /dev_stage="molling L3"
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/lab_host="XL1-Blue MRF/"
/lab_host="XL1-Blue MRF/"
/lab_host="XL1-Blue MRF/"
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/clone_lib="Onchocerca v
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/db_xref="taxon:6282"
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                                                                       Dr. Sara Lustigman (email:
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Query Match Best Local Similarity

17.7%; 78.9%;

Score 314; DB 37; Pred. No. 3.7e-53;

Length 537;

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                                                                                                                                                                                                                                                                              Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997) on Jan 14, 1998 this sequence version replaced gi:1797124. Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI322068 552 bp mkwn sWOv3MCAM12A04SK Onchocerca volvulus molting L3 larva cDNA creakuru-nvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM12A04 5',
                                                                                                                                                                                                          Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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AI322068.1 GI:4056219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                           Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
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Location/Qualifiers
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                                                                                                                                                                               genome@smith.edu
            /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                           /clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
                                                                                /burdin="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                         /clone="SWOv3MCAM12A04"
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Lambda Uni-ZAP XR;
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Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Libotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmaphybc.org)."
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RESULT
AI317885
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                           mRNA sequence.
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AI317885.1 GI:
EST.
Onchocerca volv
                                                                                                        SWOV3MCAM06H12SK Onchocerca volvulus molting L3 larva (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MC
                Onchocerca
Eukaryota;
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                               volvulus.
                volvulus
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Secernentea; Spiruria; Spirurida;
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                          aacaa-ctgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtgcatatc 518
                                                                                                                                                         atttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtatttttgtaac 459
                                                                                                                                                                                                                                                                                                                                                                        TACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCTTATA 237
ATCAAGTTGTTGTCATCTCATTCCATCCATTGTTTGTGACAAAAGTTGATCGAGCATATC
                                                                                                                     GTTTGATTCCTGTAATGTAGCACGTACACGTTCGTTAAATCCACGTGGTATTTTTTGTCAC
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Contact: Steven A.
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/lab_host="XLI_Blue MRF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-Stage Information of the I
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Molecular Parasicology OvmL3
Unpublished (1998)
On Jan 19, 1998 this sequence version replaced
Contact: Steven A. Williams
Molecular Description
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AA625020
AA625020.1 GI:2537422
EST.
Onchocerca volvulus.
Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Secernentea;
            Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Scienc
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
                                                                                                              Genes expressed in molting L3
Unpublished (1997)
On May 9, 1995 this sequence v
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                          AA625020 363 bp mRNA EST 12-NOV-1997
SWOV3MCA691SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C0691 5', mRNA
                                                                                                                                                                Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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1 (bases 1 to 363)
Email: genome@smith.edu
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AA625024
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SWOv3MCA758SK Onchocerca volvulus molting L3 larva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2 or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
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a 71 c 77 g 110 t 1 others
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(SL96MLW-OvmL3)"
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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On May 9, 1995 this sequence version replaced gi:802407
Contact: Steven A. Williams
Molecular Parasitology
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/db_xref="taxon:6282"
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/clone_lib="Onchocerca volvulus molting L3
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Institute of Cell, Animal and Popu.
University of Edinburgh
Ashworth Labs, King's Buildings, WA
3JT, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
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MB3D6AA4G10T3 Brugia malayi day 6 post-infection third stage larvae
SAW96MLW-BmL3d6 Brugia malayi cDNA clone 3D6AA4G10 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/3D6/MB3D6AA4G10T3.html
Seq primer: T3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jan 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brugia malayi
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1 (bases 1 to 354)
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          105
recombinants and average insert size was 900 base pairs.
The library was constructed by Michelle Lizotte-Waniewski.
The library is available from The Filarial Genome Project
Resource Center: contact Dr. S.A. Williams, Clark Science
Center, Smith College, Northampton, MA 01063 USA phone +1
413 585 3826 fax +1 413 585 3786 email genome@smith.edu."

81 c 84 g 84 t
                                                                                                                                                                               /dev_stage="third stage larvae, six days after infection"
/lab_host="E. coli XLl-Blue"
/note="Vector: lambdaZapII (UniZap XR); Site_1: Eco R I
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi isolated
from the peritoneal cavity of jirds six days after
infection. The mRNA was converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNASE H and DNAPOL I. The library had 2 x 10E5 independent
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/strain="TRS Labs"
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larvae SAW96MLW-BmL3d6"
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AA618952
AA618952.1
EST.
                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405277.
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA618952 459 bp mRNA EST 12-NOV-1997 SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C02020 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                           Fax: 4135853786
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                                                                                                                                                                                                                                                                                                          genome@smith.edu
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by
                                                                                                         /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                              /clone_lib="Onchocerca volvulus
(SL96MLW-OvmL3)"
                                                                                                                                                                                 /clone="SWmL3CO2020"
                                                                                                                                                                                              /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                     /organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                        Location/Qualifiers
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85.0%;
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Pred. No. 3.3e-44;
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TITLE
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Best Local Similarity 77.8
Matches 318; Conservative
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Unpublished (1997)
On May 9, 1995 this sequence version replacement of Biology 11 Sciences, Sience Northampton, MA, 01063, USA
Tel: 4135853826
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                                                                                                                                                                                                                                                                                                                                                                                             AA625010 395 bp mRNA EST 12-NO SWOV3WCA318SK Onchocerca volvulus molting L3 larva cDNA
                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                                                                                                           Onchocerca volvulus
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a 85 c 91 g 150 t 2 others
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Pred. No. 2.7e-43;
0; Mismatches 91;
                                                                                                                     version replaced
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/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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/lab_host="XL1-Blue MRF'"
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84.0%;
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Pred. No. 1.9e-42;
""smatches 57;
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Search completed: April 16, 2000, 03:08:58 Job time: 6182 sec

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                                                                                                                                                                                                                                                                                                                                            Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in molting L3 larvae of Onchoce Unpublished (1997)
On Sep 12, 1996 this sequence version replaced Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onchocerca volvulus.
Onchocerca volvulus
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
AA618952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, S.A., Lizotte Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA618952 459 bp mRNA EST 12-NOV-1997 SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C02020 5',
                                                                                                                                                                                                                                                                                                                             Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                             Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA618952.1 GI:2522828
EST.
                                                                                                                                                                                                                                                                        /dev_stage="moiting L3"
/lab_host="xL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Nnote="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O; volvulus molt to fourth-stage larvae by
                                                                                                                                                      /clone_lib="Onchocerca volvulus molting L3 larva
(SL96MLW-OvmL3)"
                                                                                                                                                                                                        /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                     /clone="SWmL3CO2020"
                                                                                                                                                                                                                                        organism="Onchocerca volvulus"
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                                                                                                                                                                                                                                                                                                                                                                        Science Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                          gi:1405277
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a volvulus
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TITLE
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Best Local Similarity
Matches 318; Conserv
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Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 413853826 Fax: 4135853786
                                                                                              Williams, S.A., Lizotte-Waniewski,M., Genes expressed in molting L3 larvae Unpublished (1997)
On May 9, 1995 this sequence version Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                 Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                AA625010 395 bp mRNA EST 12-NOV-1997 SWOVJMCA318SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWmL3CO318 5',
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                                                                                                                                                                                                                                                                                                                                                                     sequence.
AA625010
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                                                                                                                                                                                                                                           Filarioidea; Onchocercidae; Onchocerca.
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                                                                                                                                                                                                                                                                                                                                                GI:2537412
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77.88;
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Pred. No. 2.7e-43;
0; Mismatches 91;
                                                                                                                                                                              Laney, S. and Lustigman, S of Onchocerca volvulus
                                                                                                                                        replaced
                                                        Science Center,
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373 TGC 375
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seq primer: pBluescript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="molting L3"
/dev_stage="molting L3"
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In Indiana Uni-Zap XR; Site_1: Eco RI; Site_2: Indiana Uni-Zap XR; Site_1: Eco RI;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Search completed: April 16, 2000, 03:08:58 Job time: 6182 sec

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Database sequences: 188963
Database length: 23686106
Search time (sec): 139.2000
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-Q-/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19878/app_query.fasta.1
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-DB-A_Geneseq_36 -QFMT=fastan -SUFFIX=backtrans.rag
-GAPOP=12.000 -QAPEXT=4.000 -MINANTCH=0.100 -LOOPEL-0.000
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| Sequence of human bone proteogl
| Feline infectious peritonitis
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| GAP protein Ira2. Blocking Ras
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Peptidyl C-terminal alpha-amida
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seq_documentation_block:

ID R20112 standard: Prot
AC R20112

DT ABC R20112

O6-APR-1992 (first e
DE AE-III (peptidylhydro
Nac R20112)

DT O6-APR-1992 (first e
DE AE-III (peptidylhydro
Nac R20112)

EP AE-III (peptidylhydro
Nac R20112)

FT FI (peptidylhydro
Nac R2012)

FT P R465404-A.

PD CB-465404-A.

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A_Geneseq_36:R11110
A_Geneseq_36:R10322
A_Geneseq_36:R80530
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US-09-323-427-2/rev x R20112
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                                                                  1367
                                                                                                                                                                                                                                                                                                1467 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
         548
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Claim 4; Page 18; 28pp; English.

Chaim 4; Page 18; 28pp; English.

The sequence was deduced from a CDNA insert from pAE-III-202-4

(FERM BP-3172). The vector serves as a source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyOH -> R-NH2. It can be used to produce peptides with amidated C-termini, e.g. calcitonin, growth hormone, LH-RH.
                                                                                                                                                                                                                                542 lAlaAspGlyTyr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawahara T, Kangawa K;
WPI; 92-010570/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CIBA ) CIBA GEIGY AG.
Iwasaki Y, Shimoi H, S
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                                                     AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                  CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 1368
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; JP-141678.
; JP-210535.
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/note=."including PAM 383..935
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/product= PHL
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Gaps: 18
Percent Identity: 19.437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aspargGluAsnGly...ArgIleGlnCysPheHisAlaGluThrGlyAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT.....
                                                                                                                                                                                                                                                                                                                                                 CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT 711
                                                                                                                                                                                                                                                                                                                                                                                                                 ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCG 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisargSerValLysLysAlaGlyIleGluValGluGluIleThrGluTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...ATTACCATTAAAGAACCAAAT.....AGCGAATGTGTTCGACC
                                                                                                                                                                                                                                           alGluLysGlnThrGlnGluLysGlnGlnLys......GlnLysAsnSer
                                                                                                                                                                                                                                                                                                                                                                                 rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV 742
                                                                                                     lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
                                                                                                                                                                           {\tt aGlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG}
                                                                                                                                                                                                        TGATATCAACACCCTTGAA.....ATTAGCGATGATAATCAAGCTT 638
                                                                                                                                                                                                                                                                             GCA......GAACCGGAGAATATCATT...GATGTACGAAC
                                                                     GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT 538
                                                                                                                                       TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT 588
CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 491
                                   ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
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p81184; standard; Protein; 1594 Ar p81184; standard; Protein; 1594 Ar p81184; standard; Protein; 1594 Ar p81184; sequence encoded by the 2nd readi g Sequence encoded by the 2nd reading Sequence encoded by the 2nd reading Sequence for 1992 (1992) and 1992 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: A_Geneseq_36:p81184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc of the peplomeric gene in three reading frames. The top reading cc frame is an open reading frame of 4356 nucleotides and has a coding cc capacity for a precursor polypeptide having a mol. wt. of 160,470 cc (1452 AAS). The beginning and the end of the E2 gene are indicated comparison to the FT of N81533. The first 18 N-terminal AAS have a strong comparison to the FT of strong and the end of the E2 gene are indicated comparison. The extreme carboxy-terminal part comprises a region of 20 cpeptide. The extreme carboxy-terminal part comprises a region of 20 cpeptide. The extreme carboxy-terminal part comprises a region of 20 cpeptide. The extreme carboxy-terminal part comprises a region of 20 composition of the N-terminal part (pos. 1-790) which corresponds comparison to the N-terminal part (pos. 1-790) which corresponds to the S-part of the IBV E2 (see p81183). N.B. IBV = infectious of a stop carbon.

Cc common of the IBV E2 (see p81183). N.B. IBV = infectious contains virus. "x" in the AA sequence denotes the translation confidence of a stop carbon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-323-427-2/rev x P81184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: P81184 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoded by the 2nd reading frame of the peplomeric of FIVP strain 79-1146.
Vaccine; peplomeric protein; E2 gene.
Feline infectious peritonitis virus.
Ep-264979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840 leAlaIleAlaIlePheIleArg 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         490 TTACCATTTCGTTTAAATTTCGT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 lSerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene for feline infectious peritonitis virus - and gene produseful as antigenic protein for vaccine Disclosure; Fig 1: 13pp; English. CDNA was prepd. from FIPV straim 79-1146. N81533 gives the second was prepd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Groot RJ, Spaan WJM, Van Der Zeijst BAM
WPI; 88-114147/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1586 ACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGA 1537 :::|||::::||
                                                                                                                                                                                                                                                                                                                                                                            1486
                                                                 1386 ACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCAC 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 SerThrIleMetAlaLeuSerHis.....
109 lyAsnHisLeu.....
                                                                                                                                                                                                                     CAAGAAGGTTGCCGTAATGAAGGAGGTGGACGTCAAGTTGCCGGAATTTC 1387
                                                                                                                                                                                                                                                                                                                                                                    ATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGAT 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uAspThrProLysPheLysCysArgCysAsnAsnAlaLeuIle.ValAsn
                                                                                                                                                                                                                                                                                          LeuLysGluLysGluLeuAsnGluMetVal.....valGlyLeuLe 92
                                                                                                                                       uArgLysGlyLysLeuLeuIleArgAsnAsnGlyLysLeuLeuAsnPheG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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0.376
45.783
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27
18.072
                           .ValAsn
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671 396	CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA ::::::::::::::::::::::::::::::::::	712 380
713 380	61 GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGAT. ::: ::::::::::::::::::::::::::::::::	76 36
762 363	CACAATGTTCAGAAC ::: ::: LeuThrSer	811 349
812 348	2 CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTTCGAC ::::: ::: ::::: 3 laLeuLeuProGlyAsnThrValLeuHisMetLeuThrLysValPhe	33 8
853 333	AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGAT	893 316
894 316	ATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC:::	943 313
944 312	93 GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATA ::: :::::::: ::: 98 erGlyMetMetThrLeuLeuGlnLeuIleLeuValValValLeu	993 298
994 298	36TTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGT	103 28
103 7 281	65 SerProProThrSerGlyIleProHisValArgValLeuThrGluLysPh	26
1037 264	8AATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGC :::	24
1079 248	2 CATA :::: 1 lLeuLeuT	108 23
1083 231	GACCAACCGGTCAACCAGTTCA ::: ::::: MetHisValValAsnHisTyrT	1132 215
1133 214	leTyrMetProPheIleLe	1141 198
1142 198	2CAGTATGCCGTTATGAAATTT ::::: 1 yThrThrAlaLeuGluGlnLeuGluLeuProPheSe:	1162 181
1163 181	AAATCACAA :::::: LysLysLysGluVa	1201 165
1202 164	CATGGAAGCTGATAAAACAGTTA:: :::	1245 148
1246 148	91TATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTA ::: :::::::::::::::::::::::::::::	1291 131
1292 131	36 GTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTGATCCAT	133 11

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seq_documentation_block:
ID R87953 standard; Protein; 332 AA.
AC R87953;
DT 20-MAR-1996 (first entry)
DE Bovine neurotrophic biglycan.
KW Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
KW neurotrophic; central nervous system; CNS; memory loss; dementia;
KW learning.
OS Bos taurus.
FT region 7. .23
FT w09530432-A1.
PD 16-NOV-1995.
PF 09-MAY-1994; WO-E01479.
PF 09-MAY-1994; WO-E01479.
PF 09-MAY-1994; WO-E01479.
PR 09-MAY-1994; WO-E01479.
PT memory deficit (s) in the elderly and patients with dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: A_Geneseq_36:R87953
Mueller HW; WPI; 95-403938/51.

Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 TTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522 ...PheThrMetAlaGlnLeuLeuAsnIle***GluHisTyrHisProVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 erArgSer...Ala***LeuThrAspHisAspThrValMetTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 heHis***IleGlnGlnValValSerPheLeuLysPheHisValIleVal 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 hrīleSerLeuAlaHisPheLeuLeuValValTyrLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 CTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTATTCAGTA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACC
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alignment_scores:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 8: 60pp; English.
Bovine biglycan (R87953) is a chondroitin sulphate proteoglycan with Bovine biglycan (R87953) is a chondroitin sulphate proteoglycan with Bovine biglycan (R87953) is a chondroitin sulphate proteoglycan and remarked in the structure and function of CNS neurons the survival and maintain the structure and function of current ageing as well as after pathological and/or traumatic during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients with Jamanaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                     432 TCGAAGCAATA.....
                                                                                                                                                                                                                                160 GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy 176
                                                                              186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProLeuArg......LysLeuGlnLysLeuTyrIleSerLy 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euValLeuValAsnAsnLysIleSerLysIleHisGluLysAlaPheSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGCACCTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568
                                                                                                                                                                                                                                                                                                                                                                                       lGluLeuArgIleHisAspAsnArgIleArgLysValProLysGlyValP 143
                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAATCAGAAGGCATAAAAATAATGTTAGA.....ATCA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....LeuProSerSerLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 518
                                                                                                                                                        rLeuArgIleSerGluAlaLys......LeuThrG
                                                                                                                                                                                                                                                                                                            heSerGlyLeuArgAsnMetAsnGluIleGluMetGlyGlyAsnProLeu 159
                                                                                                                ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC
                                                                                                                                                                                            TATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA 358
LeuAspHisAsnLysIleGlnAlaIleGluLeuGluAspLeuLeuArgTy
                                        ATCARAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA
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                                                                            .....ProLysAspLeuProGluThrLeuAsnGluLeuHis
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seq_documentation_block:
ID R87951 standard: Prot
AC R97951 standard: Prot
AC Poly Control
AC R87951 standard: Prot
Biglycan: proteoglyca
KW learning.
OS Rattus Sp. Locat
FT peptide 1.3
FT peptide 1.3
FT peptide 1.3
FT peptide 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) proteoglycan cpds., partic. chondroitin of the CNS and attenuating proteoglycan cpdficit(s) in the elderly and patients with dementia proteoglycan (R87951) is a chondroitin sulphate proteoglycan with cc neurotrophic activity for brain neurons. Recombinant biglycan, cc obtd. by expression of encoding cDNA (T08768) in eukaryotic host cc cells, can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after can discompany companies and 
                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                  US-09-323-427-2/rev x R87951
                                                                                       Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                      Percent Similarity:
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Rat neurotrophic biglycan; chondroitin sulphate; neuron protection;
Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
Biglycan; central nervous system; CNS; memory loss; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R87951 standard; Protein; 369
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775 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA 726
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CTCA.....AGAAAAGAT.....

103

eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 120

.....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 668

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seq_documentation_block:

ID R87952 standard; Protein; 369 AP AC R87952;
DT 20-MAR-1996 (first entry)
DE Human neurotrophic biglycan.
KW Biglycan; proteoglycan; chondroi
KW neurotrophic; central nervous sy
KW learning.
OS Homo sapiens.
FH Key 11.37
FT region /label= Sig_pept
FT region /label= Hypervar
PN W09530432-Al.
PD 16-NOV-1995.
PF 09-MAY-1994; WO-E01479.
PP 09-MAY-1994; WO-E01479.
PP 09-MAY-1994; WO-E01479.
PP NOMAY-1994; WO-E01479.
PP NOMAY-1994; WO-E01479.
PP NOMAY-1994; WO-E01479.
PP P O9-MAY-1994; WO-E01479.
PP P O9-MAY-1994; WO-E01479.
PP P O9-MAY-1994; WO-E01479.
PP P O9-MAY-1994; WO-E01479.
PP FOTEOGRAPH MANNHEIM GMBH
PI Hasenoberla R, Huston J, Jungha
PI Mueller HW;
PP O9-MAY-1994; WO-E01479.
PP POTEOGRAPH MANNHEIM GMBH
PI Hasenoberla R, Huston J, Jungha
PI Hasenoberla R, Huston J, Jungha
PI GO-MAY-1994; WO-E01479.
PP O9-MAY-1994; WO-E01479.
PP O9-MAY-1995.
PP O9-MAY-1995.
PP O9-MAY-1995.
PP O9-MAY-1995.
PP O9-MAY-1995.
PP O9-MAY-1995.
PP O9-MAY-1994; WO-E01479.
PP O9-MAY-1995.
PP O9-MAY-19
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US-09-323-427-2/rev x R87952
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                                                                                                                                                                                                                                    148
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Human biglycan (R87952) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patient with Ammentia
                                                                                                                                                                                                                                                                                                                                                                                   137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 120
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Biglycan; proteoglycan; chondroitin sulphate; neuron protection; neurotrophic; central nervous system; CNS; memory loss; dementia;
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GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT
                                                                                                                                              AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 518
                                                                                                                                                                                                                             sAsnHisLeuValGluIleProProAsn....
                                                                                                                                                                                                                                                                                         CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568
                                                                                                                                                                                                                                                                                                                                                            ProLeuArg.....LysLeuGlnLysLeuTyrIleSerLy
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC
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/label= Hypervariable_region
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Gaps: 13
Percent Identity: 20.401
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432 180

TCGAAGCAATA.....

heSerGlyLeuArgAsnMetAsnCysIleGluMetGlyGlyAsnProLeu

CCAAATCAGAAGGCATAAAAATAATGTTAGA.....ATCA 433

.....Va

163

157

157

lGluLeuArgIleHisAspAsnArgIleArgLysValProLysGlyValP 180

GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy

213 408 196

.....ATAAAACTGCCATA

TATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA 358

ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC rLeuArgIleSerGluAlaLys............LeuThrG

308 223

lyIle......ProLysAspLeuProGluThrLeuAsnGluLeuHis

163 467 517 157 567 148 617 137 667 120 712 103

GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTTCGT 468

AAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAA 518 sAsnHisLeuValGluTleProProAsn..... CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568 euValLeuValAsnAsnLysIleSerLysIleHisGluLysAlaPheSer 136

ProLeuArg.....LysLeuGlnLysLeuTyrIleSerLy 148

CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC

618

seq_name: A_Geneseq_36:R87952

313 129

leThrLysValGlyIleAsnAspPheCysProMetGlyPheGlyVal 328 TCACAAATTATACCTTG.....TATTGCCCCAATTTTTATGGGCATC 89 163 280 164 263 207 253 257 237 307 223 357 213 407 197 421

yLeuProAspLeuLysLeuLeuGlnValValTyrLeuHisSerAsnAsnI

LeuArgGluLeuHisLeuAspAsnAsnLysLeuSerArgValProAlaGl 296

.....ATTTTATTCTAACAGTTTATCATTTGTGATAATA 130

isAsnGlnIleArgMetIleGluAsnGlySerLeuSerPheLeuProThr

164 279 164 263 208 253

ATGAATAGTTTCGTTTGTTATTATCA...TCATTATCAACTTGTCCT...

rSerLysLeuTyrArgLeu......GlyLeuGlyH

TTCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC

LeuAspHisAsnLysIleGlnAlaIleGluLeuGluAspLeuLeuArgTy ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA

DET PR	35 22 30 30 25 25 25 27 27 27 27 27 27 28 29 30 30 30 30 30 30 30 30 30 30 30 30 30	158 467 163 432 180 421 197
p94856; p94856; p94856; 27-JUN-1990 (first entry) p94856; 27-JUN-1990 (first entry) pour-soion plasmid pUCPICI799 BglII gene product. Expression plasmid puCPICI799 alpha amidetic. Expression plasmid splan amide; ds. Synthetic. Expression plasmid splan amideting enzymes of xenopus laevis of yellows, kitano k, tano k, ta	7 ATATATAGTATGTAGGANATAATTACTGTAATACAATAAGCATATATACAATAAGTATATAGTATAGTATGTAGGANATAATTACTGTAATACAATAAGCATTATAGTAGTATATAGTATATAGCTTTATATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGCTTTATAGGTTAAAAGCTTATAGGTAAGGTTTAGGGTAGAGGTTAGGTTAGGTTAGGGTAGAGGTTAGGTTAGGGTAGAGGTTAGGGTAGAGGTTAGGGGAGTGGAGAGTTAGGGGAGTGAGAGGAG	CCAAATCAGAAGGCATAAAAATAATGTTAGA. CCAAATCAGAAGGCATAAAAATAATGTTAGA.

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US-09-323-427-2/rev x P94856
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Percent Similarity:
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seq_name: A_Geneseq_36:P94854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1517 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also N93060.
Sequence 693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1467 AGGACATGTTTATGTGAAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1417 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 1368
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                                                                                                                                                                                                                                                                                                                                                      1183 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     545 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 545
                                                                                                                                                                                                                                                                                                                                                                                                                                          562 AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                                                                                               1083 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTG 1034
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577 uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 593
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                                                                                                                                                                                                                                                                 593 laValSerTyrAlaPro......Gly 599
                                                                                                                                                                                                        611 rGly.......AspSerThrProValGlnGlyPhe....... 620
                                                                                       629 ......IleLeuAspThrPheIleProAlaArgLysAsnPh 640
                                                                                                                    983 AATGCTGATGGATGTGCTCTTGATAAATATTTG......CTAAATAATTT 940
                                                     640 eGluMetProHisAspIleAlaAlaGlyAspAspGlyThrValTyr 655
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0.945
43.103
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Gaps: 12
Percent Identity: 21.552
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seq_documentation_block:

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alignment_scores:
Quality:
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EP-299790-A.
18-JAN-1989.
15-JUL-1988; 306508.
17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
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 632 laValSerTyrAlaPro....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.

Plasmid pAx799 contains a sequence derived from Xenopus laevis. The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.

Although the gene product is similar to that of pXA457 at the N-terminus, it has an area of hydrophobic elements suggesting a membrane function. See also N93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUNR) Suntory Ltd.
Obsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno
WPI; 89-017279/03.
N-PSDB; N90791.
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P94854;
P94854;
C-terminal prepro-C-terminal alpha-amidating enzyme of pxA799.
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                                                                                                                                                                                                                                                                           nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
                                                                                                                                                                                                                                                                                                                                                                                    AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
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                                 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 1134
                                                                uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
                                                                                                 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 1184
                                                                                                                                     AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                                                                                                     AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 1231
                                                                                                                                                                                                         leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla 600
                                                                                                                                                                                                                                            ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
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0.945
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12
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638
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seq_documentation_block:
ID R73053 standard: Prot
AC R73053;
DT 06-NOV-995 (first e
DE Peptidyl C-terminal a
KW Peptidyl C-terminal a
FT Peptidyl 
                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-323-427-2/rev x R73053
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                                                        1467 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                       1517 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
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Increasing protein prodn. from cultured animal cells - by adding Increasing protein prodn. from cultured animal cells - by adding a trichostatin to the medium, effective at low concn. and not injurious to host cells

Disclosure; Page 10-15; 19pp; English.

3mu-15 cells (i.e. CHO cells expressing a peptidyl C-terminal alpha-amidase enzyme (AE)) were suspended in F-12 medium to which aliquots of trichostatin were added. Cells were cultured for 3 days at 37 deg and then assayed for AE. Without trichostatin, AE productivity was 708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities were respectively 866, 1897, 1894 and 3359 U/ml.

Sequence 875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1133 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 1084
546 lAlaAspGlyTyr...
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                                                                                                                                   CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
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enzyme;
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Ratio:
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US-09-323-427-2/rev x W13825
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Ratio: 0.393
Percent Similarity: 47.648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1003 GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1053 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG 1004
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                                                                                                                                                                                                                                                                            384
                                                                                                                                                                                             401 HisValGlnLeuLeuTieAsnLeuLysIleSerProLeuMetLysSerGl 417
748 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCACAGATTGAGG.....TATCTGAAATCACAAC 1192
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                                                                                                                                                                                                                                    CAC...AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA 831
                                                                                                                                                                                                                                                                          eulleSerSerGlyLeuLeuTyrLeuGlnAspSerAsnAspLysPheVal 400
                                                                                                                                                                                                                                                                                                             TCACGTAT .....ACAAATATGCGGATCGAT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....pheSerAlaGlnLysArgValValSer 356
                                                                                                                                                                                                                                                                                                                                                      .....ileThrTyrGlyIleIleLysValProThrTyrIleArgLysL 384
                                                                                                                                                        A.....ATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA 793
                                    AG.....GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG 749
                                                                                                                    1226 ĀA;
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Gaps: 24
Percent Identity: 19.632
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seq_name:
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                                   InLeuIleSerLeuLys 714
                                                                                                                                     CCCAATTTTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTT
                                                                       GCATTATTGCAATTAAA 41
                                                                                                         tSerIlePheLeuLysArgLysAspPheThr..
                                                                                                                                                                                                            TTCTAACAGTTTATCATTTGTGATAATATCACAAATTATACCTTGTATTG
                                                                                                                                                                                                                                                erLysGlnPheGlnLysAlaArgAsnAsnVal......
                                                                                                                                                                                                                                                                                     ATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCCTATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euLysAsnAspLysSerGluValLeuLysValTyrSerMetIleAsnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gIleGluLeuGlnSerValTyrAsnAspGluLysLeuLysThrGluLysL 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATACAATAAGTGATATTTTC.....ATCAAAACTTCTTCTA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eLeuPheThrLysThrPheIlePheIleTyrLysLysValLeuLysGluL 569
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                                                                                                                                                                                                                                                                                                                       lAsnIleArgPheLeuLeuHisAsnSerGluIleIleAspThrAsnThrS
                                                                                                                                                                                                                                                                                                                                                       .....TTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC
                                                                                                                                                                                                                                                                                                                                                                                             SerAsnGlnAlaValGlyGlnThrTrpAsnPheProGluValPheGlnVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lnLeuLeuSerAsp......IleGluSerLeuGluAlaLeuMetAsp
                                                                                                                                                                            \dots. {\tt MetLeuLeuIleAlaThrAsnLeuLysGlnTyrAsnLysPheMe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \tt uGluValPheHisHisPhePheLysTrpIleGluPheIleValTyrHisG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etValAlaGluTrpTyrLeuSerHisLeuCysSerGlyIleLeuSerSer
A_Geneseq_36:R99462
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                                                                                                       .AsnLysAsnLeuIleG
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alignment_block:
US-09-323-427-2/rev x R99462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                             1496 ATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGG 1447
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                                                                     1446 TCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  916 IleSerIleAsnProAsnProLysValAspSerAspLeuGlnLeuLys.. 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 83-94; 145pp; English.

The DNA sequence (T34137) which encodes the biosynthetic enzymes of icosapentaenoic acid (EPA) can be used to transform Escherichia coll The DNA sequence allows efficient microbial production of EPA, which is a raw material for drugs, agrochemicals, foods and animal feedstuffs. EPA is also useful for lipid balance correction and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an antihypertensive, antiinflammatory and anticancer agent. Sequence 2756 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of icosapentaenoic acid using transformed DNA coding for icosapentaenoic acid synthase derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAGA ) SAGAMI CHEM RES CENTRE.
Kato S, Kondo K, Yamada A, Yazawa
WPI; 96-342288/34.
N-PSDB; T34137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shewanella putrefaciens. W09621735-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; anticancer agent.
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Biosynthetic enzyme of icosapentaenoic acid synthase.
Icosapentaenoic acid synthase; EPA; drugs; agrochemicals; foodstuffs; animal feed; lipid balance correction; anthypertensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R99462 standard; Protein; 2756 AA
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13-JAN-1995; JP-004299.
       S
                                                                                                                                                                                                                                                            PG1y.....AlaArgValPheValGluPheGlyProLysAsnIleLeuG
                                                                                                                                                                                                                                                                                           TGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA.... 1500
                                                                                                                                                                                                                                                                                                                                  ArgPheThrSerGlnLeuGluAlaMet......TyrAsnAs
                                  lnLysLeuValGlnGlyThrLeuValAsnThrGluAsnGluValCysThr
                                                                                                                                                                                                                                                                                                                                                                      GCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAA 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATT 1596
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                                                                                                                                                                                                                                                                                                                                                                                                           ysīleLysAlaSerPheLysLysHis.....MetLeuGlnSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aLeuTyrSerAsnAlaThrGlyGly...LeuTyrGluSerThrAlaAlaL
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 .GGAATTTCACTT...
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0.389
46.800
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Gaps: 23
Percent Identity: 18.400
.CCATTTGATTCATGCAAT 1365
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from She
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seq_documentation_block:

ID R05159; standard; prot
AC R05159; standard; prot
AC R05159; of first e
DF 09-CCT-1990 (first e
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US-09-323-427-2/rev x R05159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632 GTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAAT 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582 ACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 TGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone matrix DNA and proteins used in detection, diagnosis and treatment involving skeletal and/or connective tissue disease states.

and/or connective tissue disease states.

pisclosure; p; English.

probes and Abs raised to the proteins can be used to determine probes and Abs raised to the proteins can be used to determine their levels useful in diagnosis of associated conective tissue their levels useful in diagnosis of sosteo/rheumatoid arthritis, diseases states such as osteoporosis, osteo/rheumatoid arthritis, paget's disease, artherosclerosis and periodontal disease.

Proteins may also be used to induce or block biological function. Sequence 368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence of human bone proteoglycan I (biglycan).
Osteoporosis; rheumatoid arthritis; Paget's disease;
atherosclerosis; periodontal; human bone matrix; proteoglycan.
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3-NOV-1989; US-432044.
(USSH) Nat Inst of Health.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA 726
                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                              712
                                                                                                                                                                                                                                                                                                                                                                                                                                              102 eSerGluLeuArgLysAspAspPheLysGlyLeuGlnHisLeuTyrAlaL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   725 CTCA.....AGAAAAGAT......713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||:::::: |||::::::||||||::::|||
86 LysGluIleSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspIl 102
laGluThrAlaLeuSerAlaThrLysValGlnAlaThrMetLeuGluVal 1265
                                                                                                                                                                                                                                                                                                     ||| ||| |||| ::::::||| ::::::|||
euvalLeuvalAsnAsnLysIleSerLysIleHisGluLysAlaPheSer 135
                                                                                                                                                                                                                                                                                                                                                                      CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 668
                                                                                                                                             ProLeuArgAsnVal......GlnLysLeuTyrIleSe 146
                                                                                                                                                                                                                         CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 618
                                                                            CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568
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0.730
41.472
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Gaps: 14
Percent Identity: 19.732
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seq_name: A_Geneseq_36:R88469
                                                                                                                                                                                                                                                                                                         documentation_block:
R88469 standard; Protein; 1464 AA.
DNA encoding feline infectious peritonitis I virus spike protein - used in a vaccine for prevention and treatment of FIPV-I infection claim 1; Page 14-17; 23pp; Japanese.
                                                                                                                                                                                                             Feline infectious peritonitis 1 virus spike protein. Feline infectious peritonitis 1 virus; FIPV-I; spike vaccine; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                          312
                                                                                                                                                                                                                                                                  R88469;
14-AUG-1996 (first entry)
                                                                                            10-JUN-1994; 129300.
10-JUN-1994; JP-129300.
(KITA) KITASATO KENKYUSHO
                                                                                                                                                           J07327683-A.
19-DEC-1995.
                                                                                                                                                                                             Feline infectious peritonitis 1 virus
                                                               N-PSDB; T10166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 yLeuProAspLeuLysLeuLeuGlnValValTyrLeuHisSerAsnAsnI
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                                                                                                                                                                                                                                                                                                                                                                                                  leThrLysValGlyValAsnAspPheCysProMetGlyPheGlyVal 327
                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuArgGluLeuHisLeuAspAsnAsnLysLeuAlaArgValProSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt is AsnGlnIle ArgMetIle Glu AsnGly Ser Leu Ser Phe Leu ProThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAATAGTTTCGTTTGTTATTATCA...TCATTATCAACTTGTCCT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAspHisAsnLysIleGlnAlaIleGluLeuGluAspLeuLeuArgTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATATTCGTTTCTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ATTTTATTCTAACAGTTTATCATTTGTGATAATA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heSerGlyLeuArgAsnMetAsnCysIleGluMetGlyGlyAsnProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lAspValArgIleHisAspAsnArgIleArgLysValProLysGlyValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAATCAGAAGGCATAAAAAATAATGTTAGA......ATCA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rLeuArgIleSerGluAlaLys.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyIle.....ProLysAspLeuProGluThrLeuAsnGluLeuHis 235
                                                                                96-072341/08.
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                                                                                                                                                                                                                              spike protein;
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875

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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                    1035 TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1305 TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1390 TTTCACTTCCA.....TTTGATTCATGCAAT.....GTTGCGCGT 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               974 GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA
                                                                                                                                                                         985 TA.....AATGCT.....GAT
                                                                                                                                                                                                                     890 r.....TyrValCysAsnGlyAsnThrHisCysLeuLysLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 alAsnGlnThrAspLeuPheGluPheValAsnAsnThrGlnAlaArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host cell with the spike protein DNA and expressing the sequence such that the spike protein can be isolated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     739 LysAsnSerThrThrGlyGluIlePheThrValValProCysAspLeuTh
GlyAlaArgLeuGluSerLeuMetLeuAsnAspMet
                                                                                                                                                                                                                                                                                                            TyrIleGlnIleGlnValLysProValValValAsp.....CysAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                   hr {\tt GlyAsnIleSerIleProLysAsnPheThrValAlaValGlnAlaGlu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rHisValGluIleValAspAspSerIleGlyValIleLysProValSerT 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA 1206
                                                                                                                                 euThrGlnTyrThrSerAlaCysGlnThrIleGluAsnAlaLeuAsnLeu
                                                                                                                                                                                                                                                                                                                                                         TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT 1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAA 1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oGlnPheTyr.....TyrIleThrLysTrpAsnAsnAspThrSerSerA 818
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0.508
46.597
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Gaps: 16
Percent Identity: 19.895
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US-09-323-427-2/rev x W88310
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1552 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1461 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1502 ATAACAATCAATTTTAATACACGTAATGCATTCGAAGGAC......A 1462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1361 GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGT 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1411 GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1311 TGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG...ATCGTGCAT 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                             1214 ATTGAGGTATCTGAAACTGAAACTGCTTTTCAAACTCAAATTGTCCCGAT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1264 ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAG 1215
                                                                                                                                                                                                                                                                                                                                                                                1164 GCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAG 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1048 CTTTCTGCGCGCTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGAT 999
                                                                                                                                                                                                                                                                                                                                                                                                                        125 gLeu.....SerAspPheLeuAlaSerIleThrThrAsnValS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 ThralaHisAsnLysAsnGluGlyGlyAsnAlaArgMetPheCysTyrAr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 erPhePheArgAlaLeuPheGinValLysLysIieIleValAlaLeuLys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 ......ileHisTyrValAsnMetAspLysAsnPheArgS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 LysasnLysIleValGluIleProAsnPheIleAsnThrAsnLysPheAs 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 ....... 92
                                                                                                                                             998 ACTGTGGAA.....ATTCTAAATGCTGATGGATGTGC 967
                                                                                                                                                                               169 pPheAspIleAsnValArgLysLysThrArgAspAlaPheAsnLeuLysA 186
                                                                                                                966 TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGAT...... 924
                         209 alleAsnHisLeulleLeuSerLysThrSerAsnCysAsnAspPhelleL 226
                                                                                                                                                                                                                                                                                                                                                             erLysGluAlaValGlnGluPhe.....IleAlaArgLysAlaThrPro 152
                                                                                                                                                                                                                                                           ......AAATGGACATGCGATTCTGAAACCGTTGATA 1049
Quality:
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0.533
46.281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 363
Gaps: 18
Percent Identity: 21.763
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1742 ACTGCAGCAACAACAACAACAACAACAAACAACAACAACAA
Align seq 1/1 to: R59926 from: 1 to: 3079
alignment_block: US-09-323-427-2/rev x R59926
alignment_scores: Quality: 89.00 Length: 752 Ratio: 0.264 Gaps: 42 Percent Similarity: 44.814 Percent Identity: 18.617
Case the case that the case th
8/5 CAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAA837

917	TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGG (966
2592	LeuLeuIleAspValGlyProArgGluLeuArgSerSerLeuHisGlnL	2575
967	TGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	1016
1017 2575	ATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTTGTC::: ::: LeuLeuValGlnMetTyrLeuProGluIleLeuPheIleValSe:	1066 2561
1067 2560	ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG 	2544
2544	AlaMetThrGlnSerTrpSerG	2537
1117	CCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACC	1166
1167 2536	AWATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG :::::: ::: ::	2525
52	LeuProThrThrGluValAlaAsnAsnIleileGlnLysIleLeuAla	50
1217	CTGATAAAACAGTTAGTGCAC	1237
2508	::::: ::: uArgAspSerGluAsnArgAspTrpLysLysThrIleSerLeuLeuThrV	2491
1238	TGCTTTTACATGGAA	1259
1260 2491	CGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGA	2475
2474	spPheLysAlaValTyrMetGlnTyrValTrpLeuLeuLeuLeuL	2458
1304	GAATCCACGTGGTATTTTGT	1344
2458	nIleSerHisIlePheArgIleLeuIleArgLeu	2441
1345	TCACTTCCATTTGATTCATGCAATGTTGCGCGTACACC	1388
2441	AsnLeuTyrGlnHisValTyrLeuAlaAspAspGluGluGlyPr	2425
ءَ د	TAGATGATTATTT THEOLOGY TO BE TAGATGATGATGATTATTT TO THE TAGATGATGATGATGATGATGATGATGATGATGATGATGA	1423
2 2	GAAAGGTCTTTATGATCAAGAAGGTTGCC	1452 2408
2408	AlaTyrMetPhe.IleTyrValLeuGluAlaLeuLysAs	9
1453	ACAATCAATTTAATACACGTAATGCATTCGAAGGAC	9
2391	heLeuGlyValIleGlyL	2375
1500	GGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACC	1544
2375	rHisPheHisArgSerProGluValTyrValProGluAspThrThrTh	2358
1545	· · · · · · · · · · · · · · · · · · ·	1559
2358	TyrAsnLeuIleAlaAlaThrGluAlaSerPheGlyLeuAsnPheGly	2342
1560	ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTC	1607
2341		2325
9	TTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAA	1648
ω c	::::::::::::::::::::::::::::::::::::	2316
164	B AGCAATAATAACCCCCATCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAG	1698

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ID R42452 standard; Protein; 1634 AA.

RA R42452;
AC R2452;
DT 27-MAY-1994 (first entry)
DE Enzyme involved in elcosapentaenoic a
Enzyme involved in elcosapentaenoic a
Enzyme involved in elcosapentaenoic a
Enzyme involved in elcosapentaenoic a
Enzyme involved in elcosapentaenoic a
Enzyme involved in elcosapentaenoic a
Eph; elcosapentaenoic acid synthetase
KW hypolipemic; hypoglycemic; antihypert
KW foodstuf; additive.
OS Shewanella putrefaciens.
PN W09323545-A.
PD 25-NOV-1993; J0641.
PN 15-MAY-1993; J0641.
PN 15-MAY-1993; JP-147945.
PR (SAGA) SAGAMI CHEM RES CENTRE.
PA (SAGAMI CHEM RES CENTRE.
P
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                                                                       alignment_block:
US-09-323-427-2/rev x R42452
                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                           Ratio:
percent Similarity:
Align seg 1/1 to: R42452 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2874 GluHisGlnIleAsnGlnLysSerAspHisTyrLeuCysTyrMetPheLe 2890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2857 ysSerThrAlaPheAspPheLeuLysMetMetPheArgAsnSerTyrPhe 2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2890 uLeuTyrPheValLeuAsnCysAsnGlnPheGluGluLeuLeuGlyAspV 2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2924 LysIleLeuLeuGluTrpLeuSerSerAspAsnGluAsnAlaAsnIleTh 2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2940 rLeuTyrGlnGlyAlaIleLeuPheLysCysSerValThrAspGluProS 2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TATGCATACTATTGTAAATGTTTCATCA......TTAGGCCATG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2974 IleCys.....AlaLeuArgPheTyrSerValIleArgAsnGluIleAr 2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2957 erargpheargphealaLeuIleIleargHisLeuLeuThrLysLysPro 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 CTTGTAT ..... 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 AATAGTTTCGT.....TTGTTATTATCATCATTATCAACTTGTCCT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2988 gLys 2989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q51128.

Gene coding for eicosa-penta:enoic acid synthetase - is isolated for from Pseudomonas, Alteromonas or Shewanella and used for recombinant prodn. of eicosa-penta:enoic acid claim 6; Page 52-63; 106pp; Japanese.

Claim 6; Page 52-63; 106pp; Japanese.

EPA is useful as a drug, having anticoagulant, hypolipemic, hypolycemic, antihypertensive and anticancer activity. It is also hypolycemic, antihypertensive and anticancer activity additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1993.
14-MAY-1993; J0-0641.
15-MAY-1992; JP-147945.
15-MAY-1992; JP-147945.
(SAGA) SAGAMI CHEM RES CENTRE.
(SAGA) KONDO K, Yamada A, Yazawa K;
WPI; 93-386577/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzyme involved in elcosapentaenoic acid (EPA) synthesis. EPA; elcosapentaenoic acid synthetase; drug; anticoagulant; hypolipemic; hypoglycemic; antihypertensive; anticancer; perfoodstuff; additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AAAA 8 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alAspPheGluGlyGluMetValAsnIleGluAsnLysAsnThrIlePro 2923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GCTTCTGAAAAGCTTATTCATTAT...TCAGTAATCTTTTA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTT
                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                          88.00
0.376
46.800
                                                                                                                                                                                             Gaps:
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18.200
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99	TAACGGTGAT ::: nTyrGlyGlu	042 081
1043	GCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCT	092
1093 1068	TGCTATCATTGGTCA ::: :: nSerIleSerGlyAs	142 054
1143 1053	CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATT : :	.192
1193 1037	CTGAAATCACAA :::::::::::::::::::::::::::::::	1020
1240 1020	CGTGCATATCGAGTACAATGCTTTTACATGGA :::::: GluvalGluLysTleValGluLysValValGl	ō ä
1290 1003	TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTA ::: ::: ::: ::: ::: ::: :::	80 (2)
ω .	aAsnHisIleSerLysAlaThrArgAlaLysMetAlaLysSerLeuGluT	970
1329		1329
1329 970	GTTGCGCGTACACGATCTCTGAATCCACGTGGTATT	1364 954
1365 953	CCGGAATTTCACTTCCATTTGATTCATGCAAT	1396 938
1397 938	TCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTG	1446 932
1447 931	ATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATG :::::: ::: :::::: ::::::::::	1496 916
, <u></u>	 InLysLeuValGlnGlyThrLeuValAsnThrGluAsnGluValCysTh	ió.
4	AC	1499
1500 899	5 TGGTGTCGAAGGTGAGCCAGAAATTGAATGTTGGACCAACTTCAATA	1545 884
1546 884	: 1	159! 87:
1596 872	5 TTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCGTCTTATT :::	164 85
1646 859	5 AATAATAACCCCATCAAGTGGAGGAAGAAGAAGAAGGAAG	169 84
1696 843	-> CUGNITGUAGCAACAACAACAACAACAACAACAACAACAACAACAACA	827

532 TGTT 1249 laG1	582 ACTT	632 GTTG 1228 Val.	682 GAAC 1211 hrTh	713 1197 oThr	761 GCAC 1181 Alav	811 CAC/ 1173 erG]	861 ATG0 1163 aPro	911 CAA(::: 1147 Ser/	935 1130 lnA	969 TGC	998 ACT 1097 Thr
TATGGGTTTAAGCAT) ::: uThrAlaLeuSerAla	GCTGCAGTACAAAAT(:::::::::::::::::::::::::::::::::	ATTTACGTCACCGTG	TGATATCAACACCCT' ::::: AlaValGlnThrAl	TCTGCAGAACCG	CAAAACCTGCTGCAG: ::::: ::: alGlnProValIles	CACAATGTTCAGAACCACAA ::: erGlnValValGlnSerGln	CAGATCAGTATTACC	;AAGCTCACGTATACA ::: snIleAlaAlaLeuA	aGlnThrLeuGlnSe	CTTGATAAATATTTG ::: 1leProGluSerLeu	TGGAAATTCTAAATG : heThrThrLeuMetT
TGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATT ::: ::: laGluThrAlaLeuSerAlaThrLysValGlnAlaThrMetLeuGluVal	ACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAA ::::::::::: nThrSerValAlaThrThrThrProSerAlaPheSerA	GTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAAT	GAACTGATATCAACACCCTTGAAATTAGGGATGATAATCAAGCTTTGCCA :::::	TCTGCAGAACCGGAGAATATCATTGATGTAC ::: :::	GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA	CACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC ;:: erGinValValGinSerGinthr	ATGCCAGATČAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTTCGAC	CAAGAAGCTCACGTATACAAATATGCGGGATCGATCACAGCTTTTCTATCA :::::	TATCCAACAGATTTAATGGCTGGC	TGCTCTTGATAAATATTTGCTAAATAATTTGGAA	ACTGTGGAAATTCTAAATGCTGAT
			AATCAAGCTTTGCCA ::: ArgGlnAlaAlaPro	GAGAATATCATTGATGTAC AlaProValT	ACTCAAGAAAAGA :::::::::: sValSerGluGlnPr	AAAACAGGTGGTGCC	GCGAATGTGTTCGAC :: :::::::: snGluAlaIleGlns	ACAGCTTTTCTATCA CALACTATTTCAL	GATTTAATGGCTGGC:::::::::::	lnPheHisGlnLeuG	GGATG uAlaSerSerGlyVa
483 1265	533 1249	583 1236	633 1227	683 1211	714 1197	762 1180	812 1173	862 1163	912 1146	936 1130	970

1911

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL=frame+_n2p.model -DEV=xlp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-800-825A-5 - 81.50 112.59 2.49 /cgn2_6/ptodata/1/iaa/PCTUS9_COMB.pep:PCT-US94-10166-5 - 81.50 112.59 2.49 /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-872-302-5 - 81.00 131.00 1.16 /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-392-806A-6 - 81.00 125.54 1.49
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 324-167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GUT, JIRITITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1,193
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORREY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC
OPERATING SYSTEM: DOS
SOFTWARE: WORDERfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                      ORGANISM:
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                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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94306-1840
                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                          Ratio:
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: United States of America
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NELSON, RICHARD, C.
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CRYPTOSPORIDIUM ANTIBODIES, DNA
AND RNA ENCODING THEM, HYBRID
VECTOR AND TRANSFORMED HOST AND
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                                                Length: 273
Gaps: 18
Percent Identity: 23.077
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Align seg
seq_documentation_block:
                                 seq_name:
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                                                                                                                                                                                                                                                                                                                                                            АТТСТСААССССВААТССВАГААСАСААТССВАТААСТСТАСТАСЛАВААС 1594
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                                                                                                                                                                                                .....CysValLeuIleG 155
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                                                                 u***CysCysCysCysCys 215
                                                                                               ....TGCTGCAGTCGGTGT 1748
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Sequence 35, Application US/08415751 patent No. 5643772
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US-08-415-751-35
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                                                                                                                                 alignment_block:
US-09-323-427-2 x US-08-415-751-35
                                                                                                                                                                          Ratio:
Percent Similarity:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                  Align seg 1/1 to: US-08-415-751-35
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: MAY 29, 1992
ATTORNEY/AGENT INFORMATION:
ANAME: Hana Dolezalova
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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1706 FIGHTEGTTGTTGTTGTTGTTGTTGCTGCAGTCGGTGT 1748
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                            FEATURE:
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                                        135 CysCysCysLeuAsnTrpThrLeuTrpTrpTyrGlyCysCysCysCy
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                                                                                                                                                                                                                                                                                                                           ORGANISM:
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                                                                        TGCTTCCTGTCTTCCTCCACTTGATGGGGTTATTATTGCTGTTGTTG 1705
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NELSON, RICHARD, C.
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                                                                                                                                                                                                                                                                                  identified as Xaa.
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Tune 1, 1993
TIMBER: 07/891,301
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6.056
58.065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIAGNOSIS AND KIT
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                                                                                                               from: 1
                                                                                                               to: 362
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0
51.613
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151 sCys***LeuTrpTyrAsnCysCysCysCysPheCysCys 165

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STATE:
COUNTRY: USA
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION 
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LENGTH: 3200 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-451-8
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    Quality:
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Ratio: 0.537
Percent Similarity: 41.501
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Patent No. 5928865
GENERAL INFORMATION:
655 CTAATTTCAAGGGTGTTGATATC.....AGTTCGTACATCAATGATATT 698
                                                                                                                                                                                                                                                                                                                   774 alasnPheLeuSerGlnPheLeuIleProLysProTyrLeuThrGluIle 790
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                                                                                                                                                                              791
                                                                                                                                                                                                                                             699 CTCCGGTTCTGCAGATCTTTTCTTGAGTAAACGAAGTTGCGCAGCTGCAG 748
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                         IleAsnPheIleMetProPhe......GlnArgGluAlaArgCysLe 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Chiron Corporation 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 453
Gaps: 24
Percent Identity: 22.075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 3200
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03	:: ::: : leLeuIlePheAlaIlePheG	1020
1635	GAAAGCAATAAGACGAATCATTTCAGAAGATTTAGTAAATTCG	1586
1585 1020	"TUGACACCATTGTCAACCGGAATCGAATAAGACAATGCAATAAGTGTAG"	1005
00	alPheAsnPheAsnProPheTrpIle.	ق د
1535	AATTGATTGTTATTGAAGTTGGTCCACATTCAATTTCTGGCT	1489
1488 995	CATAAAGACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTA : ::: eIleGInSerCysIleL	1439 989
989	:::	982
1438	TACGGCAACCTTCTTG	1389
981	eLysValAl	0 0
69	LeuLeuIleAspAspHisIlePheAsnGlyI	957
1338	AATGGATGAAACGAAATGACAACAGTTGTTGTTACAAAAATACCACG	1289
5	 eAsnPh	946
1288	CCATGTAAAAGCATTGTACTCGATATGCACGATCAACT	1239
5 0	ulleGlyArgLeuLeuTyrProThrGluIleThrArgCysPheSer	929
J	OKOMKMEMENDALOKOVA OKOMONA OKOMANA	1197
29	::::::	91
1196	CATCGGGACAATTTGAGTTTGAAAAGCAGTTGT	1163
16	leTyrPheArgPhePheSerSerIleGluThrPheIlePhe	903
1162	· · · · TGGTCCACCATCCAAAATTTCATAACGGCAT	1128
02	::: leLeuAsnGlyLe	886
1127	AACTGGCTGACCAATGATAGCAAATTGAACTGGTTGACCG	1081
œ	LysValPheArgLysSerCysGl	873
1080	CAACCGCGCAGAAAGTATCAACGGTTTCAGAATCGCATGTCCAI	1031
73	::: ::: eValIleGluIleSerLysPheCysIleGlnLe	857
	TCACCGTTACCATCATCGACAAAGCAGG	999
856	::: 	848
998	GCACATCCATCAGCATTTAGAATTTCCACAG	949
847	eIleAsnPhe	844
948	GAGCTTCTTGGCCAGCCATT	899
844	LeuSerValAsnGlyPhePheLysAlaSerCysLeuProCysPheLeuPh	828
868	CTGATCTGGCATTGATAGAAAAGCTGTGATCGATCCGCATATTTGTAT	849
827	LeuIleGluSerValAsnPheCysIleTyrLeuPheSerAsn	814
848	ATTCGCTATTTGGTTCTTTAATGGT	799

PRIOR APPLICATION APPLICATION NUMB FILING DATE: 30 FILING DATE: 30 ATTORNEY/AGENT INE AMME: VILLAMIZE REGISTRATION NUMB REFERENCE/DOCKET TELECOMMUNICATION TELEFAX: (919): TELEFAX: (919): INFORMATION FOR SEQUENCE CHARACTEN SEQUENCE CHARACTEN JUNE AMINO ACITYPE: MAINO ACITYPE: MAINO ACITYPE: PI MOLECULE TYPE: PI	NUMBER OF SEASON NUMBER: OF SEASON NUMBERS: CORRESSED CIBA-GEIGY CO STREET: 7 SKyline Drive CITY: Hawthorne CITY: Hawthorne STATE: New York COUNTRY: USA ZIP: 10532 ZIP: 10532 ZIP: 10532 ZIP: 10532 ZIP: 10532 COMPUTER READABLE FORM: COMPUTER: IBM PC COMPAT TYPE: Floppy dis COMPUTER: IBM PC COMPAT COMPUTER: USAPPLICATION UMBER: USAPPLICATION UMBER: USAPPLICATION UMBER: JP APPLICATION UMBER: JP FILING DATE: 01-UN-19: FILING DATE: 01-UN-19: PRIOR APPLICATION UMBER: JP FRIOR APPLICATION DATA: APPLICATION UMBER: JP PRIOR APPLICATION DATA: APPLICATION UMBER: JP PRIOR APPLICATION UMB	documentation_block: Sequence 2, Application Sequence 2, Application GENERAL INFORMATION: APPLICANT: Iwasaki, APPLICANT: Shimoi, F APPLICANT: Suzuki, F APPLICANT: Ghisalba, APPLICANT: Kangawa,	1636 ATTTTTAGAAAAAC
ON DATA: UMBER: JP 329911/90 30-NOV-1990 INFORMATION: izar, JOAnn NUMBER: 30.598 NUMBER: 4-18110/A/CGJ 44 KET NUMBER: 4-18110/A/CGJ 44 ON INFORMATION: 914)785-7120 914)785-7120 914)785-7120 9141-8689 25EQ ID NO: 2: TERISTICS: amino acids ACID ACID NOTED ACIDS ACID NOTED ACIDS ACID Protein	DDRESS: DDRESS: DDRESS: Line Drive Line Compatible Line Drive Line Compatible Line Drive Line Drive Line Compatible Line Drive Line Drive Line Compatible Line Drive Line Dri	Yasuno Hiroko Kenji A. Oreste A. Oreste A. Takashi A. Takashi No. 5196316el Enzyme and DNA Coding Therefor	TTTTTAGAAAAAC

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-070-301-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1
FILING DATE: 15-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    840 leAlaIleAlaIlePheIleArg 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 TTACCATTTCGTTTAAATTTCGT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 lSerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       807 ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      710 GCA.....GAACCGGAGAATATCATT...GATGTACGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                   STREET: 1233 20t
CITY: Washington
STATE: D.C.
                                                                       FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 20036-8218
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT 588
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5871995
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KATO, Ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KISHIMOTO, Jiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKAMOTO, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YANAGI, Mitsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAMINUMA, Toshihiko
                                                                                                                                                                                                                                                                                                                                                                      Wegner, Cantor, mus
233 20th Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIDA, Toshio
                                                                                             24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                      Cantor, Mueller & Player, P.C
                          JP 1-209687
                                                                                                                                                                 #1.25
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alignment_block:
US-09-323-427:2/rev x US-08-070-301-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-070-301-16 from: 1 to: 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                            1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: |
ORIGINAL SOURCE:
ORGANISM: Fro
                                         1230 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 1184
                                                                                                                                                                                                                                                                                                                                                                                              1367 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA..... 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1467 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1517 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1417 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              658 lAlaAspGlyTyr.....
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REFERENCE/DOCKET NUMBER: P-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEPAX: (202) 835-0605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-
FILING DATE: 02-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 2-106412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 989 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 1-FILING DATE: 31-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 744
                                                                                     AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl 728
                                                                                                                                                                                                                                                                   nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 696
                                                                                                                                 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 1231
                                                                                                                                                                                                                                                                                                                                                         Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 679
                                                                                                                                                                              leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla 712
                                                                                                                                                                                                                     .....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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0.965
43.103
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                                                                                                                                                                                                                                                                                                                                                                                                                                   .....Cys 663
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12
21.552
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US-08-540-804-12

alG1 alG1 alG1 alG1 alG1 alG1 alG1 alG1	AGTATGCCGTTATGAAATTTTGGATGGT
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alignment_block:
US-09-323-427-2/rev x US-08-540-804-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 93.50
Ratio: 0.403
Percent Similarity: 47.444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1141 TGGATGGTGGACCAACCGGTCAACCAGTTCAAT.....TTGCT 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1191 TGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1222 .....GTGCACAGATTGAGG......TATCTGAAATCACAAC 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 TyrValAspGlnAsnProLeuThrMetHisLysIleIleGlnLeuIleLe 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1003 GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1053 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 uTrpSerIleHisProSerArgGlnPheAspHisTyrGluSerAsnGlnL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 ...SerThrAspGluAspLeuHisGluPheGlnIleGluAspAlaIleTr 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu........... 369
                                                                                                                                                                                                                                                                                                                                                                                     401 HisValGlnLeuLeuIleAsnLeuLysIleSerProLeuMetLysSerGl 417
                                                                                                                                                                                                                                                                                                                                                                                                                      877 CAC...AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                              903 TCACGTAT.....ACAAATATGCGGATCGAT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           953 TIGCTAAATAATITGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGC 904
                                                                                                                                                                                                                                                                                                         830 A.....ATAGCGAATGTGTTCGACCACAATGTTCAGAACCACA 793
                                                                                                                                                                                                                                                                 792 AG.....GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG 749
                                                                                                                                                                                                                                648 TAATC.....AAGCTTTGCCAGTTGATTTACGTCACC 617
                                                                         461 nLeuSer.....LysThrProLeuSerIleLysIleM 472
                                                                                                               698 AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 649
                                                                                                                                                      451 ArgIleLeuSerAsn....
                                                                                                                                                                                        748 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ......ileThrTyrGlyIleIleLysValProThrTyrIleArgLysL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....pheserAlaGlnLysArgValValSer 356
etValAlaGluTrpTyrLeuSerHisLeuCysSerGlyIleLeuSerSer 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 489
Gaps: 24
Percent Identity: 19.836
                                                                                                                                                          .....AspIleThrAsnLeuGl 461
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seq_documentation_block:
; Sequence 12, Applicati;
; Patent No. 5922585
                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-218-265-12
                                                                                                                                                                             Sequence 12, Applicating Patent No. 5922585
GENERAL INFORMATION:
APPLICANT: Young, Richard A.
APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
NUMBER OF SEQUENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
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                                                                                                                                                                                                                                                                                                                                                                                                       GCATTATTGCAATTAAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAATTTTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTAACAGTTTATCATTTGTGATAATATCACAAATTATACCTTGTATTG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCCTATTTTA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lAsnIleArgPheLeuLeuHisAsnSerGluIleIleAspThrAsnThrS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATACAATAAGTGATATTTTC.....ATCAAAACTTCTTCTA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                      tSerIlePheLeuLysArgLysAspPheThr...AsnLysAsnLeuIleG 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTAGCTAACAAATATATAGTAT.....GTAGGAAATAATTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleLeuLeuCysTyrGlnLysLeuPheSerGlnPheIleAsnAspHisIl 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnLeuLeuSerAsp......IleGluSerLeuGluAlaLeuMetAsp 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValAsnArgThrValLeuLeuLysIlePheLysIlePheCysIleAspLe 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....CTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAACTAA 371
                                                                                                                                                                                                                               Application US/08218265
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alignment_scores:
Quality:
Ratio:
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US-09-323-427-2/rev x US-08-218-265-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                    1003 GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTTCTTGATAAATAT
                                                                                                                                                                                                     1053 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1222 ......GTGCACAGATTGAGG.....TATCTGAAATCACAAC 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1267 CATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA.....
                                                                                                                                                                                                                                                                                                                                                                                                                         312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 uTrpSerIleHisProSerArgGlnPheAspHisTyrGluSerAsnGlnL 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
TYPE: amino acid
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/218,265 FILING DATE: 25-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTT 1142
                                                                                                                                                                                                                                            pSerLeuValPheGlnLeuAlaLysAsn........
                                                                                                                                                                                                                                                                                                                                                                     TGGATGGTGGACCAACCGGTCAACCAGTTCAAT.....TTGCT 1104
                                      .....IleThrTyrGlyIleIleLysValProThrTyrIleArgLysL
                                                                                  TyrMetMetProSerLeuTyrArgLeuLeuAsnIleLeu
                                                                                                                                                                                                                                                                                         ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 1054
                                                                                                                                                                                                                                                                                                                                SerThrAspGluAspLeuHisGluPheGlnIleGluAspAlaIleTr 338
                                                                                                                                                                  .....PheSerAlaGlnLysArgValValSer
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02173
R PT
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617-861-9540
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0.403
47.444
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Percent Identity:
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24
19.836
    384
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400 400 417 417 417 417 417 417 417 417 417 417	07 ATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCCTATTTTA	TTTTATATGCATACTATTGTAAATGTTTCATCATAATGTTTATATATGCATACTATTGTAAATGTTTTCATCATATATGTAAATGTTTTCATCATATATGTAAATGTTTTCATCATATATGTAAAATGTTTTCATCATCATATATGTAAAATGTTTTCATCATCATATATGTAAAATGTTTTCATCATCATCATATATGTAAAATGTTTTTATATATA	snGlnAlaValGlyGlnThrTrpAsnPheProGluValFileGliiva		TTTCTGAAAAGCTTATTCATTATTCAGTAATC ysSerGluvalLeuLysValTyrSerMetIleAsnAsn	ATCAAAACTTCTTCTA ::: ::::::: pGluLysLeuLysThrGluLysL	ATGTAGGAAATACTG 3 ::	OGTTTCTTATCATCCTTCTAATAACTAA : : : : : :	rGTTAGAATCATCGAAGCAATAATAAAA	ATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGCAI4	GTTTAAGCATTGCATTGATTGCTGCCG 4 ::: ::: ::: ::: IleGluSerLeuGluAlaLeuMetAsp 5	AGTACAAAATGGAATCTGCATGTCACC 5 :::: ysTrpIleGluPheIleValTyrHisG 5	TTCTGCAACATAAT 5	AAGCTTTGCCAGTTGATTTACGTCACC 61 ::: HisLeuCysSerGlyIleLeuSerSer 48	PATCAACACCCTTGAAATTAGCGATGA 6	8 CTGCAGCTGCGCAACTTCGTTACTCAAGAAAAGATCTGCAGAACCGGAG 6	AGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG 7	4 7	TTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA 8 :: :: euLeuIleAsnLeuLysIleSerProLeuMetLysSerGl 4	::: ::::::
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-07-906-349A-6
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                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: 1i
; MOLECULE TYPE:
US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/07906349A Patent No. 5434064
                                                                                                                                                                                                                                                   alignment_scores:
Quality:
                                                                                                                                    alignment_block:
US-09-323-427-2/rev x US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTE READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: LBM PC compatible
COMPUTER: 30-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/643,237
APPLICATION NUMBER: 07/643,237
FILING DATE: 18-JAN-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
TELEPHONE: 202-673-73-73-9
                                                                                     Align seg 1/1 to: US-07-906-349A-6 from: 1 to: 801
                                                                                                                                                                                                       percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 801 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 TICTAACAGTITATCATTIGTGATAATATCACAAATTATACCTTGTATTG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L.
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES
TITLE OF INVENTION: TARGET PROTEINS
TITLE OF INVENTION: TARGET PROTEINS
TITLE OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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CITY: Washington
STATE: D.C.
573 ThrThralaalaalaThrCysalaCysThrGlyCysThrGlyCysThrCY 589
                                            798 ACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAGCAAAACCTG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                       SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                              3.000
40.260
                                                                                                                                                                                                                                                            93.00
                                                                                                                                                                                                            Length: 77
Gaps: 1
Percent Identity: 28.571
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seq_documentation_block:
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                                                                                                                                                 TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GUT, JIRI
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: MAY 29, 1992
ATTORNETY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFILING DATE: 03-APR-1 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 TAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATA 599
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         NAME/KEY:
                                                                                                   TOPOLOGY:
                                                                                                                 STRANDEDNESS:
                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                     Hana Dolezalova
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Positions coded by nonsense
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                                          Cryptosporidium parvum
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                                                                                                 linear
                                                                                                                                                                                                                                (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette - 3.5 inch, 1.44 Kb storage
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                                                                                                                   single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRYPTOSPORIDIUM ANTIBODIES, DNA AND RNA ENCODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYPEPTIDES BINDING ANTI-
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   codons are
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-303-238-3
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US-09-323-427-2/rev x US-08-415-751-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
US-08-415-751-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08303238 Patent No. 5654270
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                               APPLICANT:
                                                      APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 yMetArgAsn***ProHisArgGluLeuLeuHisGluLeuValValLysG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SerAsnLeuLeuGlnHisSerArgArgHisPhePheGluArgLeuGl 36
                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uCysCysCysGlyCysCysSerLysIleTrpAspAsnCysCysCysSerL 130
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SAN
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4370 LA JOLLA VILLAGE DRIVE, SUITE 700 NN DIEGO
                                                                                                                                                                               HARPER, JOHN R.
                                                                                                                                                                                                  WHITBY, DAVID J.
                                                                                                                                                                                                                       RUOSLAHTI, ERKKI I.
LONGAKER, MICHAEL T.
                                        CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identified as Xaa.
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1.220
49.669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.828
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                                                                                               SCARRING
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517 GCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGT	GGCTTCTCAATGTTTATGGGTTTAA 51 -::::: UValGlu	CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACCTCAC 61 ::: :::: :::: :::: :::: ::::	SLEUTYRAIAL 11 TGATATCAACA 66 ::: ysalaPheSer 13	Align seg 1/1 to: US-08-303-238-3 from: 1 to: 368 775 AAACAGGTGGTGCCGCAACAACCTGCTGCAGCTGCGCAACTTCGTTTA 726 111::::: 111::: 86 LysGluileSerProAspThrThrLeuLeuAspLeuGlnAsnAsnAspI1 102		ignment_scores: 91.50 Length: 299 Quality: 91.50 Gaps: 14 Ratio: 0.738 Gaps: 12 Percent Similarity: 41.472 Percent Identity: 19.732	COUNTRY: UNITED STATES COUNTRY: UNITED STATES ZIP: 92122 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: PATENTIA SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIA Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/303,238 FILING DATE: 17-NOV-192 APPLICATION NUMBER: US 07/978,931 APPLICATION NUMBER: US 07/978,931 APPLICATION NUMBER: JS 0
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7 7	Align seg 1/1 to: 5340934-2 from: 1 to: 368	alignment_scores: 90.50 Length: 299 Quality: 90.50 Gaps: 14 Ratio: 0.730 Gaps: 14 Percent Similarity: 41.472 Percent Identity: 19.732	<pre>seq_documentation_block: patent No. 5340934 patent No. 5340934 papticanT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.</pre>	<pre>seq_name: /cgn2_6/ptodata/1/iaa/backfiles1.pep:5340934-2</pre>	29	163ATTTTATTCTAACAGTTTATCATTTGTGATAATA 130 ::: ::: 295 yLeuProAspLeuLysLeuLeuGlnValValTyrLeuHisSerAsnAsnI 312	79 LeuArgGluLeuHisLeuAspAsnAsnLysLeuAlaArgValProSerGl 2	207 ATGAATAGTTTCGTTTGTTATTATCATCATTATCAGTTGTCLI	257 TYCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC 208	AACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 2 	η ω	TATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA	421	Leu

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seq_documentation_block:
   Sequence 67, Application US/08325071
   Patent no. 5587311
   GENERAL INFORMATION:
                                                                                                                               seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-67
                                                                                                                                                                                                                                                                                                                           .279 LeuArgGluLeuHisLeuAspAsnAsnLysLeuAlaArgValProSerGl 295
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    APPLICANT:
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                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   262
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                                                                                                                                                                                                        TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 89
                                                                                                                                                                    leThrLysValGlyValAsnAspPheCysProMetGlyPheGlyVal 327
                                                                                                                                                                                                                                                                                                                                                                                                       isAsnGlnIleArgMetIleGluAsnGlySerLeuSerPheLeuProThr 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGAAGCAATA..... 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProLeuArgAsnVal..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCAC 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......IleProProAsnLeuProSerSerLeu.....Va 162
COBON,
                                                                                                                                                                                                                                                                                        .....ATTTTATTCTAACAGTTTATCATTTGTGATAATA 130
Stewart Gary
Joanna Terry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......GlnLysLeuTyrIleSe 146
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alignment_block:
US-09-323-427-2/rev x US-08-325-071-67
                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-325-071-67
                                                                                                                                                                                             alignment_scores:
                                                   Align seg 1/1 to: US-08-325-071-67 from: 1
                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
1476 TGCATTCGAAGGACATGT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242
FILING DATE: 06-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202,672,5300
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-NOV-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DAIL.
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: AU PI2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-OCT-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202
TELEFAX: 202
TEX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: RIDING, George Älfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 27-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20007-5109
                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                650 amino acids
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SRISKANTHA, Alagacone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                          90.00
0.612
40.947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: AU PH9196
27-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMBER: PCT/AU87/00401
27-NOV-1987
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                                                                                                                                                                                                                                                                                                                                                       67:
                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                            60042/111 BIAU
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                                                   to:
                .....TTATG 1454
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22
21.727
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35 ACTTCGT
785 GGAGCTGTTAAAACAGGTGGTGCGCAGCAAAAACCTGCTGCAGCTGCGCA 736
GATTC 78
AATGCCAGATCAGTATTACCATTAAAG 83 ::: 1aileArgThrSerileGlyLysGluV 37
AGCTCACGTĀTACAAATATGC 8 ::: HisCysLysArgTyrGl 3
AATTTGGAA 93
AAATTCTAAATGCTGATGGAT 9 :::
yrCysProTr 32
ACTITCTGCGCGGTTGTCCATTCCTGC 1
TAAATGGA 107
ATTTTGGATGGTGGACCAACCGG 112 ::: ::: ThrValLeuCysGluCysProTrpAs 283
TTGTCCCGATG 116. hrCysArgProThr 266
IGGAAGCTGATAAAACAGTTAGTGCACAGATTG 121 ::: :: : 250 slalaGluAspGlyIleThrCysLysSerIle: 250
ATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG 1 :::
AACAACTGTTGTCATTTCG 130 ::: ::: ::: sLysasnalaCysargThrLysGluAlaGlyPheV 217
GTAAC
CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 13 ::::::::::::::::::::::::::::::::::
<u> </u>
147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163

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seq_documentation_block:
Sequence 22, Application US/08477451;
Patent No. 5928865;
Patent No. 1928865;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-477-451-22
                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-08-477-451-22
                                                                                                                                                                                                            alignment_block:
US-09-323-427-2/rev x US-08-477-451-22
                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                              Align seg 1/1 to: US-08-477-451-22 from: 1 to: 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      701 GAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGA 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 yGlnAsnLysCysValLysValAsp 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENT POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMEE: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY, AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
REFERENCE/DOCKET NUMBER: 035.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                       1447 GTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTT 1398
                                       1397 GCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA...... 1355
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CITY: Emeryville
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94608-2916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                10 ValileLeuValTyrProIleLeuPheLeuPheAlaLeuIleIleLys. 25
.ProSerPhePheTyrTyrThrThrTyrLeuLeuLeuLeuValSerLeuS 42
                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chiron Corporation
                                                                                                                                                                                                                                                                                89.50
0.393
40.426
                                                                                                                                                                                                                                                                             Length: 564
Gaps: 28
Percent Identity: 18.085
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ω	AT 71	·····AACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAG	754
6	uT 32	ysSerAspLysThrAlaAsnLysMetSerValSerGlnValArgLe	· 0
ĊΊ	75	GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAA	
9	Se 30	AsnMetGlySerAlaLeuValGlyAsnGlyPheGlySer	
Ĭ	79	ACCACAAG	799
2 0	AG 80 :: sp 29	.CAAATAGCGAATGTGTTCGACCACAATGTTC ::: ::: ::: nPheMetalaGluValLeuLysasnGlyPheA	276
6	Г ом 27	LeuMetMetGlyLeuAsnGluAlaLeuGlyLysLysPheA	259
12	A. 84	CAATGCCAGATCAG	868
	uMe 25	erSerAspLeuPhe.SerMetIleLeuAsnPheLeuPhePheLe	243
50 5	Y L 24	AAGAAGCTCACGTATACAAATATGCGGGATCGATCACAGCTTT	\vdash
5 E) to	TAPAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGG	960 226
26	G1 22	ProAs	210
51	GA 96	GGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	1010
909	-0 -	::::	196
1011	-	TCCATTCCTGCTTT	1033
034 95		<pre>TCTGAAACCGTTGATACTTTCTGCGCGGTTG </pre>	179
79	Le 1	euValTrpTrp.GlnAsnIlePheValCysAspTrpTr	16
065	:	TGGTCAGCCAGTTTATCATAAATGGACATGCGA	1098
66	pL 1	uIleLeuIleLysIleCysTyrAsnGluIleLysThrLysArg	149
099	:	.TCAACCAGTTCAA	1122
49	Le 1	/alser	13:
123	:	ATGCCGTTATGAAATTTTGGATGGTGGACCAACCG	117
33	neC 1	eTrpTyrSerAsnP	116
171	GT 1	CAAACTCAAA	1184
.185	B-1	:::	0 (
	:	Partory reduys intry strengted SerAlaTyrThr	
.235	rc 1	CCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATO	128 9
ž.	TleL 9	LysThrPheArgGluIleSerLeuPheProAsnIleSer	7
285	TTGT 1	CAACTGTTGTCATTCGTTTCATCCATTAT	131
15	:: :: lnLy 7	LeuIleIleLeuMetThrGlnTrpGlnAsnTrpPheLeuPheVal(ن.
) (133
no i	S	::: ::: 2 erIleIleSerLysTyrTyrLeuLeuSerHisAlaLysPheThrMet	4
1334	:		1354

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Sequence 61, Application US/08325071 Sequence 61, Application US/08325071 Patent No. 5587311 GENERAL INFORMATION: APPLICANT: COBON, Stewart Gary APPLICANT: MOORE, Joanna Terry APPLICANT: WILLADSEN, Peter APPLICANT: WILLADSEN, Peter APPLICANT: KEMP, David Harold APPLICANT: KEND, David Harold APPLICANT: RIDING, George Alfred APPLICANT: RIDING, George Alfred APPLICANT: RAND, Keith No. 5587311man TITLE OF INVENTION: DNA Encoding A Cell Membrane TITLE OF INVENTION: Glycoprotein Of A Tick Gut CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS:	471 AlametArgThrSerGluPheSerAspValPheMet 4 eq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-	ACTTGTCCTATTTATTCTAACAGTT	280 GCTTCTGAAAAGCTTATTCATTATTCAGTAATCTTTTATATGCATACTAT ::: ::::::::::::::::::::::::::::::	380 TAATAACTAATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACT ::::: 415 eArgGly	::: LeuGlyPhePheLeuLeuH1sArg	TTATGG	80 TTGCTGCAGTACAAAATGGAATCTGCAT	PAATCAAGCTTTGCCAGTTG	12 c 12 c 43 L	

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TOPOLOGY: 11;

MOLECULE TYPE:
US-08-325-071-63
                                            AFFLICATION

FILING DATE: 27-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 60042/111 BIAU

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 672 5300

TELEFAX: 202 672 5399

TELEX: 904136

INFORMATION FOR SED ID NO: 63:

SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
DBTOP NORTHORNIANDER: US-MT/242,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/AU87/00401
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU D14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION UMBER: AU P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION DATA:
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Sequence 63, Application US/08325071
Patent No. 5587311
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APPLICANT:
APPLICANT:
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington, D.C.
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MOORE, Joanna Terry
JOHNSON, Law Anthony York
WILLADSEN, Peter
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alignment_scores:

885 GGATCGATCACAGCTTTTCT	935 TATCCAACAGATTTAATGGC	970 GTGCTCTTGATAAATATTTG :::::: 334 ysbeuLeuAsnGluTyrTy	1007AACGGTV 320 pLysSerArgLysProGlyI	1022 TTTGTCGATGATGGT ::: 304 PheMetAspCysGlyValTyrMet	1072 CATGCGATTCTGAAACCGTTGATACTTTCTGC	1122 TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCAT : :::::: ::: 283 nGlnHisLeuvalGjyasp	1163 CCAGTATGCCGTTATGAA. ::: 267 GluAspCysArgValHist.	1210 AGGTATCTGAAATCACAACTGCTTTTCAAACTGAAATTGTG :::::	1251 CTTTTACATG	1301 TTTCATCCATTATTTGTTA	1317AACTGTTGTCAT	1353 ACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC ::::: :::: 187 ProProAlaAspSerTyrCysSerPro	1403 CAAGTTGCCGGAATTTCAC	1453 TGAAAGGTCTTTATGATCA ::::: ::: 163 SGluLySASnLeuLeuGln	1476 TGCATTCGAAGGACATGT ::: 147 CysValProThrThrCysLeuA	Align seg 1/1 to: US-08-325	alignment_block: US-09-323-427-2/rev x US-08-	rercent similarity: 40.390
GATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG 836 	TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC 886 :::	GTGCTCTTGATAAATATTTGCTAAATAATTTGGAA 936 :::::: ysLeuLeuAsnGluTyrTyrThrValSerPheThrProAsnIleSer 350	AACGGTGATACTGTGGAAATTCTAAATGCTGATGGAT 971 ::: ::: pLysSerArgLysProGlyProAsnValAsnIleAsnGlyC 334	TTTGTCGATGATGGT100 :: PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 320	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC 102 	TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 107 	CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGG 112 :: :: :: 	AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG 116 :: ::	TTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG 121 ::: ::: :::	TTTCATCCATTATTTGTTACCAAAGTTGATGGTGCATATCGAGTACAATG 125 	AACTGTTGTCATTTCG 1302	CGATCTCTGAATCCACGTGGTATTTTTTGTAACAAC	AAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGGGTAC 135	TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 140 ::::: ::: sGluLysAsnLeuLeuGlnArgAspserA 173	GTTTATG 145 	071-63 from: 1 to: 650	-071-63	Percent Identity: 22.284

GluasnLeuCysaspSerLeuLeuLysasuvilusiusiusiusiusiusiusiusiusiusiusiusiusiu
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TTACTCAAGAAAAGATCTGCAGAACCG 702
 LeuArgLysLeuGlnAlaCysGluHisProIleGlyGluTrpCysMetM 418
ACTTCGT
IleLysAlaArgLeuIleAlaGluLysProLeuSerAsnHisVa 401
GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 736
375 alPheLysValGluIleLeuAsnCysThrGlnAsp 386
835 AACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTC 786

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pir2:715789
pir1:A35269
pir2:A36054
pir2:S05356
pir2:S05356
pir1:VGBE11
pir2:E71615
pir2:H71616
pir2:H71616
pir2:H71616
pir2:F71613
pir2:F71633
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pir2:D71606
pir2:T15789
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pir2:F71606
pir2:B26696
pir1:RNZQBF
pir2:S78177
pir2:A0970
pir2:C71607
pir2:G71613
pir2:S55098
pir2:C71618
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pir2:S57242
pir2:T03099
pir2:S52967
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pir2:S27799
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Query: US-09-323-427-2
Query length: 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database sequences: 142080
Database length: 47169319
Search time (sec): 178.310000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM of: US-09-323-427-2 to: PIR_62:*
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                                                                                                                   : $23344
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8 | cuticlin 1 - Caenorhabditis ele
10 | DNA-directed RNA polymerase (EC
22 | probable multiple transmembran
3 | hypothetical protein 1 (CYb-COI
124 | DNA-directed RNA polymerase (FC
125 | hypothetical protein 717 - Recl
126 | nandlin 1 - human (fragment)
                                                                                                                                   probable amine transporter PFH
S-layer protein precursor - Ba
SERA antigen/papain-like protein
hypothetical protein prB0555c
DNA mismatch repair protein (mu
guanidine nucleotide exchange
hypothetical protein pEB0495w
hypothetical protein 2136 - 11
probable chloroquine resistand
origin recognition cmplx subuni
hypothetical protein PFB0755w
adenylate cyclase (EC 4.6.1.1)
proteoglycan I - mouse
biglycan precursor - rat
c-kit-related kinase 1 (XKrkl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! hypothetical protein PFB0745w | hypothetical protein PFB0470w | probable membrane protein YMR21 | hypothetical protein PFB0315w | hypothetical protein PFB0315w | hypothetical protein PFB0316w | hypothetical protein PFB0870w | twitchin - Caenorhabditis eleg | mucin, submaxillary - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Documentation
                                                                                                        hypothetical protein 7.9 - :
                                                                                                                                                                                                                                                                                           peptidylglycine monooxygenase (glycoprotein H precursor - saim
                                                                                                                                                                                                                                                                                                                                                                                     NADH dehydrogenase (ubiquinone)
ATP-dependent Clp proteinase (I
hypothetical protein PFB0800c
hypothetical protein C41A3.1
                                                                                                                                                                                                                                                                                                                                   hypothetical protein (clone pLF
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pir2:S37621
pir2:T09079
pir2:G71607
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US-09-323-427-2/rev x A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cuticle protein cut-1 - Caenorhabditis elegans ()Species: Caenorhabditis elegans C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994 C:Accession: A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: cut-1 a Caenorhabditis elegans gene coding for a dauer A;Reference number: A49772; MUID:91323673
A;Accession: A49772
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Sebastiano, M.; Lassandro, F.; Bazzicalupo, Dev. Biol. 146, 519-530, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:M55997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-423 <SEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
cuticle protein cut-1 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: A49772 from: 1 to:
                                                                                                                                                                                                                                    1242 GGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAA 1193
                                                                                                                                                                                                                                                                                                                                                                                               1442
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                                                                       CTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATT 1143
TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA 1093
                                                         hrAlaPheGlnThrGlnValValProMetProValCysLysTyrGluIle
                                                                                                                tGluSerAspLysThrValSerThrGlnIleGluValSerAspLeuThrT 141
                                                                                                                                                                            TTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACAT
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snPheAsnThrAfgAsnProPheGluGlyHisValTyrValLysglyLeu
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Gaps: 6
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| probable chloroquine resist
| probable integral membrane
| biglycan precursor - human
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cuticlin : Caenorhabditis elegans (fragment)
C;Species : Caenorhabditis elegans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_C
C;Accession: S27799
R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
Submitted to the EMBL Data Library, July 1991
Submitted to the EMBL Data Library, July 1991
A;Bescription: CUT-1 a Caenorhabditis elegans gene coding
A;Bescription: S27799
A;Reference number: S27799
A;Molecule type: DNA
A;Molecule type: DNA
                                                                                                                                                                          seq_name: pir2:S27799
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                                                                                                                                                                                                                                                                                                                                                                                                                  ATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT 610
                                                                                                                                                                                                           uValSerGlu.....GluSerValArgArgArgAlaThrSerThrGlyI 387
                                                                                                                                                                                                                                                                                                                                                          TCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA 560
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                                                                                                                                                                                                                                        TTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCA 465
                                                                                                                                                                                                                                                                     leSerSerThrProIleGlyLeuProSerPheLeuGlyMetArgThrIle
                                                                                                                                                                                                                                                                                                  TCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....GCGCAACTTCGTTTACTC...AAGAAAAGATCT...G 710
                                                                                                                   #text_change
                                                                                                                                                                                                                          418
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                                                            for a dauer specific non
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                                                                                                                        09-Sep-1997
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colla

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A;Residues: 1-308 <SEB>
A;Cross-references: EMBL:M55997; NID:g156271; PID:g156272
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: CUT-1
A;Introns: 245/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-323-427-2/rev x S27799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1203
                                                                                                                                                                                                                                                                                                                                                                                                      1103 ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 1054
                                                                                                                                                                                                                                                                                                                             1003 GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCC
                                                                                                                                                                                                                                                                                                                                                                                     TCACGTATACAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGA 854
                                                                                                                                                                                                                                aHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnI 139
                                                                                                                                                                                            TCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGT
                                                                                                                 aHisAlaAlaAlaAlaProGlnAlaGlyValGluValGlnAlaAlaP
                                                                                                                                                        TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAA 754
                                                                           roValGlyAlaAlaProValAlaAlaProValAlaAlaAlaAlaAlaAla
                                                                                                                                    ACCTGCTGCAGCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
           AAGATCT...GCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA 671
ProAlaValProArgAlaThrLeuAlaGlnLeuArgLeuLeuArgLysLy
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3.989
74.503
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Percent Identity:
                                                                                                  .GCGCAACTTCGTTTACTC...AAGAA 718
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alignment_block:
US-09-323-427-2/rev x S72284
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: rpoC2
A;Genome: plastid
A;Genome: plastid
A;Note: this apparently degenerate plastid is referred to as the apicoplast C;Keywords: nucleotidyltransferase; plastid; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues; 1-960 GWIL>
A;Cross-references: EMBL:X95275; NID:g1171583; PID:e220245; PID:g1171589
A;Note: the success of this protein involves a -1 frameshift in the codon for residue
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyt J. Wol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa A;Reference number: S72277; MUID:96346169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid
N;Alternate names: RNA polymerase record
C;Species: plastid Plasmodium falciparum
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C;Accession: 572284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S72284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                   1297 ATCCATTATTTG ...TTACCAAAGTTGATCGTGCATATCGAGTACAATGC 1251
                                                                                                                                                                                                                                            1335 TGGTATTTTTGTAACAACAACTGTTGTCATTTCGT......TTC 1298
                                                                                                                                                                                                                                                                                                                                                                         1385 CTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACG 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1435 AAGAAGGTTGCCGTAATGATGATGAGGTGGACGTCAAGTTGCCCGGAATTTCA 1386
1250 TTTTACATGGAAGCTG......ATAAAACAGTTAGTGCACAGAT 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 etArgThrIleValAlaThrAlaLeuSerAlaThrIlePheTyrValAla 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 rserThrGlyIleSerSerThrProIleGlyLeuProSerPheLeuGlyM 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 ACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     620 CACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGT 571
                                                                                                                                                                                              41
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                                                                     58
                                                                                                                                                                                                                                                                                                                        28
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LysLysLeuIleIlePheLysTyrAsnIleSer.......
                                                       IleTyrLeuLeuIleLeuTyrLysAsnLysIleAsnAsnIleTyrAsnAs 74
                                                                                                                                                                                        yrSerPheLeuTyrAsnTyrSerLeuAsnIleLysAspPheSerAsnPhe 57
                                                                                                                                                                                                                                                                                                        .PheLysIleLeuHisGluLeuLeuTyr.....LeuGlyTyrGluT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTT 471
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0.436
44.608
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Gaps: 34
Percent Identity: 21.078
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	74	nLysTyrTyrGluIleLysAsnAsnTyrIleAsnValPheLeuAsnAsnT 9	91
	1212	TGAGGTATCTGAAA	1199
	91	lIleAsnLysIleGlnGlyIleLeuAsnAsnAsn	107
	1198	TCACAACTGCTTTTC 1	1184
	108	PheAs	124
	1183		1151
	1150	ATGAAATTTTGGATGGACCAACCGGTC	1121
	141	<pre>!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!</pre>	157
	1120	AACCAGTTCAAT	1109
	158	leTyrGluTyrIleLeuSerCysTy	174
	1109		1109
	174	spThrAlaLeuLysThrAlaAspSerG 1	.91
	1108	ATTGGTCAGCCAGTTTATCATAAAT 1	.076
	191	ysArgLeuIleAsnIleThrSerAsnPheIleIleLys 2	07
	1075	CCGTTGATACTTTCTGCGCGGTTGTCCATTCC 1	026
	208	GluLeuAsnCysLysSerProPheIleLeuLysTyrIleLeuAsnMetAs 2	24
	1025	GGTAACGGTGATACTGTGGAAATTCTAAATGC 9	79
	224	euProLeuAsnIleLeuArgPheLysIleL 2	41
	978	· 5×	29
	241	sn 2	49
•	928	CTCACGTAT8	96
	250	AsnGlyThrPheIleTyrThrLysAsnThrTyrIleThrLysTyrIleLe 2	66
	895 266	ACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCAA ::: ::::::::::::::::::::::::::::	83
	855	CCATTAAAGAACCAAATAGCGAAT8	21
	283	SerValTyrLeuCysAsnIleTyrAsnAsnIleCysAsnThrCysLeu 2	99
	820	CAATGTTCAGAACCACAA 7	92
	300	nLeuTyrLysTyrAsnLeuGlyGlnHisIleGlyValIl 3	16
	791	GATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGC 7	42
	3 L 6	erSerGluAlaIleSerGluProSerThrGlnMetValL 3	30
	741	ATCTGCAGAACCGGAGA 6	98
	330	aSerSerIleLeuLysAspLysPheAsnPheAsn 3	46
	697	ATATCATTGATGTACGAACTGATATCAACACCCCTTGAAATTAGCGATGAT 6/	648
	347	eTyrLysIleTyrLeuTyrLysLeuAsnIleAsnLysIl 3	63
	647	AATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT 6:	10

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seq_documentation_block:

probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium probable multiple transmembrane domain protein PFB0770c - malaria parasite (Plasmodium probable multiple mult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir2:F71606
A; Molecule
                        ;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \verb"euIlePheLeuMetAsnLysIleLeuTyrAsnTyrAsnAsnIleLeuPhe"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluTyrLys.....TyrIleLeuGlnAsnGlnTyrIleLy 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACTGTAATA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAATAAAACTGCCATATATATTCGTTTCTTCTTATCATCCTTCTAATAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sCysAsnPheIleTyrAsnSerIleSerLysAsnPheLysTyrAsnLeuA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \verb"nTyrAsnPheIleAsnSerAsnTyrTyrPheLysLysMetAsnPheIleL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGCTTATTCATTATTCAGTAATCTTTTATATGCA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |||:::||| :::|||:::
rTyrLeuTyrTyrH1sI1eLysPheTyrAsnLeuTyrAsnLysGlyI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euLys......AsnPheAsnAsnIleGlnIleLeuAsnLysLeu 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTATTTGCATTATTGCAATTAAAAAGTAT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ysLysLeuPheIleTyrLeuAsnIleIle.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAGGCCATGAATAGTTTCGTTTGTTATTATCATCATTATCAACTTGTCC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTATTGTAAA.....TGTTTCATCA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| ||||||||||||| 573
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A;Residues: 1-1122 <GAR>
A;Cross-references: GB:AE001417; GB:AE001362; NID:g3845271; PID:g3845273; TIGR:PFB077
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0770c
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    Quality:
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US-09-323-427-2/rev x F71606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1404 TCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA 1355
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                                                                                                                                                                                                      615
                                                                 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CysAsnAsnHisThrSer...AspAsnAsnThrCysAsn....... 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGC 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....AsnHisThrCysAsnAsnHisThr
                                                                                                                                                                                                                                                                                                                                                                                                                                             ....TCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGC 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....AsnHisThrCys....AspAsnAsnThrCys.....
                                                                                                                                                                                                                                                                                                      TGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTTGGAATATCCAA
                                                                                                                                                                                                                                                                                                                                                                 GTCGATGATAGGTAACGGTGATACTGTGGGAA......ATTCTAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                             snLysLysGluThrHisAsnAsnPhe.....
                                                                                                                                                                                                                                   CAGATTTAATG...GCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT
                                                                                                                                                                                                                                                                                                                                           .....SerHisAsnAspThrGlnGluAsnAsnIleMetLysAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AsnAsnHisThrLeuGlyAsnPro 564
                                                                                                 AAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG
                                                                                                                                 eLysLysIleIleGluLeuAsnThrThrLysLeuValGluGluArgAsnA
                                                                                                                                                                 CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC
                                                                                                                                                                                                      :::::|||::: ||| ::: ::::|||||| 631
                              CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT
                                                               sn....SerLeuLeuAspIleAsnGluTyrAsnAsnAsnSerAsnAsp
LeuAsnGluTyrPhe.
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   .AspAsnLeuIleGluAsnAsnIleLe
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seq_documentation_block:
hypothetical protein 1 (CYb-COII intergenic region) - Leishmania tarentolae mitochondric
C;Species: mitochondrion Leishmania tarentolae
                                                                                 seq_name: pir2:B26696
                                                                                                                                                                                                                                                      131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    588 TGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCT 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 693 leMetAsnLysLeuMetTyrThrAsnValSerAsnAsnGluArgTyrArg
                                                                                                                                                                  81 ATTCTGTAAACAATTCA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 CGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATA.....
                                                                                                                                                                                                     yrAsnAsnAsnAsnAsn
                                                                                                                                                                                                                                                                                                                                                                      nPheIleAlaTyrIleIleArgProPheIleLysAsp...... 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleIleArgAsn...IleTyrPhePheLeuCysAlaLeuSerGlyArgGl 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATTCAGTAATCTTTTATATGCATACTATTGTAAA.......
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lTyrAsnGluValPheGluIlePheLeuArgAsnIleLysGlnProAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rAspTyrLysMetTyrPhe...LysLeuPheGluHisLysAsnIleIleP 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGCATAAAAATAATGTTA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|| |||:::||
uMetIleProTyrIleThrTyrCysLeuGlyLysIleAlaMetSerIleV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerPheIle..PheLeuSerSerPhePheGluValValLeuSerThrLeu 809
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                                                                                                                                                                                                                                                                                                                                     TCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....TTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ......LeuTh 761
                                                                                                                                                                                                                                                                                                                                                                                                                    .....TGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCA 182
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A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: hypothetical protein 1 (CYb-COII intergenic region)
C;Keywords: mitochondrion
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A;Residues: 1-443 <SIM>
A;Residues: 1-443 <SIM>
A;Cross-references: GB:M10126; GB:J02707; GB:M10127; GB:M11022; GB:M64690; GB:N00030;
A;Note: the authors translated the codon ATT for residue 388 as Phe and TTC for resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Simpson, L.; Neckelmann, N.; de la Cruz, V.F.; Simpson, A.M.; Feagin, J.E.; Jasmer, J. Biol. Chem. 262, 6182-6196, 1987
A;Title: Comparison of the maxicircle (mitochondrial) genomes of Leishmania tarentola A;Reference number: A92643; MUID:87194837
A;Accession: B26696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: B26696 from: 1 to: 443
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1059 AACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTC.....
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                                                                                                                                                                                                                                                                                                                   ATCTGAAATCACAACTGCTTTTCAAACTCAAATTG...TCCCGATGCCAG 1160
                                                                                                     TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA 1060
                                                                                                                                                             TyrLysIleLeuIleLeuTrpTyr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTA 1257
                                                  \verb|nLeuIleAsnPheIleLeuLeuPheValLeuLeuTyrTyrMetIleLeu|.
                                                                                                                                                                                                             TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA 1110
                                                                                                                                                                                                                                                                                                                                                                           eIleSerIleLeuPheGluLeuPhe..... 109
                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGT 1207
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0.463
44.485
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                                                                                                                                                           .. TyrTyrMetIleAs
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29
19.853
                                                        152
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     1017
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seq_documentation_block:
pNA-directed RNA polymerase (EC 2.7.7.6) beta chain - plasmodium falciparum plastid C:Species: plastid Plasmodium falciparum C:Species: plastid Plasmodium falciparum C:Date: 31-Dec-1990 #sequence_revision 15-May-1998 #text_change 11-Jun-1999 C:Accession: S72282; S10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A;Residues: 1-1024 <WIL>
A;Cross-references: EMBL:X95275; NID:g1171583; PIDN:CAA64572.1; PID:e220243; PID:g117
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A;Cross-reference number: S10438
A;Reference number: S10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; W. J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium A; Reference number: S72277; MUID:96346169
A;Accession: S72282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir1:RNZQBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: this apparently degenerate plastid is referred to a C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase; plastid; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X52177; NID:g9879; PIDN:CAA36427.1; PID:g9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 328-1024 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S10438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Genome: plastid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-323-427-2/rev x RNZQBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 yPhePheLeuLysValPheCysLeuLeuLeuHisLeuSerTyrLeuGlyI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390
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                                                                                                                                                                                                                                                                                                                                                  1633 AATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACT 1584
                                                                                                                                                                                                                                                                             1583 ACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATG.....
1499 ACAATCA.....ATTTTAATACACGTAATGCATTCGAAGGACATGT 1459
                                                                                                                                                                                     102 rophelleTyrAsnAsnIleIleIleLeuAsnGlyLeuTyrLysThrCys 118
                                                                                                                                                                                                                                                                                                                        86 eAsn...IleAsnLysIleIleLysPheAsnIleLeuIlePheIleLeuP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATAATATCACAAATTATACCTTGTATTGCCCCAATTTTTATGGGCATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCCTATTCTGTAAACAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....TyrPheArgLeuIleIleAsnIle......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .PhellePheSerTyrGlnPhe 404
                                          IleGlnLeuPheLysLysAsnAsnLysIlePheIleIleLysPheLysAs 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                             .GTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATA 1500
                                                                                                                                                                                                                                                                                                                                                                                                                     to: RNZQBF from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112.00
0.373
45.113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 665
Gaps: 28
Percent Identity: 17.594
                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1024
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                                                                                                                                                                                                                                                                                                   1544
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728		728
390	ThrAsnGluGlyLeuThrCysGlyLeuValAsnTyrLeuThrThrAs	374
728	AGCTGCGCAACTTCGTT	745
7	:::::::::::::::::::::::::::::::	357
4	AAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTG	
357	ysileAsnMetileThrThrGlyLeuAsnSerLysPheileLeuAsnA	
-	11.28 ANIITAIIGUST TOTOTOS CONSCITALITA ANIXA A FINANCES	5 1
• 0	GAACCAAATAGCGAATGTTCGACCACAAT	847
323	rileAsnileIeLeuGluAsnileAsnIleAsnProLeu	310
848	CAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTA	897
	::: snIleTyrAsnAsnIleThrLeuLeuLeuAsnAsnLysLysT	
868	ATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGT	
حک د	GTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTA	766
280	LysSerLys	7
998	GGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATA	4
1048 277	CATGCGATTCTGAAACCGTTGATAC :::::: ::: :::: eTyrAsnLysLysPheTyrSerIleIleAspAsnLeuLeuI	260
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43	leTyrIleAsnLe	236
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1159 236	ICTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGA1 	1208 219
219	yrAsnTyrIleLysPheIleTyrSerLysTyrAsnAsnIle	205
1209	CAATGCTTTTACATGGAAGCTGATÀAAACAGTTAGTGCACAGAT	1258
204	<pre>::: :::::::::::::::::::::::::::::::</pre>	191
1259	TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATC	1308
9	snAsn	179
1309	acacgatetetgaateeaegtggtatttttgtaacaacagetgi	1358
1359 179	GACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCG	163
6	<pre>reLeuAsnIl</pre>	7.57
4	TATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGA	n un
152	nAsnAsnLysAsnIleIleTyrValTyrIleTyrIleSer	135

	ed name: pir2:S78177	e O
	70 AATTCACTTATTTGCATTATTGCAATTAAAAAGTATTTC 32	
71 646	leIle	
630	THE STATEMENT OF THE STREET	
613	7 TyrSerLeuGlyAsnAsnLeuLeuValGlyTyrGlySerTyrLeuGlyTy	
146		
179 596	228 TAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCATCA : :::	
580		
229		
230 563	268 CTTATTCATTATTCAGTAATCTTTTATATGCATACTATT	
546	:: ::: ::: 31 luGlyIleValIleTyrValSerCysIleLysIleIleIleArgAsp	
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531	TASNPhelleLeuAsnLysTyrLeuAsnHisLeuIleIleSerTyrGlnG	
514	ASHLEGGERASHLIE	
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505	::	
404		
454 489	TTTAAATTTCGTCCAAATCAGAAGGC :::::::::: :: .1leHisTyrAsnAspSerIleArgA	
473	467 PheAsnTyrLeuLeuSer	
504	ATTGATT	
466	Pro	
554	AGTACAAAATGGAATCTGCA	
604 457	638 TTGCCAGTTGATTTACGTCACCGTGCACTTCTGCA : ::: :: ::::: 440 eAsnLysThrThrIleLeuThrIleAsnLysAsnThrPheLysIleCysA	
440	PheTyrAsnIleSerPheAsnAsnIleTyrLeuLysLysAsnIleAs	
639	688 ATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCT ::: ::::: ::: :::::	
423	ıArg	
689	727TACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTG	
407	390 nIlePheLeuAsnLeuLysTyrLeuPheValIleTyrTyrLysHisIleP	

seq_name: pir2:S78177

seq_documentation_block:

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TCTGAAATGATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGC 1
1672 GAAGAAGACAAGCAATCTTAGTTTTTCTAAAAATCGAATTTTACTAAA 1623 ::: ::: ::: 261 sp
1722 CAACAACAACAACAACAACAACAACAACAATAATAACCCCATCAAGTGGAG 1673 :::: :::::: :::::: 244 rGluGlyLeuArgGlyThrGluThrThrLeuAlaLeuProMetAlaSerA 261
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alignment_block: US-09-323-427-2/rev x A40970
alignment_scores: Quality: 108.00 Length: 396 Ratio: 0.527 Gaps: 21 Percent Similarity: 51.768 Percent Identity: 21.212
F;157-240/Jomain: fibronectin type III repeat homology <fn3a> F;255-338/Domain: fibronectin type III repeat homology <fn3b> F;347-427/Domain: fibronectin type III repeat homology <fn3b> F;347-652/Domain: fibronectin type III repeat homology <fn3d> F;547-632/Domain: fibronectin type III repeat homology <fn3e> F;641-723/Domain: fibronectin type III repeat homology <fn3e> F;641-723/Domain: fibronectin type III repeat homology <fn3f> F;731-818/Domain: fibronectin type III repeat homology <fn3g></fn3g></fn3f></fn3e></fn3e></fn3d></fn3b></fn3b></fn3a>
A;Residues: 1-843 <jus> A;Cross-references: GB:M64108; NID:g340081; PIDN:AAA36794.1; PID:g340082 C;Superfamily; collagen alpha 1(XIV) chain; fibronectin type III repeat homology; von Wi C;Keywords: glycoprotein</jus>
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular ma;Reference number: A40970; MUID:91373351 A;Accession: A40970 A;Molecule type: mRNA
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40 AAGTATTTCATTTGTGAAAAAAAAAAAAAAAAAAAAAAA
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131 TATCACAAATTATACCTTGTATTGCCCAATTTTTATGGGCATCATTTCCT 82
181 TCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAA 132 :: 563 TyrLeuLys
228 TAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCA 182 :: ::::::::::::::::::::::::::::::::::

ز	768 TGGTGCCGCAGCAAAACCTGCTGCAGCTGCGC AACTTGCTTTACTGA 7	
G.	46 lPheGlnThrGlyIleArgAsnLeuV 5	
69	TTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGG 7	
819 546	868 TCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGT 8 ::: ::::::: 531 ThrGluProAlaThrThrIleValDroThrThrSerValThrSerVa 5	
369	09 AGAAGCTCACGTATACA ::::: ::: 14 rGluSerGluVal.valThrAlaVa	
910 514	38GAATATCCAACAC	
939 497	GCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTG ::::::::::::: 	
986 483	1007AACGGTGATACTGTGGAAATTC 9	
1008 466	1055 GTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTGTCGATGATGGT:: ::: :::	
1056 449	1105 CTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACC ::	
1106 433	TGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTG :::: :: :: :::	
1150 417	CAGTATGCCGTTA :::::: hrIleAlaIlePh	
1191 400	0 AAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACT ::	
1241 384	ATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGG :::::::: ::::::::::::::::::::::::::	
1291 370	CCACGTGGTATTTTTGTAACA	
1341 363	e:: 13	
1391 348	1440 TGATCAAGAAGGTTGCCGGAATGATGAAGGTGGACGTCAAGTTGCCGGAA : ::: :::	
1441 331	1487 AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTA	
1488 318	1525 AAATTGAATGTGGACCAACTTCAATAACAATCAATTTT	
1526 302	1572 ATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAG	

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GATCAAGAAGGTT :::::: ThrLysHisValI
CCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACA :: ::: :::!:::::::::::
61 CG#
1611 GATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTAT1 1502 365
1705 CAACAACAGCAATAATAACCCCATCAAGTGGAGGAAGAACACHG 1006 :::::: :::
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alignment_scores: Quality: 107.00 Length: 689 Quality: 107.00 Gaps: 38 Ratio: 0.354 Gaps: 38 Percent Similarity: 43.832 Percent Identity: 19.303

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C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Accession: G71613
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, i.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                 seq_name: pir2:G71613
                                                                                                                                                                                                                                                                                                                      ::|||:::|||
879 luLysGluLys 882
                                                                                                                                                                                                                                                                                                                                                                                                            862 uValLeuLysThrValGluGluGluLysGluGluGluGluGluLysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 TAAATGTTTCATCATTAGGCCATGAATAGTTTCGTTTGTTATTATCATCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 774 eGluLysAsnLeuSerHisLeuLeuAsnIleTyrTyrGlnHisLysIleV 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            759 IleCysAsnAspAsnThrTyrValAlaHisSerSerIle...TyrCysIl 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            699 alAsnLysAsnAsn......AsnIleCysSerLysIleLysAsn 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleArgIleSerGluTyrValLeuSerLysTyrPhePheArgAsnGlyLe 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGCAATTAAAAAGTATTTCATTTGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euPhe.....ValCysGly 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTTGCATT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eIleAsnAlaLeuSerLysMetCysTyrThrTyrGluMetTyrValValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAAAT.....TATACCTTGTATTGCCCAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATAATAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAlaMetProLysLysTyrIleAspLeuIleIlePheSerAsnIl 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTGAAAAGCTTATTCATTATTCAGTAATCTTTTATATGCATACTATTG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ······GATATTTTCATCAAAACTTCTTCTATCGCTTTTATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC.....TGTAATACAATAAGT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATAAAAATAATGTTAGAATCATCGAAGCAATAATAAAAACTGCCATAT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uProTyr...ValAsnThrIleValGluArgGlnIlePheLysLeuLeuV
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A;Accession: G71613
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: 1-1346 <GAR>
A;Residues: 1-1346 <GAR>
A;Cross-references: GB:AE001397; GB:AE001362; NID:g3845192; PID:g3845193; TIGH A;Experimental source: clone 3D7 C;GenetLos:
C;GenetLos:
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US-09-323-427-2/rev x G71613
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Ratio: 0.319
Percent Similarity: 46.036
                                                                                                  1206
                                                                                                                                                                                                                                                               1270 GTG......CATATCGAGTACAATGCTTTTAC 1245
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    1159 ...TATGCCGTTATGAAATTT
                                                                                                                                                                         1244 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG.....T
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649 AsnHisGluAsnSerArgAsnLysIleAlaAsnTrpGlnAsnLysIleGl 665
                                       yrLeuTyrLeuGluIleLeuHisArgMetLysIleTyrAsnHisAspIle 834
                                                                                  ATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG... 1160
                                                                                                                              {\tt sPhePheIleLeuLysGluAsnTyrTyrTyrLeuSerIleAspAsnLeuT}
                                                                                                                                                                                                                     IleSerLeuSerLeuCysAspIleLysTyrLeuAsnLeuTyrAlaLeuCy
                                                                                                                                                                                                                                                                                                            {\tt luGlnAsnLeuAsnHisGluAsnMetLysTyrIleIleHisAsnLeuMet}
                                                                                                                                                                                                                                                                                                                                                                                                   AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....GluValProHisAsnPheGluIleHisLeuAspAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAGGTGGACGTCAAGTTGCCG...GAATTTCACTTCCATTTGATTCA 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCG...TCTTATTGCTTTCTGTAC.....TACACTTATTGCATTGT 1568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ATTTACTAAATCTTCTGAAATGATGAT 1606
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TGGATGGTGGA 1131
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21.280
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probable membrane protein YMR216c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein YM8261.10c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998
C;Accession: S55098
C;Accession: S55098
C;Rocedman, K.; Brown, D.; Bowman, S.
                                                                                                         R; Dedman, K; Brown, D.; Bowman, S.
submitted to the EMBL Data Library, June 1995
symbolited to the EMBL Data Library, June 1995
A; Reference number: $55089
A; Accession: $55098
A; Accession: $55098
A; Molecule type: DNA
A; Residues: 1-742 CDED>
A; Residues: 1-742 CDED>
A; Cross-references: EMBL: 249809; NID: 9854459; PID: 9854468; MIPS: YMR216c
A; Experimental source: strain AB972
C; Genetics:
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A;Map position: 13R
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F;241-257/Domain: transmembrane #status predicted <TMM>
                                                                 A;Gene: SGD:SKY1
A;Cross-references: SGD:S0004829; MIPS:YMR216c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1149 sTyrpheGlnLeuLysLysIleAspLeuGluTyrIleAsnSerAsnIleA 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1183 IleAsnTyrArgTyrGlnTyrGlnSerValHisLysAlaIleGlnLeuPh 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|||:::: |||||| :::|||:::|||:::
1166 snAsnLysLysLysAsnThrTyrAsnAspPhePheAsnGluAsnAsn 1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 ATAATGTTAGAATCATCGAAGCAATA......422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTT...TATGGGCATCATTTCCTATTCTGTAAACAATTCACTTATTTGCA 55
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alignment_block:
US-09-323-427-2/rev x S55098
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                                                                              1094
   1044 CTGCGCGGTTGTC
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                                                                     CAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTT 1045
                                                                                                     alLeuLeuGlyAlaPro.....
                                                                                                                                  TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT 1095 ::||| |||:::|||
                                                                                                                                                                                rAsnSerIleGlnThrArgGluTyrArgSerPro......GluV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATT 1288
                                                                                                                                                                                                                    AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGA 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....AsnAsnAspAsnSerLysAsnLysAsnAsnAsn.AsnAsn 480
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0.816
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Gaps: 13
Percent Identity: 20.462
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1032
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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: C71618
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A;Cross-references: GB:AE001386; GB:AE001362; NID:g3845148; PID:g3845151; TIGR:PFB031
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: C71618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: PFB0315w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:C71618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: C71618 from: 1 to: 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-323-427-2/rev x C71618
                                                       1144 TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT 1095
                                                                                                                                                                                                                                                                                                           1244 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                      1294 CATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTAC 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1391 ATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAA 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1102 MetLysLysLysLysThrGlnGluTyrValAspIleGlu.....Th 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1441 ATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGA 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1116 rValTyrGluTyrValIleGluLysTyrLysArgValHisValLeuTyrL 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1031 .....CATTCCTGCTTTGTCGATGATGGTAAC...GGTGATACTGTGGAA 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               989 ATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTT 940
:::|||:::|||
625 LeuleuGly.......GluleuProSerTyrLeuleuArgAsnGl 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637 yLysTyr 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 939 GGAATAT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608 luGlyHisSerTyrThrLysAspAspAspHisIleAlaGlnIleIleGlu
                                                                                                                                                                                                                                                                                                                                                                     LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euGlyArgLeuLeuGlnIleValGluLysLeuPheLysLysTyrIleLeu 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TC...CACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATC 1295
                                                                                                                     ysLeuGluPheLeuIleLysLysMetGlnHisTyr......
                                                                                                                                                                                      AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 1145
                                                                                                                                                                                                                                                tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 1183
.....PheAsnHisIleIleAsnSerTyrGl 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt aCysLeuIlePheGluLeuIleThrGlyAspPheLeuPheGluProAspG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104.50
0.477
44.422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 493
Gaps: 20
Percent Identity: 18.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624
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seq_documentation_block:
hypothetical protein PFB0870w - malaria parasite (Plasmodium falciparum)
C;Species; Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Date: 13-Nov-1998 #sequence, L.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
C;Accession: E71604
A;Accession: E71604
A;Accession: E71604
A;Accession: E71604
A;Accession: E71604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: PFB0870w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-323-427-2/rev x E71604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: E71604 from: 1 to: 2380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1518 LeuThrLysIleGlu.ValPheValIleCysValGlnAsnPheVal.... 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1501 spvalLeuGlnLeuTyrAspLysTyrProTyrIlePheGlnTyrLysAsp 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 TCATCAAAACTTCTTCTATCGCTTTTA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1652 TTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1699 CAGCAATAATAACCCCCATCAAGTGGAGG...AAGAAGACAGGAAGCAATC 1653
                                                                                                                                                                                                                                                                                                                                          1602 TCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTAT...TCGATTC 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 nasnasnasnasnGlyTyrLysLysLysIleLysAsnLysAsnLysAsnL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1505 TCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTA 1456
                                                                                 548 erIleAspAsnAsnVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ......TTCGTCCAAATCAGAAGGCATAAAAATAATGTTA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......GTTTCTTCTTATCATCCTTCTAATAACTAATTTTAGCTAAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                     ysAsnLysLysAsnLysLeu.....Asn
                                                                                                                                                                       CGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACT 1506
                                                                                                                                                                                                                                                             AsnTyrAsnAspAsnPheValSer.ValAsnGlySerTyrAspAsnTyrS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104.50
0.415
47.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 528
Gaps: 24
Percent Identity: 19.886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....ThrLeuTyr 1535
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598	647 AATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACCTTCTGCAACATAA ::: ::: ::: ::: ::: :::
800	erAlaIleIleAlaSerCysAsnIleProMetTyrLeu
648	97 ATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTTAGCGATG
698 785	74/ TGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGA
774	64lleThrGlnIleLeuProT
748	AGCAAAACCTG
763	51 IleTyrLeuAsnAsnArgIleGlyAsnValPheValGly
) (TACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACATTTTTTTT
848 750	897 ATACAAATAWGCGGARCGATCAGCTTTTCTATCAATGCCAGATCAGTA ::::::: ::: 737LeuAsn1leGluLeuAsnLysTyrLeuTyrGluAspSerTyr
736	0TyrGlnLysLeuGluAsr
898	TATCCAACAGA
729	::::: ::: leIleSerAsnValTyrLysHisG
948	CTGATGGATGTGCTCTTGATAAATATTTGC
713	697 lySerIleCysAlaCysCysLeuSerVa
o u	35 TGTCCATTCCTGCTTTTTTTTTTTTTTTTTTTTTTTTTT
0	TTGATACTTTCTGCGCGG
683	0ProTyrHisLeuGlyValSer
1086	GETCAGCCA
669	GlyIleSerPheS
1136	CAAACTCAAATTGTCCCGATGC
1186 658	. ₽ ∪
ω	15AsnThrHisAsnMetHisAsnThrHisAsnTleHisAsnGluLy
1236	85 TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACAT
626	: ::::::::::::::::::::::::::::::::::
ည	GGTATTTTTGTAACAACAGTTGTCATTTCGTTTCATCCATTTATTT
1336	1364 GTTGCGCGTACACGATCTCTGAATCCACG ::: :::
593	4 ysLysTyrAspThrSerTyrSerPhe
1365	GATTCA
1406	1455 TGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGATGAAGGTGGAC
567	

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A; Molecule type: DNA
A; Residues: 792-6839 ABL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898
A; Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898
A; Experimental source: var. Bristol
R; Benlan, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 45-50, 1989
A; Title: Sequence of an unusually large protein implicated in regulation of myosin ac
A; Reference number: S06797; MUID:90044042
A; Accession: S06797
A; Status: nucleic acid sequence not shown
                 A;Experimental source: var. Bristol R;Benlan, G.M.; L'Hernault, S.W.; Morris, M.E. Genetics 134, 1097-1104, 1993
A;Title: Additional sequence complexity in the
                                                                                                                   A;Molecule type: DNA
A;Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,'I
A;Cross-references: EMBL:X15423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Benian, G.
submitted to the EMBL Data Library, November 1989
A;Reference number: S07571
A;Accession: S07571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: Additional sequence complexity within twitching of Caenorhabditis eleg, A;Reference number: S57242
A;Accession: S57242
A:Mainania:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 18-Jun-1999. C;Accession: S57242; S07571; S06797; S57218 R;Benlan, G.M.; L'Hernault, S.W.; Morris, M.E. submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; MoLecule type: DNA
A; Residues: 1-6839 <BEN1>
A; Cross-references: EMBL:L10351
A; Experimental source: var. Bri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: myosin-regulating protein N;Contains: protein kinase (EC 2.7.1.-) C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      twitchin - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               902 ArgLysIlePheAspTyrTyrThrPheVal 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 TCAGTAATCTTTTATATGCATACTATTGTA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 TCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 TATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                835 eLysValSerProPheAspSerAspTyrValGlyIle...GlyAsnLysA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597
Additional sequence complexity in the muscle gene, unc-22, and its encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuPheIleCys.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt snAsnSerValIleSerProHisLeuIleLysTyrAsnHisIleLeuPhe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCATTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGCATAAAA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCAC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leGluLysAspTyrLeuPheLeuIleGluAsnLeuLysAspIleLeuGlu 901
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0 CGC
1410 TGGACGTCAAGTTGCCGGAATTTCACTTCCACTTGATTCATGCAATGCTTG 1301 ::: :::::: ::: 3415 .AsnArgGlnGlyThrSerAlaProLeuThrSerAspHisAlaTleValA 3431
1501 TAACAATCAATTTTAATACACGTAATGCATTCQAAGGACATGTTTAT 1433
lva 3 CAA 1 erA 3
356valvalLeuLys 335
335
333
CA 16 sn 33
1749 ARCACCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA
US-09-323-427-2/rev x S57242
Ratio: 0.479 larity: 40.485 Percent Identity: 19.
-194, 'Q', 196-206;374-468;658-753 See: var. Bristol e: var. Bristol 71: 6808; 176/3; 264/2; 387/3; 413/3; 143/2; 176/3; 264/2; 387/3; 413/3; 16808; 176/3; 264/2; 387/3; 413/3; 6808; 176/3; 176/3; 176/3; 176/3; 176/3; 176/4, 1
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790 GATTCGGAGCTGTTAAAACAGGTGG	3679 TrpGlnGluValGlyThrPheProAspCys 837 AGAACCAAATAGCGAATGTGTTCGACC	913 GCCAAGAAGCTCACGTATACAAATATGC 913 GCCAAGAAGCTCACGTATACACAATAGCC 872	TAAATAATT	995GTGGAAAI	1003 GTGATACT 3618 lyLysaspThralaGlnCysasnVal	038 GGTTGTCCAT 601 aValArgGlyAspThrGlyValTyr	1046	1085TATCATAAATGGACATGCGATTCTG	.112CAAT :::: :551 sAlaGlyThrProIleLysLeuAspI	1113	1142TTGGATGGTGGACCAACCGG	1173 TGTCCCGATGCCAGTATGCCGTTATGAI :::: :::: 3501 uThrProGlyGluThrTyrGlnPheAr	1223 AGTGCACAGATTGAGGTATCTGAAATCAC 	271	12723452 pHisValAspLeuGluTrpLysProProAla	:::::: 1 laLysAsnProPheAspGluProAspAl 1 daLysAsnProPheAspGluProAspAl 0 GTCATTTCGTTTCGTTCATCCATTATTTGTTA
AGGTGGTGCCGCAGCAAAACCTGCTGCAGCT 741	ThralatysValAsntyste 309 ACAATGTTCAGAACCACAAG 791 ::::::	THE TRANSPORT OF THE TR	AATATCCAACAGATTTAATG :: ysproproThraspAsnGly	TCTAAATGCTGATGGATGTGCTCT 9 ::::: :: ::: uIleHisLysGluGlyCysThrLe 3			rSerAlaIleHisIlePheSerAl 3601	104 Alaarg 358	TGCTATCATTGGTCAGCCAGTT. 108 : ::: ::: ::: eAlaPheGluGlyGluProAlaP 356	aGlyLeuLeuAspLeuArgIleLy 3551	TCAACCAGTT	alAsnLysAlaG 351	AACTGCTTTTCAAACTCAAAT 117 :::: rLysalaThrAlaAspAsnLe 350	CTGATAAAACAGTT :: :: !yaspTrpValGlu	AsnAspGlyGlyAlaProI	AAAGTTGAT

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L_block: 23-427-2/rev x T03099	lignment_bl US-09-323-4
lignment_scores: Quality: 104.00 Length: 405 Ratio: 0.654 Gaps: 20 Percent Similarity: 39.259 Percent Identity: 21.975	lignment_sc Percent Sim
	Molecule t Residues: Superfamil Superfasi:
;Cross-references: GB:J03512; Cross-references: GB:J03512; Experimental source: submaxillary gland; Experimental source: submaxillary gland; Experimental source: Submaxillary gland; Foundadje, A.; Johnson Jr., W.C.; Hill, Biol. Chem. 262, 11339-11344, 1987; Title: Structural properties of porcine submaxillary gland apomucin.; Reference number: A92606; MUID:87280230	Experiment; Eckhardt, Eckhardt, Biol. Che. Title: Str Reference
LUH: AZ8028 le type: mRNA es: 12139-12167,'T',12169-12641 <tim></tim>	Molecule ty Residues:
m. 263, 1081-1088, 1988 cine submaxillary gland apomucin contains toumber: A28528; MUID:88087170	;Title: Por ;Reference
;Residues: 12139-12167,'T',12169-13288 <ec3> ;Residues: 12139-12167,'T',12169-13288 <ec3> ;Cross-references: GB:M61883; NID:g454837; PID:g164374 ;Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.</ec3></ec3>	Residues: Cross-refe; Timpte, C.
s a cystine-rich, cart	Holecule t
Molecule type: mRNA Residues: 1-13288 <eck> Cross-references: EMBL:AF005273; NID:g2581863; PID:g2581864 Eckhardt, A.E.; Timpte, C.S.; Abernethv. J.I.: Zhao, v. Hill B.</eck>	<pre>White Molecule 1 Residues: Cross-refe Eckhardt,</pre>
Reference number: 214839; MUID:98070526 Accession: T03099 Status: preliminary; translated from GB/EMBI/DDR.I	Reference; Accession; Status: pi
R.L.	<pre>?;Eckhardt, f. Biol. Che ;;Title: The</pre>
<pre>seq_documentation_block: nucin, submaxillary - pig NyAlternate names: apomucin ;Species: Sus scrofa domestica (domestic pig) ;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Sep-1999 ;Accession: T03099; A40009; A28528; B29789</pre>	<pre>seq_documentation_ nucin, submaxillar nucin, submaxillar ny,Alternate names:)Species: Sus scr)Spate: 24-Mar-199 ;Accession: T0309</pre>
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	690 TG : 3729 eA
0 GCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCAT 691 :: :: 0 GluGluProIleIleAlaLyssnGlnPh 3729	740 GC 3720 G1
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13123 snAspThrCysCysGluIle......GlyHisCysGluLysArgThr 13136
                                                                                                                                                             13106 oSerProProThrCysLysThrGlyGluArgLeuIleLysPheLysAlaA 13123
                                                                                                                                                                                                                                                                       13090 CysThrCysThrGluAlaLysThrValAspCysLysProLysGluCysPr 13106
                                                                                                                                                                                                                                                                                                                                                                                    13073 euGlyGluGluLysSerProGlyAspValTrpThrAlaAsnCysHisLys 13089
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                                                                                                          1006 ACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAA 957
                                                                                                                                                                                                              1038 GGTTGTCCATTCCTGCTTTGTCGATGAT......GGTA 1007
                                                                                                                                                                                                                                                                                                                              1076 TGGACATGC...GATTCTGAAACCGTTGAT......ACTTTCTGCGC 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                           1126 CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1234 ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAA...ATCACAACTGCT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||
|12982 ......ValGlyThrThrGluAlaGlyIleSerSerGlyAsnSerP 12995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12962 lySerGlyThrThrSerSerProGlyGlyValLysThrGluAlaThrThr 12978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1281 CAAAGTTGATCGTGCATATCGAGTACAATGCTTT...TACATGGAAGCTG 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1331 ATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTAC 1282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1422 TAATGATGAAGGTGGACGTCAAGTTGCCCGGAATTTCA.....CTTC 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1472 TTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCG 1423
1519 AATGTGGACCAACTTCAATAACAATCAATTTTAATACACGT...AATGCA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1557 TCCGGTTGACAATGGTGTCGAA......GGTGAGCCAGAAATTG 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1607 ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT 1558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1707 AACAACAACAGCAATAATAACCCCCATCAAGTGGAGGAAGAAGACAGGAAG 1658
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696 13211	744 13194	772 13177	806 13162	85i	13145	906	13137
696 TATCATTGATGTACG 682 ::: 13211 TyrasnGlyCysThr 13215	744AGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAA 697 ::: :::	772 CAGGTGGTGCCGCAGCAAAACCTGCTGC. 745 773 CAGGTGGTGCCGC		856 AGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAA 807 :::::::::::::::::::::::::::::::::::		906 AGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCC 857	

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Swissprot 38: PGS1_HUMAN -
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Swissprot 38: CO3_MOUSE -
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Swissprot 38: YF61_METJA -
Swissprot 38: YF61_METJA -
Swissprot 38: SW5M_NEGCR -
Swissprot 38: SW5M_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database: SwissProt_38:*
Database sequences: 82229
Database length: 29864866
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                                            Documentation
                                                                                                                                                  i Q0974 schizosaccharomyces
i Q39575 chlamydomonas reinha
p01027 mus musculus (mouse),
i P25823 drosophila melanogast
i Q58956 methanococcus jannasc
i Q58956 methanococcus jannasc
i P05510 neurospora crassa. na
i P14772 saccharomyces cerevia
i P1837 paramecium primaurel
i P27801 saccharomyces cerevia
i P27801 saccharomyces cerevia
                                                                                                                                                                                                                                                                                                                                                                                          P47853 rattus norvegicus (rat)
1 008853 plasmodium falciparum
1 P21810 homo sapiens (human).
2 P75802 escherichia coli hyr
2 P12890 xenopus laevis (afric
2 P25648 saccharomyces cerevi
2 P47179 saccharomyces cerevi
3 P47179 saccharomyces cerevi
4 P47179 saccharomyces cerevi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P17889 bacillus subtilis. tra
i P98991 bos taurus (bovine).
i P14198 dictyostelium discoid
i P16492 herpesvirus saimiri (
i P16491 schizosaccharomyces (
i 010211 schizosaccharomyces (
                   ! 002678 canis familiaris (do:
P30938 rattus norvegicus (rat
                                                                                                                                                                                                                                                                                                                                                                            ! P23351 neurospora crassa.
                                                             ! P38692 saccharomyces cerev
! P38198 saccharomyces cerev
! 080957 human papillomavirus !
! P19158 saccharomyces cerev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! P09975 marchantia polymorp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P12021 sus scrofa (pig). apor
P34855 apis mellifera ligust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q59633 pseudomonas aeruginos
! Q03100 dictyostelium disco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q09276 caenorhabditis elegar
P21809 bos taurus (bovine)
Q03656 saccharomyces cerevis
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P21421 plasmodium falciparı
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SwissProt_38:SYA_MYCPN -
SwissProt_38:RMAR_CANGA -
SwissProt_38:UL52_HSV7J -
SwissProt_38:AMD_HUMAN -
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                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               SUBDITIES (APR-1995) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: COMPONENT OF THE CUTICLES. IT FORMS A RIBBON APPROXIMATELY 2 MICRONS WIDE RUNNING ALONG THE LATERAL LINES UNDERNEATH THE ALAE. CONTRIBUTES TO THE FORMATION OF EXTRACELLULAR ENVELOPES PROTECTING THE ORGANISM FROM THE ENVIRONMENT.

-I- SUBCELLULAR LOCATION: SECRETED

-I- TISSUE SPECIFICITY: LOCALIZED IN A NARROW BAND NOT EXPOSED TO THE EXTERIOR, RUNNING UNDERNEATH THE ALAE.

-I- DEVELOPMENTAL STAGE: EXPRESSED DURING DAUER LARVA FORMATION.

-I- DOMALN: THE SMALL REPEATS A-A-P-(AVI) ARE ALSO PRESENT IN MANY PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES.
                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                         EMBL; M55997; AAA27995.1; ALT_INIT.
EMBL; Z99125; CAA88934.1; -.
PIR; A49772; A49772.
HSSP; P04002; 1ATF.
                                                                                                                 REPEAT
                                                                                                                                                                       DOMAIN
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MEDLINE; 91323673.

SEBASTIANO M., LASSANDRO F., BAZZICALUPO P.;

"Cut-1 a Caenorhabditis elegans gene coding 1

noncollagenous component of the cuticle.";

Dev. Biol. 146:519-530(1991).
                                                                                                                                REPEAT
                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                Cuticle;
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01-FEB-1994 (Rel. 28, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                              WORMPEP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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CUT-1 OR C47G2.1.
Caenorhabditis elegans
Cukaryota; Metazoa; Nematoda;
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G -> P (IN REF. 1).
P -> G (IN REF. 1).
A -> G (IN REF. 1).
MISSING (IN REF. 1).
CL -> SG (IN REF. 1).
FA -> LP (IN REF. 1).
IG -> MR (IN REF. 1).
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CUTICLIN 1.
4 X 4 AA REPEAT OF A-A-P-[AVI].
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! P21358 candida glabrata (
! P52468 herpes simplex vir
! P19021 homo sapiens (human
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alignment_block:
US-09-323-427-2/rev x CUT1_CAEEL
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Similarity: 80.769
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                                               AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC
                              ysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnIleSerIleThr
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seq_name: SwissProt_38:RPOB_PLAFA
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01-CCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7)
                                                                                                                                                                                                                             MEDLINE: 95107345

GARDNER M.J., GOLDMAN N., BARNETT P., MOORE P.W., R. STRATH M., WHYTE A., WILLIAMSON D.H., WILSON R.J.M. "Phylogenetic analysis of the rpoB gene from the plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPOB_PLAFA
                                                                                 GARDNER M.J., WILLIAMSON D.H., WILSON R.J.M.;
"A circular DNA in malaria parasites encodes an RNA polymerase like
that of prokaryotes and chloroplasts.";
MOL. Blochem. Parasitol. 44:115-124(1991).
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALXZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                      STRAIN-BW(C10)
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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             MISCELLANEOUS: THIS RNA POLYMERASE IS ENCODED ON A CIRCULAR DNA. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                          SUBSTRATES.
CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N
                                                                                                                                                                                                                 Biochem. Parasitol. 66:221-231(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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404	453 ATAAAAATAATGTTAGAATCATCGAAGCAATAATAAAACTGCCATATATA . ::::::::::::::::::::::::::::::
489	3 eIleGluAsnLeuIleProPheIleHisTyrAsnAspSerIleArgA
454	CTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCCAAATCAGAAGGC
504 473	553 TGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATT ::::::: 467 PheAsnTyrLeuLeuSer
554 466	603 ACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCA
604 457	638 TIGCCAGTIGATITACGTCACCGTGCACTTCTGCA : ::: ::::: 440 eAsnLysThrThrIleLeuThrIleAsnLysAsnThrPheLysIleCysA
639 440	ν 8
689 423	727TACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTG
407	390 nIlePheLeuAsnLeuLysTyrLeuPheValIleTyrTyrLysHisIleP
728	
728 390	745 CAGCTGCGCAACTTCGTT :::
746 373	795 ACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCGAGCAAAACCTGCTG :: :::::::::::::::::::::::::::::
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. 323	897 ATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTA
310	947 AATAATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGT
295	:::
2 2	97 CTGTGGAAATTCTAAATGCTGATGGATGTGCTTCTTGATAAATATTCTT
9	TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGA
1048	1079 AAATGGA
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Quality:
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US-09-323-427-2/rev x YQH3_CAEEL
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Ratio: 0.559
Percent Similarity: 47.229
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NP_BIND
SEQUENCE
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141 hrIleProTyrGlySerGluCysAspValThrLeuThrAspLeu...... 155
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     1117 CA......GTTCAATTTGCTATCATTGGTCAGCCA... 1089
                                                                  1155 CCGTTATGAAATTTTG......GATGGTGGACCAACCGGTCAAC 1118
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495 AA;
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178 ATP (POTENTIAL).
55068 MW; 09C77468 CRC32;
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seq_documentation_block:
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NEAME P.J., CHOI H.U., ROSENBERG L.C.;
"The primary structure of the core protein of the small, leucine-rich proteoglycan (PG I) from bovine articular cartilage.";
J. Biol. Chem. 264:8653-8661(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGS1_BOVIN
P21809; P792
01-MAY-1991
                                                                                                                                                                                                  "Primary structure of bovine cloned CDNA.";
                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1030 ATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAT
                                                                                               MEDLINE; 89255324.
                                                                                                                                    SEQUENCE OF 38-369.
                                                                                                                                                                              Biochem. Mol.
                                                                                                                                                                                                                                 XU J.H., RADHAKRISHNAMURTHY B.,
                                                                                                                                                                                                                                                                               TISSUE-AORTA
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364
                                                                                                                      TISSUE=CARTILAGE
                                                                                                                                                                                                                                                          MEDLINE; 96113563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BONE/CARTILAGE PROTEOGLYCAN I
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 lAsnAspGlnIleTyrPheSerLysPheArgThrPheArgPheGlyAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgArgThrThrArgSerAlaProThrAspAspAsnGlySerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTG 636
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                                                                                                                                                                                                                                                                                                                                         Bos.
                                                                                                                                                                           Biol.
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                                                                                                                                                                           Int.
                                                                                                                                                                     37:263-272(1995)
                                                                                                                                                                                                           aorta biglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRECURSOR (BIGLYCAN) (LEUCINE-RICH PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                   SRINIVASAN S.R.,
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alignment_block:
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CARBOHYD
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DISULFID
CONFLICT
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CONFLICT
                     775 AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA
                                                                                                                                                                    CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal;
SIGNAL
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REPEAT
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REPEAT
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REPEAT
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PIR; A33701; A33701.
PFAM; PF00560; LRR; 8.
PFAM; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 264:2876-2884(1989).

-!- TISSUE SPECIFICITY: FOUND IN THE EXTRACELLULAR MATRICES OF SEVERAL CONNECTIVE TISSUES, SPECIALLY IN ARTICULAR CARTILAGES.
-!- PTM: THE TWO GLYCOSAMINOGLYCAN CHAINS ATTACHED TO BIGLYCAN CAN BE EITHER CHONDROITIN SULFATE OR DERMATAN SULFATE.
-!- SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
REPEAT
                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=CARTILAGE;
MEDLINE; 89123388.
CHOI H.U., JOHNSON T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DS-PGII, from bovine articular cartilage and sepharose chromatography.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, from bovine articular cartilage and skin isolated by octyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEAME P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE OF 38-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 10\,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY
                                               1/1
                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
                                                                                                               Ratio:
                                               ;
0
                                                                                                                                                                                         Connective tissue; Extracellular matrix; Proteoglycan;
                                             PGS1_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Leucine-repeat
                                                                                                 106.50
0.873
40.803
                                                                                                                                                                                         355
152
188
354
                                                                                                                                                                   41509
                                                                                                                                                                   MW;
                                                                                            Length: 299
Gaps: 13
Percent Identity: 20.736
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C -> E (IN REF.
A -> R (IN REF.
KK -> Y (IN REF.
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                                                                                                                                                                                                                                                                                      LRR
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                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                 F1CC673B CRC32;
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                                                                                                                                                                            (IN REF.
                                             369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated by octyl-
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seq_documentation_block:
ID KM65_YEAST STAN
                                             seq_name: SwissProt_38:KM65_YEAST
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                                                                                                                                            296 yLeuProAspLeuLysLeuLeuGlnValValTyrLeuHisThrAsnAsnI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....CTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProLeuArg.....LysLeuGlnLysLeuTyrIleSerLy 148
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sAsnHisLeuCysGluIleProProAsn......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATATAGTATGTAGGAAATAATTACTGTAATACAATAAGTGATATTTTC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rLeuArgIleSerGluAlaLys.....LeuThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATATTCGTTTCTTATCATCCTTCTAATAACTAATTTTAGCTAACAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluAsnSerGlyPheGluProGlyAlaPheAspGlyLeuLysLeuAsnTy
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                                                                                                                                                                                                           LeuArgGluLeuHisLeuAspAsnAsnLysLeuSerArgValProAlaGl 296
                                                                                                                                                                                                                                                                                                                                                                          TTCAGTAATCTTTTATATGCATACTATTGTAAATGTTTCATCATTAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                         LeuAspHisAsnLysIleGlnAlaIleGluLeuGluAspLeuLeuArgTy
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCAAAACTTCTTCTATCGCTTTTATAGCTTCTGAAAAGCTTATTCATTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyIle......ProLysAspLeuProGluThrLeuAsnGluLeuHis 236
                                                                                                          TCACAAATTATACCTTG.....TATTGCCCAATTTTTATGGGCATC 89
                                                                                                                                                                                                                                                                            isAsnGlnIleArgMetIleGluAsnGlySerLeuSerPheLeuProThr 279
                                                                                                                                                                                                                                                                                                          ATGAATAGTTTCGTTTATTATCA...TCATTATCAACTTGTCCT... 164
                                                                                                                                                                                                                                                                                                                                       ATTTTATTCTAACAGTTTATCATTTGTGATAATA 130
                                                                              leThrLysValGlyValAsnAspPheCysProValGlyPheGlyVal 328
        STANDARD;
                                                                                                                                                                                                                                        PRT;
           742
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE SERINE/THREONINE-PROTEIN KINASE YMR216C (EC 2.7.1.~).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMR216C OR YM8261.10C
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-i- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. SIMILAR TO S.POMBE DSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetaceae; Saccharomyces.
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DEDMAN K., BROWN D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00069; pkinase; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z49809; CAA89931.1;
HSSP; P24941; 1AQ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transferase; Serine/threonine-protein kinase;
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                                                                                                                                                                                                                                    TACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCG 1538
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                                                                                                                ....AsnAsnAspAsnSerLysAsnLysAsnAsnAsn.AsnAsn
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ATP (BY SIMILARITY).
BY SIMILARITY.
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seq_name: SwissProt_38:APMU_PIG
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                                                                                                                                                               Sus scrofa (Pig)
Sus scrofa; (Pig)
Eukaryota; Metazoa; Chordata; Cran
Cortart iodactyla; Suina;
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                                                       MEDLINE;
ECKHARDT
                                                                                                                                                                                                                                 01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
APOMUCIN (MUCIN CORE PROTEIN) (FRACMENT).
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            carboxyl-terminal
                                                                                                TISSUE=SUBMAXILLARY GLAND;
                                                                                                                         SEQUENCE FROM N.A.
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                                    Porcine
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       A.E., TIMPTE C.S., submaxillary mucin terminal domain in
                                                                        91236743
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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  ABERNETHY J.L., ZHAO Y., HILL R.L.; contains a cystine-rich, addition to a highly repetitive,
                                                                                                                                                                                        Craniata; Vertebrata;
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                                                                                                                                                                    Suidae;
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    PRESENTATION OF THE PROPERTY O
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              Glycoprotein;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "GERKEN T.A., OWENS C.L., PASUMARTHY M.;

"Determination of the site-specific O-glycosylation pattern of the porcine submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:galnac transferase peptide binding site.";

J. Biol. Chem. 272:9709-9719(1997).

-:- FUNCTION: APOWUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECKHARDT A.E., TIMPTE C.S., ABERNETHY J.L., TOUMADJE JOHNSON W.C. JR., HILL R.L.; "Structural properties of porcine submaxillary gland J. Biol. Chem. 262:11339-11344(1987).
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                       PFAM; PF00007;
                                                                                                                                                                                                                                                                                 PROSITE;
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J. Biol. Chem วีเดียง
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYDRATE-BINDING SITES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 87280230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 45-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIMPTE C.S., ECKHARDT A.E., ABERNETHY J.L., H: "Porcine submaxillary gland apomucin contains identical sequences of 81 residues.";
J. Biol. Chem. 263:1081-1088(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-SUBMAXILLARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: EXTENSIVELY O-LINKED GLYCOSYLATED ON SER AND THR RESIDUES (THE REPEAT UNITS. HIGHEST GLYCOSYLATION APPEARS TO OCCUR ON SER RESIDUES WHICH HAVE GLY AT POSITIONS AT +2 OR -2 FROM THE GLYCOSYLATION SITE OR, WHERE GLY IS THE PENULTIMATE RESIDUE. THI PRESENCE OF PROLLINE (USUALLY AT POSITION +3 OR -3) APPEARS TO ALLERS OF THE PENULTIMATE RESIDUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENVIRONMENT.
SUBUNIT: INTERMOLECULAR DISULPIDE BONDS COULD
MULTIMERIC MUCIN STRUCTURE.
SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECLFICITY: SUBMAXILLARY MUCOSAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN:
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                                                                                                                                                                                                                                                                          PS01185; CTCK_1; 1.
PS01225; CTCK_2; 1.
PS01208; VWFC; 1.
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                                           6 (INCOMPLETE).
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2.
4.
                                                                                                                                                           (FRAGMENT).
                                                                                                                                                                                   AA TANDEM REPEATS
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ns tandemly repeated,
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BY SIMILARITY. POTENTIAL.	APMU_E U_PIG GACTGG : rThrV rTAATA :: alarg cTAAAA TTTTTT TTTTTT TTTTTTT	91 93 94 95 96 98 98 98 100 100 100 100 110 111 111 111 111 11	i . i . i . i . i . i . i . i . i . i .
	rom: 1 to: 1150 CAACAACAACAACAACAACAACAACAAC 1::	POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. COMPANDA F7C55CCE CRC32; MW; F7C55CCE CRC32; Length: Gaps: Gaps: Percent Identity: 21.97	Y SIMILARITY Y SIMILARITY Y SIMILARITY Y SIMILARITY X SIMILARITY

772 CAGGTGGTGCCGCAGCAAAACCTGCTGC
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ATGTGTTCGACCACAA 80 CysvalThrTyrSer 10
G
06 AGCTCACGTA
956 TATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC
GlyHisCysGluLysArgThr
oSerPr
rTTGTCGATGATGGTA 10
1076 TGGACATGCGATTCTGAAACCGTTGATACTTTCTGGGC 1997 ::::::::: 1076 TGGACATGCGATTCTGAAACCGTTGATACTTTCTGGGC 1997
::
OLGUPTOFICELOFICEATCHTTGGTCAGCCAGTTTATCATAAA 1
5 .ATTG
.snGluAsnLysThrGlyCysProAlaPr 924
1234 ATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCT 1188
hrserVals 891
AlaSerGluThrThrThr
1381 CATTTGATTCATGCAATGTTGCGCGTACACGATCCTCTGAATCCACGTGGT 1332
TARTICAL TOTAL TOT
1472 TTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCG 1423
24 lySerGlyThrThrSerSerProGlyGlyValLySThrGluAlaThrThr
AATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATG
807 rGlvTleSerThrGlyProGluAsnSerThrProGlyThrThrGluThrG 824

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Se de la Cocción                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-323-427-2/rev x NU5M_APILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: NU5M_APILI from: 1 to: 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1315 CTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCA 1266
                                                                                                                                     1233 TAAAA.....
                                                                                                                                                                                                                                                                                                  1265 TATC......GAGTACAATGCTTTTACATGGAAGCTGA 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L06178; AAB96805.1; --
PFAM; PF00361; oxidored_q1, 1.
PFAM; PF00662; oxidored_q1_N; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 554 AA; 65590 MW; 9E256E2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1056 yrThrCysLysSerSerCysLysProSerProValAsnValThrValArg 1072
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P34855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=THORAX;
MEDLINE; 93114603.
CROZIER R.H., CROZIER Y.C.;
                                                                      44 etLysPheAsnPheLeuLeuLleaspTyrLysSerLeuMetPheIle 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization."; Genetics 133:97-117(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
                                                                                                                                                                                                                        27 rLeuAsnLysGluPhePhePheGluTrpAsnIleTyrThrPheAsnSerM 44
                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apis mellifera ligustica (Common honeybee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).
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                                                                                                                                                                                                                                                                                                                                                                                 LeuPheGluPheSerPheLeuMetMetLeuMetSerLeuTyrLeuLeuTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103.00
0.396
46.931
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.....CAGTTAGTGCACAGATTGAGGTA 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 554
Gaps: 34
Percent Identity: 21.480
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61	PheLeuValSerMetIlePheSerMetIleIleIleTyrSerIleSerTy	77
1205	CACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG	1156
1155	TATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTG	1106
91		95
1105 96	TTTATCATAAATGGACATGCGATTCTGAAACC ::::::: ::: TyrMetLeu1leLeuSerPr	1056
1055	TTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATG	1013
106	nMetLeuSerIleIleLeuGlyTrpAspGlyLeuGlyLeuIleSerT	123
1012	TOTAL	, 0
123	CysLeuValIleTyrTyrMetLysMetLysSerPheThrSerGlyMet	139
1009 140	CTAAATGCTGATGGATGTGCTCTTGAT	960
959	TTGCTAAATAATTTGGAATATCCAA	Ñ
153	:::: :::::: uMetThrTyrTyrGlySerTrpAsnLeuSerPhe	170
929		929
170	${ t MetAsnGluPheMetMetIleTyrIleLeuLeuMetAlaP}$	186
928	CAGATTTAATGGCTGGCCAAC	902
201	ysseralaGinileProPheserThrTrpLeuProMetAlaMetMetAl	Ö
203	aProThrProValSerSerLeuValHisserSerThrLeuValThrAlaG 2	220
ū	ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCAC	906
C	YI1eTyrLeuLeuIleArgTy	234
235		1 9
ω	.AAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCA	
251	::: LeuLysLysValValAlaTyrSerT	9
753 268	ACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAGATCTGCAGAAC 7 ::	04
703	GAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGC	54
284	: :::[] aMetPheLy	00
53	ATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCA 6 :::	04
00	tPheMetCysValGlySerTyrMetHisTyrMetTyrSerA 3	15
315	ACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA 5	60
559	CTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCATT 5	13
332	et.IleLeuIlePheSerIleLeuSerLeuCysGlyPheProPheL 3	48

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Sequence of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IF2_BACSU STANDARD; PKT; /10 AA. P17889; O31757; O1-NOV-1990 (Rel. 16, Created) O1-NOV-1990 (Rel. 16, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) TRANSLATION INITIATION FACTOR IF-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
                                                       "Isolation and molecular genetic characterization of the Bacillus subtilis gene (infB) encoding protein synthesis initiation factor
                                                                                                                                                            MEDLINE; 90236932.
SHAZAND K., TUCKER J., CHIANG R., STANSMORE K.,
SPERLING-PETERSEN H.U., GRUNBERG-MANAGO M., RABINOWITZ J.C.,
                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
                                                                                                                                                                                                                                                              STRAIN-168
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                               LEIGHTON T.;
                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGAAGGCATAAAAATAATGTTAGAATCATCGAAG......CAATA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysGluAspLysIleMetCysIleSerMetMetMetMetIlePheSe 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTAGGAA.....ATAATTACTGTAATACAATAAGTGATATTTTC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATCATCCTTCTAATAACTAATTTTAGCTAACAA.....ATATATAGT
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   Bacteriol. 172:2675-2687(1990)
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US-09-323-427-2/rev x IF2_BACSU
                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                              Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M34836; AAA22673.1; ...
EMBL; Z18631; CAA79234.1; ...
EMBL; Z99112; CAB13536.1; ...
PIR; A35269; A35269.
PIR; B35269; B35269.
PIR; B35269; B35269.
PIR; B35269; B35269.
S1994; B31994.
HSSB; PD2990; 1ETU.
SUBTILIST; BG10268; INFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBSTITUTE OF PRODUCTS: IT IS PROBABLE THAT BY USING ALTERNATIVE FORDERS IN THE STAME.

SUBMITTATION SPONTANDOUS HYPE OF THE ENSEMBLACTOR FOR THE INITIATION OF PROTEIN SYNTHESIS IN VITRO, PROTECTS FORWLMETHIONYL-TRUM FROM SPONTANDOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S SPONTANDOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S DEALING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX.

1. SUBCELLULAR LOCATION OF THE 70S RIBOSOMAL COMPLEX.

1. SUBCELLULAR LOCATION SOF THE TOS RIBOSOMAL COMPLEX.

1. SUBCELLULAR LOCATION SOF THE SAME READING FRAME, THE GENE TRANSLATES INTO TWO ISOZYMES: ALPHA AND BETA.

1. SIMILARITY: BELLONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 93259931.
SHAZAND K., TUCKER J., GRUNBERG-MANAGO M., RABINOWITZ J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities.requires a license agreement (See http://www.isb-sib.ch/announce/
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NP_BIND
NP_BIND
                                                 CHAIN
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Initiation factor; Protein biosynthesis; GTP-binding;
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nAsnAsnAsnLysAsnGlnHisGlnGlnLysProValLysProLysLysG
                                                                                                               PheAsnLysAsnLysLysAsnAsnAsnLysLysAsnLysArgAsnAs
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Ratio:
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226
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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R -> A (IN REF. 3).
ACB9B730 CRC32;
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962	······GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTG	1004
419	spLysGlyArgGlySerValAlaThrLeuLeuValGlnThrGlyThrL	403
1005	CATTCCTGCTTTGTCGATGATGGTAAC	1033
02	:: snArgGlnAlaLysGlyThrValIleG	386
0 (AAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGC	1083
1084	GGACCAACCGGTCAACCAGTTCAATTTGCTATTGGTCAGCCAGTTTA : ::: :::::::::::::::::::::::	1133 369
369	GlyGluThrIlePheValProLeu.SerAla	353
1134	AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG	1183
1184 353	PARGValMetGlnGluLeuThrGluTyrGlyLeuValProGluAlTrpG PArgValMetGlnGluLeuThrGluTyrGlyLeuValProGluAlaTrpG	336
ω ω	eValalavalAsnLysIleAspLysGluSerAlaAsnProA	
1234	:	1250
319	alGluAla	303
1251	ATCGAGTACAAT	1300
7 303	YAlaGluValThrAspIleThrIleLeuValValAlaAlaAspAspGlyV	28
. 00		J.
1333	AATGTTGCGCGT/ ::: GlyHisAlaAla	1382 274
	luGluAsnGlyLysLysIleThrPheLeuAspThr	262
13	gttgccgtaatgatgaaggtggacgtca	1432
262	uAlaGlyGlyIleThrGlnHisIle	24
ا د	·····CATGTTATGTG	1463
. 1464 1 248	LysThrThrLeuLeuAspSerIleArgLysThrLysValValGluGlyGl	1493 232
y 231	euGluIleArgProProValValThrIleMetGlyHisValAspHi	215
. 1494	TTGAATGTGGACCAACTTCAATAACAATC	1522
215	:::::: 	198
15	· · · · · · · · · · · · · · · GAAGGTGAGCCAGA	1538
. 1539 e 198	CTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTC	1580 182
e 181	euLeuGlyValMetAlaThrIleAsnGlnGluLeuAspLysAspThrIl	б
. 1581	TTATTGCTTTCTGTACTACA	1600
16	AlaGlu.GluLeuGlyLysGluProSerGluLeuIleLysLysLeuMet	149
16	AAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCGT	1641
	:: luLeuProGluLysIleThrPheSerGlyThrLeuThrValGlyAlaLe	132
. 1642	AGACAGGAAGCAATCTTAGTTTTCT	T997

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seq_documentation_block:
ID MUCS_BOVIN STANDA
AC P$8091;
DT 01-FEB-1996 (Rel. 33,
DT 01-OT-1996 (Rel. 33,
DT 01-OT-1996 (Rel. 34,
DE SUBMAXILLARY MUCIN-LI
OS BOS taurus (Bovine).
OC Eutheria; Cetartiodac
CC Eutheria; Cetartiodac
COC Eutheria; Cetartiodac
COC Bovinae; Bos.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBMAXILLARY G
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBMAXILLARY G
RX MEDLINR; 90370871.
RA BHARGAVA A.K., WOITAC
RT Cloning and CDNA seq
RT Proc. Natl. Acad. Sci
CC -:- SUBCELLULAR LOCAT
CC -:- SIMILARITY: TO PC
CC -:- SIMILARITY: CONTA
CC -:- SIMILARITY: CONTA
CC -:- SIMILARITY: CONTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: SwissProt_38:MUCS_BOVIN
TISSUE-SUBMAXILLARY GLAND;

MEDLINE; 90370871.

BHARGAVA A.K., WOITACH J.T., DAVIDSON E.A., BHAVANANDAN V.P.;

"Cloning and cDNA sequence of a bovine submaxillary gland mucin-like protein containing two distinct domains.";

Proc. Natl. Acad. Sci. U.S.A. 87:6798-6802(1990).

-!- SUBCELLULAR LOCATION: SECRETED.
-!- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
-!- SIMILARITY: TO PORCINE APOMUCIN.
-!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                           MUCS_BOVIN STANDARD; PRT; 563 AA. P98091; O1-FEB-1996 (Rel. 33, Created) O1-FEB-996 (Rel. 33, Last sequence update) O1-OCT-1996 (Rel. 34, Last annotation update) SUBMAXILLARY MUCIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575 AsnVal 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              586 TAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         686 GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 laArgAlaSerLysGlnLeuGluGluGlnArgSerAsp.....LysAla 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTICGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysLeuSerLeuAspAspLeuPheGluGlnIleLysGlnGlyAspValLy 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCA 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pGlnPheLeuValPheLysAspGluLysThrAlaArgSerValGlyGluA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAAT 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..ArgAlaMetValAsnAspIleGlyArgArgValLysThrAlaGlyPro 450
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128 TTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCAT 1379	28
78 AATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGG 14427 ::: 260 ThralavalvalSerGly	0 8
CAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGT 147	_
TATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGC 152	1578 TA 229
ACTAAATCTTCTGAAATGATGATGCTTATTGCTTTCTGTACTACACT 1	1628 AC :: 221 Va
GTGGAGGAAGAAGAAGAAGCAATCTTAGTTTTCTAAAAATCGAATTT	1678 GT
	1698 AGO :: 190 rG
B ACACCGACTGCAGCAACAACAACAACAACAACAACAACAACAACAACAA	1748 AC <i>P</i> 174 Thi
1/1 to: MUCS_BOVIN from: 1 to: 563	Align seg 1
nt_block: 323-427-2/rev x MUCS_BOVIN	10
nt_scores: Quality: 100.50 Ratio: 0.602 Eagps: 19 t Similarity: 42.931 Percent Identity: 21.594	alignment_sc
394 394 477 477 563 AA; 58913 MW	CARBOH CARBOH SEQUEN
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seq_documentation_block: ID AAC4_DICDI STANDARD; PRT; 317 AA. AC P14198; DT 01-JAN-1990 (Rel. 13, Created)
seq_name: SwissProt_38:AAC4_DICDI
695 ATCATTGATGTACGAAC 679 ::: 476 alasnvalThrValAsn 481
745 CAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAAAT 68
GluaspargValTyraspSerThrLysCysCy
858 CCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCAC 80 ::::::::::::::::::::::::::::::::::::
07 hrCysLeuPheAsnAsnAsnAspTyr
PheLysAspasnaspinicyscyscenter TaatggCTGC
90 AATTCTAAATGCTGATGGATGT
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1464 ACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATG 1415
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"Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters of asparagine, glutamine, or threonine.";

Mol. Gen. Genet. 218:453-459(1989).

-!- DEVELOPMENTAL STAGE: THE CONCENTRATION OF AAC-RICH MRNAS IS LOW IN DORMANT SPORES AND GROWING CELLS, BUT INCREASES DURING SPORE-GERMINATION AND MULTICELLULAR DEVELOPMENT.

-!- MISCELLANBOUS: SEVERAL PROTEINS DERIVE FROM AAC-RICH MRNA, WHICH, DUE TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS ARE

DUE TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS ARE
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01-FEB-1994 (Rel. 28, Last annotation update)
AAC-RICH MRNA CLONE PLK330 PROTEIN (FRAGMENT)
Dictyostelium discoideum (Slime mold)
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                                                                   ........AsnCysPheGluThrCysAspPheLysAlaThrGluArgGl 108
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Herpesvirus saimiri (strain 11).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
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                                                                        GLYCOPROTEIN H PRECURSOR. GH OR 22.
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MEDLINE; 92333688.

ALBRECHT J.-C., MICHOLAS J., BILLER D., CAMERON K.R., BIESINGER B.,
ALBRECHT J.-C., WITTMANN S., CRAXTON M.A., COLEMAN H., FLECKENSTEIN B.,
NEWNAN C., WITTMANN S., CRAXTON M.A., COLEMAN H., FLECKENSTEIN B.,
HONESS R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HONESS R.W., CRAXTON M.A., WILLIAMS L., GOMPELS U.A.;
A comparative analysis of the sequence of the thymidine kinase gene
"A comparative analysis of the sequence of the thymidine kinase gene
"A comparative analysis of the sequence of the thymidine kinase gene
of a gammaherpesvirus, herpesvirus saimiri.";
J. Gen. Virol. 70:3003-3013(1989).
J. Gen. Virol. 70:3003-3013(1989).
I. FUNCTION: GH AND GL FORM A COMPLEX THAT INDUCES NEUTRALIZING AND
I. FUNCTION: GH AND GL FORM A COMPLEX THAT INDUCES NEUTRALIZING AND
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"Conservation of glycoprotein H (gH) in herpesviruses: nucleotide sequence of the gH gene from herpesvirus saimiri.";
J. Gen. virol. 69:2819-2829(1988).
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J. Virol. 66:5047-5058(1992).
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D00543; BAA004
PIR; J00010; VGBE11.
Glycoprotein; Transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                   1656 AATCTTAGTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGA 1607
                                                                                                                                                                                                                                      1706 ACAACAACAGCAATAATAACCCCATCAAGTGGAAGAAGAAGACAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                   1606 TTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATT 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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17
43
59
80
128
128
444
644
613
675
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43
59
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128
444
560
613
675
82583 N
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                                                                                                                                                                                                                                                                                                                                                                                                                  99.50
0.358
42.121
....ThrLeuLeuPheGlyHisSerHisTyrLeu 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 660
Gaps: 39
Percent Identity: 20.000
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POTENTIAL.
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O:
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884GATCGATCACAGCTTTTCTATCA 862
ValLeuSerSerMetCysThrSerLeuGluIleGlyAsnLeuLeu 47
roT 45
TGIUAL 9 LYSING CECCUTOCOCO A AGA AGOTCACGI
ASPLEUILESerHislleTyrThrAlaTyrSerTyrThrTyrMet 42 ASPLEUILESerHislleTyrThrAlaTyrSerTyrThrTyrMet 42
394
59 AACCGTTGATACTTTCTGCGCGCGTTGTCCATTCCTGCTTTGTCGATGATG
ArgHis39
 367 AsnValProLysHisValIleThrSerLeuSerHisGl
.20 AAC
aserGlnAlaLeu 36
5 .GlupheLeuArgLysLeuMetGluSerCysPheGluP
ACAACTGCTTTTCAAACTCAAATTGTCCCGATGC
1246 ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC 1197
ATGCTTT
TTTCGTTTCATCCAT
::: nIleValAsnPro 296
77 p
rge-rul retrocker. CAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGA
57
474 CATTICGARGACATOLI
31 DASPVGLFIEGGELDON
24 AATTGAATGTGG
⊢ ⊢ ≀
2200

488

505

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132 ATATCACAAATTATACCTTGTATTG 108
                                                                                                                                                                                               228 TAAATGTTTCATCATT....AGGCCATGAATAGTTTCGTTTGTTATTATC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 GTCCAAATCAGAAGGCATAAAAATAATGTTAGAATCATCGAAGCAATAAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 AAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 CAAAATGGAATCTGCATGTCACCATTTTGGCTTCTCAATGTTTATGGGTTT 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581 alPheLeuLysThrSerMetIleIleSerAlaValAsn.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521 rAsnGlyPhePheGlnThrLeuHisMetArgHisHisThrSerLeuGluI 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         820 GTGTTCGACCAC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 LeuHisPheGlyGlnLysAspValLeuAspValTyrGluThrPheSerPr
                                           IleMetVal......pheIleLeuPheLeuValGlyLeuTyrLe
                                                                                           ATCATTATCAACTTGTCCTATTTTATTCTAACAGTTTATCATTTGTGATA 133
                                                                                                                                              leGluValArgGlyAlaTyrArgAlaArgLeuValAsnPheIleIleVal
                                                                                                                                                                                                                                                  pGlyAsnLeuHisIleHisTyrLeuIleLeuMetAsnAsnGlyThrvalI
                                                                                                                                                                                                                                                                                                     TGAAAAGCTT...ATTCATTATTCAGTAATCTTTTATATGCATACTATTG 229
                                                                                                                                                                                                                                                                                                                                                         ......GluAsnLeuPhe.....ThrGluHisSerProPhePheGlyAs 662
                                                                                                                                                                                                                                                                                                                                                                                                         ACAATAAGTGATATTTTCATCAAAACTTCTTCTATCGCTTTTATAGCTTC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ly......PheGlnSerMetMetTyrIleThrAspThrTyrValGln 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTAATTTTAGCTAACAAATATATAGTATGTAGGAAATAATTACTGTAAT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAACTGCCATATATA.....TTCGTTTCTTCTTATCATCCTTCTAATA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AsnAspCysLys......proTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .GlyCysProTyrCysSerSerValValLeuSerTyrAspGluSerGlnG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrValProArgArg......619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGlnGlyGlySerAlaAlaHisGln....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerIleProLeuLysAsnIle......ThrTyrValIleSerTh 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...GTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leLeuProIleIleLysCysIleLysSerLeuSerThrAspIleIleLeu 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt GluPheProGlnSerSerLeuIleAlaGlnLysGluIleAsnLeuGlyTh}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGCCAGATCAGTATTACCATT.....AAAGAACCAAATAGCGAAT 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......IleProValIleTyrAsnVal 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....AATGTTCAGAACCACAAGGATTCGGAGC 781
                                                                                                                                                                                                                                                          679
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275

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alignment_block:
US-09-323-427-2/rev x YAY3_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: YAY3_SCHPO from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                 1362 TGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTG 1313
                                                                                                                                                                                         1412 GGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGT 1363
                                                                                                                                                                                                                                                                     1462 ATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAA 1413
                                                                                                                                                                                                                                                                                                                                             1491 TITTAATACACGTAATGCATTC......GAAGGAC 1463
                                                                                                                                                                                                                                                                                                                                                                                                                         1541 GTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCAA 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z69380; CAA93342.1; -
Hypothetical protein; Transmembrane.
TRANSMEM 265 285
POTENTIAL.
TRANSMEM 564 584 POTENTIAL.
TRANSMEM 626 646 POTENTIAL.
SEQUENCE 649 AA; 74488 MW; F04F8763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q10211;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME
99 euLeuAspPhePheHisArgProTrpGluAspTyrGluProLeuTyrPro 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                   36 LeuAspGlySerValGluMetMetCysTrpPro......As 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708 uLeuTyrLysLeuPheValTyrLeu
                                                                                                                                                                                                                               isPheSerIleThrProIle...GluGlnThrSerCysLys.....
                                                                                                                                                                                                                                                                                                           \tt nPheAspSerProSerIlePheAlaArgIleLeuAspAlaArgAlaGlyH
                                                                             eLeuHisThrLysPheTyrSerGluArgGlyValLeu..
                                                                                                                                                         ·····GlnMetTyrGluProSerThrAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.50
0.554
43.672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                584 P
646 P
74488 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 403
Gaps: 23
Percent Identity: 22.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F04F8763 CRC32;
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                                                                           .....ArgL
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1283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uGluCysPheProAlaLeuAspTyrAlaArgGlnSerHisGluThrArgV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGG 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpLeuIleArgArgValSerCysIleArgGlyThrSerArgIleLysLe 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAAAGTTGATCGTGCA.....TATCGAGT 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||::|||||
alserLysIleThrGluAsnTyrTyrGlnAlaGluPheValProAlaSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCTGAAATCACA...ACTGCTTTTCAAACTCAAATTGTCCCGATGCCA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAA...... 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyAspProLysTyrIleLeuAspCysValProSerGlyAspGlnLeuLy 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lyValIleSerTyrLeuGluLeuGluGluGlyGlnGluIleThrPhe...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATGCGGATCGATCACAGCTTTTCTATCAA.....TGCCAGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pTyrValThrProAsn.....LeuValAspLysL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \verb|euGluAspSerThrLysArgTyrTrpArgAlaTrpIleGlnGlnCysVal|
                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAACCACAAGGATTCGGAGCTGTTAAAACA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sLeuLeuIleTyrGluProThrGlyAlaValIleAlaSerProThrPheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTACCATTAAAGAACCAAATAGCGAATGTGTTT...CGACCACAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrThrGlyArgTyrArgGluPheValGlnArgAsnAlaLeuThrLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                         || |||::: :::|||::::|||::::::
erLeuProGluAspLeuGlyGlyValArgAsnTrpAspTyrArgPheThr 302
                                                                                                                                                                                                                                                                     eArgAlaGluAlaValGluTyrMetSerPheIleTyrHisValLeuLysL 336
                                                                                                                                                                                                                                                                                                                                      {\tt TrpIleArgAspSerAlaPheThrIleTyrAlaLeuAlaGlnLeuGlyPh}
                                                                                                                                                                                                                                                                                                                                                                       .....GGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT.....
                                                                                                                                                                                                                                 AAAGATCTGCAGAACCGGAG....AATATCATTGATGTACGAACTGATATC 672
                                                                                                                                                                                                                                                                                               .....CGTTTACTCAAGA 719
                                                                                                                                                              AACACCCTTGAAATTAGCGATGATAATCAAGCTTTG...CCAGTTGATTT
                                                                                                                                                                                                  ysLysAsnLysAspGlyGlyIleAsnIleVal.....
                                                             uThr \verb|HisLeuArgGly.....TyrTyrAsnSerHisProValArgIle.\\
                                                                                               ACGTCAC...CGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTG
                            CTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTT 528
                                                                                                                               .....TyrSerIleHisGlyAspSerGlnAsnLeuGluGluValGluLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .Gly.AsnAlaAlaValHisHisLeuGln.LeuAspIleT
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                                                                                                                                                                                  625
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ATGGG

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Seq_documentation_block:
ID YCEZ_MARPO STANDA
AC P09975;
DT 01-MAR-1989 (Rel. 10,
DT 01-MAR-1989 (Rel. 26,
DE HYPOTHETICAL 259 KD F
GN 2502 (Rel. 250 KD F
GN YCF2.

OS MARCHANTIALES; MARCHANTIALES; MARCHANTIALES; MARCHANTIALES;
RA OHYAMA K.; FUKUZAWA I
RA OHYAMA K.;
RA OHYAMA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: SwissProt_38:YCF2_MARPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-323-427-2/rev x YCF2_MARPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: YCF2_MARPO from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X04465; CAA28078.1; -.

PIR; A05037; A05037.

PIR; S01591; S01591.

MENDEL; 5295; MARGO; ycf2;1.

PFAM; PF00004; AAA; 1.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
HYPOTHETICAL 259 KD PROTEIN (ORF 2136).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its due by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OHYAMA K., FUKUZAWA H., KOHCHI T., SHIRAI H., SANO T., SANO S., UMESONO K., SHIKI Y., TAKEUCHI M., CHANG Z., AOTA S., INOKUCHI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                  1731 AACAACAAA.......CAACAAACAACAACAACAACAAC
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SEQUENCE 2136 AA; 259911 MW; A
                                                                                                                                                                               1652 TTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG
                                                                                                                                                                                                                                                                                                                                                               709 AsnAsnLysLeuIleThrTrpLysLysIleSerAsnLysLeuValIleSe 725
                                                         TCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGG 1553
                                                                                                                                                                                                                                               rAsnSerGluTyrAsnLysIleIleTrpAsnLysLysAsnMetLysPheP
SerPheAsnIleIle......ThrValIlePheAspLys.L 770
                                                                                                                      heSerPheSerLysAsnSerValLeuAspThrPhePheAsnLysLys
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Ratio:
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Percent Identity:
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Ū	TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA :::	1503
770		786
1502 787	CATTCGAAGGACATGTTTATGT	4.
1452	GGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTC	1403
803	yrPheIleAsnGlu	10
1402	TGATTCATGCAATGTTGCGCGTACA	1353
811	::::::	815
1352	ATCCACGTGGTATTTTGT	1309
816	PheAsnAspLysGluPheAsnIleF	826
1308	TGATCGTGCATATCGA	1259
827	euGluLeuPheIleSerGluIleAsnAsnAspPheLeuM	841
1258	ACAATGCTTTTACATGGAAGCTGATAAAACA	1221
841	LysLysTyrLeuTyr.TyrArg	357
1220	GTATCTGAAATCACAACTGCTTTTCAAACTCAAATT	1171
857	heAsnProIleGluAsnArgGlnL	374
1170	GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTC	⊢
N	TCAATTTGCTATCATTGGTCAGCCAG	077
891	heIlePheHisLeuGluLysLysThrIleLysAs	07
1076	ACATGCGATTCTGAAACCGTTGATACTTTC	1039
907	LeuLeuTyr	924
1038	GGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAA 9 }	989
924		124
988	CTCTTGATAAATATTTGC	39
925	LeuLeuIl	30
938	ATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATA	889
931	LysSerPheIleGluLysLysAsnAsnL	942
888	GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTA	839
942	euPheIleLysSerGlnLeuSerAsnValLeuLeuVal 9	54
838	AATAGCGAATGTGTTCGACCAC8	9
955	erTyrLysPhePheAspAsnIlePheAsnPheHisPheLeuLy 9	71
808	AATGTTCAGAACCACAAGG 7	90
971	uLysAsnIleGluIleI	88
789	CAAAACCTGCTGCAGCTG 7	40
988	uLysSerLeuLeuLysLysThrTyrLeuLysAsnLeuAsnLeu	1002

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seq_documentation_block:
ID GALU_PSEAE STANDA
AC Q59633;
DT 01-NOV-1997 (Rel. 35,
DT 01-NOV-1998 (Rel. 1993)
GN GALU

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CC THE EUROPEAN BIOINFOR
CC SHELL WO3751; AAB0146
DR PFAM, PROD483; NTP-LU
FRANSFERSE; Kinase;
SQ SEQUENCE 279 AA;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last 
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Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: MAY PLAY A ROLE IN STATIONARY PHASE SURVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
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-i- CATALYTIC ACTIVITY: UTP + ALPHA-D-GLUCOSE 1-PHOSPHATE
PYROPHOSPHATE + UDP-GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U03751; AAB01486.1; ...
PFAM; PF00483; NTP_transferase; 1.
Transferase; Kinase; Nucleotidyltransferase.
Transferase; Kinase; Nucleotidyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                          GGT...TGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACT 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAA 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uAlaLeuAspAlaGlyLeuAsnGluIleSerIleValThrGlyArgGlyL
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                                                                      GTATT.....TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCA 1293
                                                                                                                                                {\tt sLeuLeuAspGluCysSerPheSerTyrThrArgGlnThrGlnMetLysG}
                                                                                                                                                                                                                          TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTG
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lyLeuGlyHisAlaIleLeuThrGlyArgProLeuIleGlyAspGluPro
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50.424
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ID CYAA_DICDI STANDA
AC Q03100;
DT 01-JUL-1993 (Rel. 26,
DT 01-JUL-1993 (Rel. 26,
DT 01-JUL-1993 (Rel. 26,
DT 15-DEC-1999 (Rel. 39,
DE 15-DEC-1999 (Rel. 39,
DE ADENVLATE CYCLASE, AC
PYROPHOSPHATE-LYASE)
ACAA OR ACA.
OS DictyOstellum discoid
OC Eukaryota; DictyOstel
RN 11
RN SEQUENCE FROM N.A.
PITT G.S., MILONA N.,
RY MEDLINE; 92233467.
RA PITT G.S., MILONA N.,
RT Gifferent roles in Di
CC HISTORY COORDIT
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADENYLATE CYCLASE, AGGREGATION SPECIFIC (EC 4
PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 ysvalīle 244
                                                                                                                                                                                                                                                                                                                                                                                                                        PITT G.S., MILONA N., BORLEIS J., LIN K.C., REED R.R., DEVREOTES P. "Structurally distinct and stage-specific adenylyl cyclase genes pl different roles in Dictyostellum development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold)
Eukaryota; Dictyosteliida; Dictyostel
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheAlaValValLeuAlaAspAspLeu......CysValAsnLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..ATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGT 1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leIleGlyArgTyrIleLeu.....ThrPro
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                                                                                                                                                                                                                    169:305-315(1992).

169:305-315(1992).

FUNCTION: COORDINATES CELL AGGREGATION BY SYNTHESIZING THE FUNCTION: COORDINATES CELLS

THAT INFLUENCES DIFFERENTIATION AND MORPHOGENESIS OF CELLS

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THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP

PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP

PART OF THE MECHANISM THAT ESTABLISHES THE OSCILLATORY CAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:CYAA_DICDI
                                                                                                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DEVELOPMENTAL STAGE: CELL AGGREGATION AND LATER STAGES.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                 DURING AGGREGATION
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                        903 rgValMetGlyIleLeuHisHisValLysIleSerAsnAspLysIleAsp 919
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                                                                         ATTTACTAAATCTTCTGAAATGATGATTCGTCTTATTGCTTTCTGTACTA 1583
                                                                                           luAspPheLysIleLysSerLysSerAsnSerSer.Phe...GluIleG1
                                                                                                   TCAAGTGGAGGAAGAAGACAGGAAGCAATCTTAGTTTTTCTAAAAATCGA 1633
                                                                                                                         nAsnAsnLysAsnGlnAsnAsnIleTyrGlyAsnAsnAsnAsnAsnGluG 874
                                                        uMetSerAsnIleLysLysProLysSerArg......PheIleAspA 903
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676	AACTGA
	: ::: ::: ePheProGInSerAlaLeuThrLysLeuArg
5	ACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTA
776 1153	TCGGAGCTGTTA ::: AsnPheLeuLeu
1144	8 sThrIleSerValAsnLys
826	CTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAG :::: :::
1138	.ysAlaTrpValValAsnCysLysIleAsnPh
876	AGAAGCTCACGTATACAAATATGCGGATCGATCA
1121	1110ValLeuLeuIleGlnIleCysSerSerTyrGlyMet
923	GCTCTTGATAAATATTTTGCTAAATAATTTGGAATATCCAACAGAT
—	
973	TGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATG
1104	1088 SerIleLeuIleSerProThrLeuThrAsnHisLeuTyrGluThrAspTy
1023	TCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT
1087	SerValLeuPheLeuAsnLeuP
1073	AGTTTATO
07	
	AGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACC <i>t</i>
05	:: ::::: 40 eu.IleArgPheGlnAsnProLe
16	.CTGCTTTTCAAACTCAAATTGTCCCGA
0 1	023 eAlaPhePheIleLeuLeuCysAlaPheGlyValCy
20	TACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
02	::: ::: ::: ::: : PheThrArgIlePheArgThrProLeuValTyrG
1258	CGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAG
1008	996 yrLeuValMetGlyIleAlaPheLeuValTyrIleGly
1308	. i
996	PHisIleMetAspSerAlaPro
1358	······TCACTTCCATTTGATTCATGCAATGT
979	LeuValI1eGlyLeuI1eLeuHisLeuMetPheTy
1389	GCCGGAATT
966	953 ysTyrVallleIleAsnAsnValValGluThrLysPhePhe
1416	ATGTTTATGTGAAAGGTCTTTATGATCAAGAA
953	:::::: ::: eGluAsnLeuThrThrGl
1466	1493AATTTTAATACACGTAATGCATTCGAAG
936	920 LysGluIleIleGlnIleAspGluAspPheValLysValThrLysLeuAr

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tarentolae um falcipar

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sp_invertebrate:022627
sp_invertebrate:016304
sp_invertebrate:023587
sp_invertebrate:023587
sp_invertebrate:024328
sp_invertebrate:097239
sp_invertebrate:02724
sp_invertebrate:02724
sp_invertebrate:02668
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sp_invertebrate:021540 -
sp_invertebrate:019053 -
sp_invertebrate:0293532 -
sp_invertebrate:022164 -
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sp_invertebrate:097236
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sp_invertebrate:Q19707 -
sp_invertebrate:O18479 -
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Query length: 1779
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Database sequences: 25878
Database length: 6934122
Search time (sec): 253.700000
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-Q=/C9n2_1/USPTO_spool/US09323427/runat_14042000_170514_19920/app_query.fasta.
-DH=SPTREMEL_12 -Q=FMY=fastan -SUFFIX-backtrans.rspt
-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-COOPEXT-0.000 -QGAPOP-4.500 -GGAPEXT-0.050 -XGAPOP-10.000
-XGAPEXT-0.500 -FGAPOP-6.000 -GGAPEXT-7.000 -YGAPOP-10.000
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-YGAPEXT-0.500 -TGAPOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
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.1e-29
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              version
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1 Q25802 plasmodium falciparum.
1 Q97236 plasmodium falciparum.
1 Q97288 plasmodium falciparum.
1 Q96247 plasmodium falciparum.
1 Q94648 plasmodium falciparum.
1 Q94648 caenorhabditis elegans.
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097298 plasmodium falciparum
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Seq_documentation_block:
ID Q93115
AC Q93115
AC Q93115
DT 01-FEB-1997 (TrEMBLre
DT 01-NOV-1998 (TREMBLRE
OC ASCATIS lumbricoides; Nacarid
RN [1]
OC ASCATIS lumbricoides; Nacarid
RN [1]
OC ASCATISOIN N.A.
RX MEDLLNE; 97390131.
RA TIMINOUNI M., BAZZICA
RT Gene 193:81-87(1997).
DR EMBL; U73005; AAB8664
KW Signal.
FT CHAIN
SQUENCE 385 AA; 4
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US-09-323-427-2/rev x Q93115
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sp_invertebrate:O97272 -
sp_invertebrate:O77372 -
sp_invertebrate:O97230 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIMINOUNI M., BAZZICALUPO P.; "cut-1-like genes of Ascaris lumbricoides."; Gene 193:81-87(1997).
                                                                                                                            83
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              AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
                                                         GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
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gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG
                                                                                                                                           CGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTT
                                                                                                                                                                                      MetCysArgAlaValSerPhe...LeuAlaLeuPheGlyLeuAlaAlaAl
                                                                                                                         laArgThrArgSerLeuAsnProArgGlyIlePheValThrThrThrVal
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Ratio: 4.593
milarity: 92.784
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385
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Ascaris.
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CUT-1-LIKE CUTICLIN PROTEIN.
; BDEB1169 CRC32;
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913 ! 097272 plasmodium falcipar
4981 ! 0977372 plasmodium falcipa
1423 ! 097230 plasmodium falcipa
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seq_documentation_block:
ID Q19707 PRELIMINA
AC Q19707;
DT 01-NOV-1996 (TREMBLRE
DT 01-NOV-1996 (TREMBLRE
DT 01-JAN-1999 (TREMBLRE
DE F22B5.3 PROTEIN.
                                                                           seq_name:
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 Q19707 PRELIMINARY;
Q19707;
Q19707;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-JAN-1999 (TrEMBLrel. 09, L
F22B5.3 PROTEIN.
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                                                                                                                                                                         .GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA 714
                                                                                                                                     avalAlaLeuAlaAlaAlaValValValValSerPheLysLeuArgP
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                                                                                                                                                       CATTGCATTGATTGCCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTC
                                                                                                 roGlnGlnLysAla
                                                                                                                   CAAATCAGAAGGCA 453
                                                                           sp_invertebrate:Q19707
                                                   PRELIMINARY;
              Last sequence update)
Last annotation update)
                                 Created)
                                                      PRT;
                                                      389
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alignment_block:
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BONFIELD J., BUTTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
BONFIELD J., BUTTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
BONFIELD J., BUTTON J., CONNENT R., FAVELLO A., FULTON L.,
CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., GREEN P., HAMKINS T., HILLIER L., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMNKEEN I
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMNKEEN I
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMNKEEN I
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WATERSTON R.,
THIERRY-MIEG J., THOMAS K., VALUDIN M., VAUGHAN K., WATERSTON R.,
WATESON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATESON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RIGHT M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
REGERGAD.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F22B5.3.
Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
EMBL; Z50044; CAA90355.1;
SEOUENCE 389 AA; 42983
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13 LeuValAlaSerValSerAlaIleProValAspAsnAsnValGluGlyGl 29
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                                                                                                                                          AAAGTTGATCGTGCATATCGAGGTACAATGCTTTTACATGGAAGCTGATAA 1231
                          CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTTGGATGGTGGA
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Gaps: 8
Percent Identity: 69.610
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1080

179

CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCA 1081

179

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seq_documentation_block:
ID 018479;
AC 018479;
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-NOV-1998 (TREMBLrel. 08
DE CUTICLIN-1.
GN MTCUT-1.
OS Meloidogyne artiellia.
OC Eukaryota; Metazoa; Nemato
                                                                                                                                                     seq_name: sp_invertebrate:018479
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    Nematoda;
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                                                       Created)
Last sequence update)
Last annotation update)
Secernentea; Diplogasteria; Tylenchida;
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alignment_block:
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Ratio: 4.042
Percent Similarity: 77.751
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                                                                                               GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCC
                                                                                                                                                                                                                                                                                                                   TGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAG 1226
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                                                              {\tt lyThrCysAspSerGluThrIleAspThrPheCysAlaValValHisSer}
                                                                                                                                                                                            uGlyGlnProIleGlnPheAlaThrIleAlaGlnGlnValTyrThrSerG
                                                                                                                                                                                                                                                        CGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAAT 1076
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seq_documentation_block:
ID Q9XVM7 PRELIMINA
AC Q9XVM7;
DT 01-NOV-1999 (TrEMBLre
DF 53F1.1 PROTEIN.
GN F53F1.1 PROTEIN.
GN F53F1.1,
GN F53F1.1 PROTEIN.
GN F53F1.1,
GN F53
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
F53F1.1 PROTEIN.
                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACAGGT......GGTGCCGCAGCAAAACCTGCTGCAGCTGCG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAAAGATCTGCAGAACCG...GAGAATATCATTGATGTACGAACTGAT 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alleProAlaArgValGlnArgLeuArgThrArgGlnLeuArgLeuLeuA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheAsnAlaLeuAspIleSerAspLysProPheAsnLeuProAlaHisIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTT 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rgPheIleTyrGlnGlyGlyGlnGlnValCysMetSerSerPheArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eArgHisHisHisLeuMetGluAsnLeuSerAlaGluProGlnArgA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGTCACCGTGCACTTCTGCAACATAAT.....GGACAACCTGTAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAATGTTTATGGG.TTTAAGCATTGCATTGATTGCTGCCGTCATTATTA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGCTGCAGTACAAAATGGA.....ATCTGCATGTCACCATTTGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnHisLeuLeuArgTyrGlyHisCysAsnGlyCysSerHisTrpTrpVa 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAT 484
             of contiguous nucleotide
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAACTTCGTTTACTCA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                     sequence
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                                from
                                chromosome
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                                                                                                                                                                 Caenorhabditis
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alignment_scores:
Quality:
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XX MEDLINE; 94150718.

XX MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

XX MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

XX MILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

XX MILSON R., DERTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

XX ADARDON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

XX ADARDON M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

XX ADARDON M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

XX ADARDON M., KERSHAW J., KIRSTEN J., MORTIMORE B., O'CALLAGHAN M.,

XX ADARDON S., LOVE C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XX ADALDON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

XX ADALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

XX THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

XX ADALDON N., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

XX THERRY-MIEG J., THOMAS K., WALLENSON-SPROAT J., WOHLDMAN P.;

XX THE CONTROL OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-323-427-2/rev x Q9XVM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q9XVM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1559 ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1509 AACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z81088; CABO SEQUENCE 364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
EMBL; Z81088; CABO3124.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 ValProIleGlnAsnSerLeuTyrGlyAspValGlnValGluCysAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 lephevalLysAspPheAlaSerGluGluValCysThrSerArgGlyThr 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGC 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGT 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r Arg \texttt{ThrIleSerValGlnIleLysThrGluLysProPheValGlyValI}
                                                                                                                                                                                                                                                                                                                                                                                                                            GTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGA 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyArgLeuSerAlaPheLeuGluIleGluIleGlyLeuCysGlyAlaLe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOATITCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuCysLeuTyrArgGluSerGlnValThrValAlaAsnAsnIleSe
                                                                                                                                                TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA 1110
                                                                                                                                                                                                                                                           rValAspGluIleSerThrIleSerTyrAsnValAsnLeuThrMetProT
                                                                                                                                                                                                                                                                                                                 GGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG
                                       TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 725.50
3.455
77.491
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40843 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
.ACCGTTGATACTTTCTGCGCGGTTGTCC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3FEC30BC CRC32;
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alignment_scores:
    Quality:
    Ratio:
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US-09-323-427-2/rev x Q9XYU9
                                                                                                                                                                                                                                                                                                                                                            seq_name: sp_invertebrate:Q9XYU9
                                                                                                                                                                                                         Align seg 1/1 to: Q9xxU9 from: 1 to: 206
                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                1008 TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
Q9XYU9 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9XYU9;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CUTICULIN-1 (FRAGMENT).
908 GAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG
                                                                      958
                                                                                                                                                                                                                                                                                                                                                                           "Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF125580; AAD28743.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wuchereria bancrofti.
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Wuchereria.
                                           34
                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                      ys {\tt PheLeuLeuAsnAsnLeuGluTyrProThrAspLeuMetAlaGlyGln}
                                                     y \texttt{AsnGlyAspLysValGluLeuLeuAsnAlaAspGlyCysAlaLeuAspL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTAAAACAGGT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATAGCGAATGTTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAsnGlyCysSerIleAspLysPheLeuLeuSerAsnLeuGluTyrPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCC 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aProValValGly 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGlnGluCysValArgProIleCysGluAspValGluGlyGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt isThrCysSerValAspAspGlyArgGlyGluThrSerPheLeuIleAsp}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :
pLysGlyMetIleIleLeuIleLysGluAspSerPheCysMetValValH
                                                                                                                                                                                                                                                                                                                                                            206 AA;
                                                                                                                                                                                                                                                                            695.00
4.064
86.364
                                                                                                                                                                                                                                                                                                                                                           22602 MW;
                                                                                                                                                                                                                                                                          Percent Identity:
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4
69.192
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              859
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alignment_block:
US-09-323-427-2/rev x 096775
                                                                                                                                     alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: sp_invertebrate:096775
                                            Align seg 1/1
                                                                                                             Ratio:
Percent Similarity:
1310 GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCAFATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
096775 PRELIMI
                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                             "cut-1-like genes are present in the filarial nematodes Brugia pahangi and Brugia malayi and, as in other nematodes, code for components of the cuticle.";
                                                                                                                                                                                                                                                                                                                                                                                                                         O96775;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ012617; CAA10074.1; -.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
LEWIS E.K., HUNTER S.J., TETLEY L., PAVIA NUNES C., BAZZICALUPO DEVANEY E.;
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                    Brugia malayi.
                                                                                                                                                                                                                                                                                                                                                                                                    CUT-1
                                                                                                                                                                                                                                                                                                                                                                                                             CUTICLIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 rGlnGlyIleCysMetSerIleThrGlyPheThrLeuAlaGlyMetLeuI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 spIleAsnGluGluPheThrSerLeuProAsnAlaLeuArgHisArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serLeuLeuAlaHisGluAsnGlyHisProValIleValAlaThrMetTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACA...GGTGGTGCC
|||||:::|||||||||||||||||:::||||||
| hcysthrGluProGlnGlyPheGlyAlaIleLysThrArgAsnglyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..TTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACTTCTGCAACAT...AATGGACAACCTGTAATACTTGCTGCAGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt GluAlaHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCy}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt sGlnIleSerIleThrIleLysGluProAsnSerLysCysGlnArgProG}
                                            to:
                                                                                                                                                                                             127
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                             AA;
                                          096775 from: 1
                                                                                                            662.00
5.296
98.425
                                                                                                                                                                                            127
14119
                                                                                                                                                                                            WW.
                                                                                                             Percent
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                           to:
                                                                                                                                                                                           3F738071 CRC32;
                                                                                                          Identity:
                                           127
                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA
                                                                                                          127
0
96.063
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                                                                                                                                                                                                                                                                                                                                                                   Spirurida;
               1261
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seq_name: sp_invertebrate:Q21808
alignment_block:
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                             Percent Similarity:
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                                                                                                                                                                    WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONRFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONRFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONRFIELD J., BURTON J., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN L., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
WATERSTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON OF CONTINUOUS NUCLEOTICE SEQUENCE From Chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Caenorhabditia; Rhabditida;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            COTTAGE A.;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                EMBL;
                                                                                                                                            Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
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NCE 290 AA; 33215
                                                           Quality:
                                           Ratio:
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3.306
69.965
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                                   Percent Identity:
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                                                                                                                          441587FE CRC32;
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                                                                 Length:
                                                    Gaps:
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Align seg 1/1 to: Q21808 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                  154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACA 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProThrMetHisSerLysGlnLeuAsnMetProValCysLysTyrGluVa 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGT 994
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                                                                                                                                                                                                                                                                                                                                                                                           AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                    AG...GTGGTGCCGCAGCAAAACCTGCTGCAGCTG.......CGC 737
                                                                                                                                                                                                                                CA.....
                                                                                                                                                                                                                                                                                                                                 spTyrIleIleProAsnAspAspIleIleSerLeuAsnTrpLeuGlnArg
                                                                                                                                                                                                                                                       CAAGGATTCGGAGCTGTTAAAAC
                                                                                                                                                                                                                                                                              roProArgArgArgSerAsnThrLeuProAlaProAspAspAsnIle
                           snAlaPheLeuPheIleIleSerLeuValSerIleValHisValCys 274
                                                                            ....GluLeuCysMetThrAlaIleGlyThrThrLeuLeuValPheLeuA
                                                                                                     GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 637
                                                                                                                               AsnPhe...
                                                                                                                                                      AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 687
                                                     GCCAGTTGATTTACGTC.....ACCGTGCACTTCTGC 605
                                                                                                                                .....AspMetArgIleSer....
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-323-427-2/rev x Q21540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                           1493
                                                                            1405
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
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JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SNITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
                                                                                                                                                                                        242
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Q21540 PRELIMINARY;
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Q21540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "2.2 Mb of contiguous nucleotide sequence from chromosome III of
elegans.";
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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                                                                     GTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGT 1356
                                                                                                       {\tt sTyrHisAspGluGluCysArgAlaGlyProGluLysPheProAspSerA}
                                                                                                                                            TTATGATCAAGAAGGTTGCCGT.....AATGATGAAGGTGGAC 1406
                                                                                                                                                                               ::: :::|||:::::: |||||||||||||:::||||
LysalaSerThrLysGlnProPheGluGlyAsnValPheValMetAspHi
                                                                                                                                                                                                                                                      heArgProGlyThrProGluIleIleCysGlyProAspArgIleGlyVal
                                                                                                                                                                                                                                                                                          GTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATC 1494
                                                                                                                                                                                                                                                                                                                                                                                                    ValArgValPheThrValGluSerPheGluGlnLeuAspArgAlaLeuAl 213
ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT 1306
                                rgSerIle...GlyLeuThrValProPheSerAlaCysAsnValHisArg
                                                                                                                                                                                                                     AATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAAGGTCT 1444
                                                                                                                                                                                                                                                                                                                                 a.....AspSerLeuThrTrpSerMetCysLysThrGluP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 338
Gaps: 8
Percent Identity: 40.533
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Last annotation update)
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seq_documentation_block:
ID Q19053
AC Q19053;
DT Q1-NOV-1996 (TrEMBLre
DT Q1-JAN-1998 (TrEMBLre
DE E04D5.3 PROTEIN.
GN E04D5.3.
OS Caenorhabditis elegan
OC Eukaryota; Metazoa; N
QC Rhabditina; Rhabditoi
                                                                                                                                                                                                                                           seq_name: sp_invertebrate:Q19053
   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
[1]
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Q19053; O1-NOV-1996 (TrEMBLrel. 01,
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1999 (TrEMBLrel. 09,
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                                                                                                                                                                                                                                                                                                                                                                                     GAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGAT...A 674
                                                                                                                                                                                                                                                                                alThrValLeuGlu 524
                                                                                                                                                                                                                                                                                                                 TCAACACCCTTGAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                        GluAspGlyHisHisHisHisHisProGluLysArgArgLysLeuVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATCAATGCCAGATCAGTATTACCATTAAA...GAACCAAATAGCGAAT 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTA...ATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nPheGlnCysGlnIleThrLeuCysLeuLysTyrAspGlyGlyCysGluG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTATCATTGGTCAGCCAGTTTATCATAAATGGACATGC......GAT 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pAsnGlyTyrGlyAspArgValAspIleLeuAspSerAsnGlyCysGlyL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAlaAspLysAspThrPheGlyMetLeuValHisSerCysTyrValAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laThrLeuGlyGluSerValTyrHisArgTrpGluCysIleGluValGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerMetIleThrThrValPheArgGluGlnIleTyrGlnMetProGlnCy 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt lnCysPheTyrMetGluAlaAspLysHisValThrValProLeuSerVal}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTAC
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                 oda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                     PRT;
                                                                                                                                                                                     484
                                                                                                          update)
                 Caenorhabditis
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BORTHANDAR A., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
EMBL; 266496; CAA91280.1;
SEQUENCE 484 AA; 53325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1435 AAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCA 1386
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                                                                                                                                                                                                                                                                                                                                                                                                                             TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCT 1236
                                                                                                                                                                                                                                                                                                                                                                                            TGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTG 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   luProSerCysMetThrValGlyAspGlyLysThrGlyHisArgPheGlu
                                                                                                                                                                                                                                                 GATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTT 1186
                                                                                                                                                                                                                                                                                    TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 1036
                                                                                                                                                                            TCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTTGGATG 1136
                                                                    luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
                                                                                                       GTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT 1086
                                                                                                                                            uLeuGluSerGluThrGlnLeuProValCysArgTyrGluIleLeuAsnG
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Quality:
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seq_documentation_block:
ID Q93532 PRELIMI
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                                                                                                                                                                                       alignment_scores:
Quality:
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US-09-323-427-2/rev x Q93532
                                                 Align seg 1/1
                                                                                                                                                  Percent Similarity:
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WOLSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A
BONFIELD J., BUTTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
BONFIELD J., BARY S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., CREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN A., MORTIMORE B., O'CALLAGHAN M.,
LICHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
LICHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q93532;
01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 Gln 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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           1622 TCTTCTGAAATGATGATTCGTCTTATTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
EMBL; Z78542; CAB01742.1; -.
SEQUENCE 315 AA; 35785 MW;
                                                                                                                                                                                                                                                                                                                      elegans.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alIleAspAlaAsnGlyCysSerValAspGlyValIleLeuGlnAsnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAACCAAATAGCGAATGT.....GTTCGACCACAATGTTCAGAACCA 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTA 839
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                                                                                                                                                                        Ratio:
                                                         to:
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                                                           Q93532
                                                                                                                                                      580.50
2.888
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                                                             from: 1
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Last annotation update)
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                                                                 to: 315
                                                                                                                                                              Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SHOWNKEEN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COULSON A.,
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1004
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                                 CTCACGTATACAAATATGCGGATCGA 879
                                                                                                                                     GlyLysGluValGlnIlePheAspGluAsnGlyCysAlaValAspLysTy
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                                                                                                                                                                       GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATA 955
                                                                                                                                                                                                                                              TTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAAC 1005
                                                                                                                                                                                                                                                                                                                                                       ValLeuThrGluSerLysThr...GluGluValAlaPheAlaThrValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLysLysIlePheValMetValGlyAspGluGluGlyGlyThrValSe 180
                                                                                                 hrSerProPheCysValThrValHisSerCysAsnValLysAspGluThr 262
                                                                                                                                                                                                                                                                                  TCAGCCAGTTTATCATAAATGGACATGCGATTCT.....GAAACCG
                                                                                                                                                                                                                                                                                                                                                                                           ATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                            hrGluGluArgIleSerTyrAsnValProLeuProAspCysLysTyrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGATAAAACAGTTAGTGCACAGATTGAGGTATCT.....
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erGlnValCysSerTrpThrValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCA 1338
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seq_name: sp_invertebrate:Q22164
seq_documentation_block:
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alignment_block:
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                                                                                                                                                                                                                        1416 TGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCA 1367
                                                                                                                                                                                                                                                                                               1451 AAAGGTCTTTATGATCAAGAAGGTTGCCGT......AATGA 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1601 CITATIGCTITCTGTACTACACTIATIGCATIGTCTTATICGATICCGGT 1552
1266 ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                     1551 TGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAA 1502
                                                                                                                                                                                                                                                                                                                                                                            1501 TAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTG
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FOUTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
EMBL; Z66565; CAA91480.1; -.
SEQUENCE 384 AA; 43964 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
T04F8.4 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                         26
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                                                                      ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC
                                 ValLeuIleIleSerPheHisProLeuPheLeuThrArgMetAspLysAl
                                                                                                                                                 ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA 1317
                                                                                                                                                                                   pGlnPheGlyArgProValGlyGlyIleLysLeuAsnHisGlyAlaCysA
                                                                                                                                                                                                                                                             LysGlySerTyrAsnArgProGluCysArgValAspTyrSerThrLysAs
                                                                                                                                                                                                                                                                                                                                        leAspMetGlnPheArgThrArgLysGlnPheAsnGlyLysValTyrVal 59
                                                                                                                                                                                                                                                                                                                                                                                                                 pAspAsnGluLeuIleGlyGlnProGluIleGlnCysAsnAlaAspThrI
                                                                                                              {\tt snMetAspArgGlnArgMetIleAlaProGluGlyMetMetPheSerThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546.50
2.240
61.929
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Percent Identity:
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9
31.218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COULSON A.,
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seq_name: sp_invertebrate:Q9XVN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt sThrAspArgLeuLeuLeuGlyAspProThrTyrValGluAlaLeuAsnM}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluAspGlyGlnGlyGluLysGlnMetIleIleAspGluArgGlyCysHi 223
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eLeuLysTyrAlaLysValGlyAspGlnValValHisArgTrpGlnCysA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetProThrCysSerTyrThrIleArgArgAspGlnLeuAspGlyProIl 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T.....GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                   ThrPheLysProLysAspAlaAsp.....MetPheSerGlnThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                             heLysAspAlaAsnSerAsnGluLysGlnIleValLysArgAsnAlaArg
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                                                                                                                                                                                                                                                                                                                                lTyrValMetAspLysGluAsnGlyAspSerThrSerAlaGlnAlaAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                 TTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAAC
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                                                                                                                                                                                                                                                                         luIleArgGlu.....
                                                                                                                                                            aValThrPhePheThrPheIlePheValLeuPheValThrThrIleLeuV 365
                                                                                                                                                                                      CTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTA 491
                                                                                                    alvalvalTyrHisArgTyrCysLysAsnGlu
                                                                                                                             TTACCATTTCGTTTAAATTTCGTCCAAATCAG 459
                                                                                                                                                                                                                 ...LeuAspProGlnThrIleCysLeuAlaProLysLeuLeuValValAl
        Created)
                                      PRT;
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alignment_block:
US-09-323-427-2/rev x Q9XVN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q9XVN2 from: 1 to:
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BONDRIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONDIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONDIELD J., BURTON J., DURBIN R., FAVELLO A., FULTON L.,
CRAZTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JOHNSTON L.,
GREEN P., HAMKINS T., HILLIER L., JERR M., JOHNSTON L.,
JOHNSTON L., COMMINING B., O'CALLAGHAN M.,
JOHNSTON A., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RLIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RLIFKEN L., ROOPRA A., SULISTON J.,
SMALDON N., SMITH A., SONNHAMMER B., STADEN R., SULISTON R.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON B., WEINSTON B., WEINSON B., WEINSTON B., WE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1652 TTAGTTTTTCTAAAAATCGAATTTACTAAATCTTCTGAAATGATGATTCG 1603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
EMBL; Z81086; CABO3116.1;
SEQUENCE 610 AA; 68585
                                                                                                                                                                                                                                                                                                                                                                                                                                           1526 GAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAA 1477
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1332 TATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTA 128:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 uLeuIleTyrAsnArgIlePheLeuGlnSerIleThrIleLeuIleLeuL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| ||| :::::::||| ||||:::
34 LeuArgPheGluSerValGlnPhe...LysAsnProProIleLeuLeuLe
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                                                                                                                                                                                                                                                                                                                                                                                        GluValPheCysGlyIleAspThrIleArgValLysValAsnThrGluHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysValGlnHisSerAlaAspAlaHisSerSerProGlnGluPheThrile 132
                                                                                                                                                                                                                                                                         sproPheAsnGlyArgIleTyrValAspGlyGluSerAspLysGlnHisC
                                                                                                                                                                                                                                                                                                                                  TGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTT 1427
                                                                                                                                                                                                                        GC.....CGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTT 1383
                                                      ProlleGlyAlaCysAsnMetArgArgGlnArgThrLeuHisProArgGl 149
                                                                                                         CCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGG 1333
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: Identity:
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8
35.906
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Q23097 PRELIMI
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032 CCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAAATTCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1082 CATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W01A8.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W01A8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 GluHisGlyAlaIleSerAlaTyrThrAsnAlaHisValPheLysTyrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       982 ATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTTGGAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCAAATAGCGAATGT.....GTTCGACCACAATGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt aAspLysValGinLeuTyrPheThrCysThrValGlnLeuCysTyrLysH}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAACAGAT...TTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eHisSerCysTyrAlaAspAspGlyHisGlyAsnLysPheGluLeuValA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is...AspGlyGlyCysGluGlyIleThrProProGlnCysSer 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt spAspArgGlyCysSerThrAspProPheLeuLeuProGlnIleGluTyr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisValTrpArgCysAspGlnAspAlaSerHisValTyrGlyIleLeuIl 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTAT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lAspGlnGluTyrSerLeuProValCysAlaTyrHisLeuLysAsp...G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysGlyLeuAsnAlaGluIleAspValGlyThrLeuAlaProGlnHisVa 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt lyileGluGlyHisValLeuArgPheAlaGlnValGlyGlnLysValThr}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGAT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrGlyMetAspArgAlaPheSerIleArgCysPhePheLeuGluSerIle 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166
                                                                                                                                                                                                                                                                                                                            COULSON A.,
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alignment_block:
US-09-323-427-2/rev x Q23097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RT RT RT RT RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1479 TAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1529 CCAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACG
                                                                                                                                                                                                                               211 lLysLysCysPheValThrAspGlyAspGlyGluAspHisAlaValValA
                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 lAsnPheMetValThrValIleValSerPheHisProAlaGlyPheIleT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994),
EMBL; Z71267; CAA95850.1;
SEQUENCE 387 AA; 43212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 rLysProPheArgGlyAsnIlePheValLysGlyArgAlaLysAspLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 ProLysVallleCysAlaGluAsnAspLeuAlaLeuAspIleValThrSe
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aAspSerAsnGlnLeuTyrPheThrCysGlnIleArgLeuCysGlnLysG
                                      GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTGTAACAACAGTGTTGTCATTTGTTA ...TTTGTTA 1283
                                                                                                             CCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATACAAATATGC
                                                                                                                                                    {\tt spPheAspGlyCysAlaThrAspProPheLeuLeuSerGluLeuSerTyr}
                                                                                                                                                                             CCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAA 983
                                                                                                                                                                                                                                                                                                           HisValTrpGluCys.....ThrProAlaAspMetGlyMetLeuVa
                                                                                                                                                                                                                                                                                                                                                 CATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGT 1033
                                                                                                                                                                                                                                                                                                                                                                                      {\tt lyProAsnGlyProThrLeuThrTyrAlaAsnValGlyAspIleValPhe}
                                                                                                                                                                                                                                                                                                                                                                                                                               GACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTAT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uSerAspSerMetValMetProLysCysGluTyrSerValArgArgAspG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluIleValThrGlnAsnIleAspValSerMetIleProThrThrGluLe 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGAT 1233
                                                                           AspAlaSerLeuMetArgAlaHisAlaSerSerGlnValPheLysTyrAl
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2.110
59.269
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Gaps: 11
Percent Identity: 31.593
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to:
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Sequence of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
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01-FEB-1997 (TIEMBLTel. 02,
01-NOV-1998 (TIEMBLTEL. 08,
01-JAN-1999 (TIEMBLTEL. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

WILSON R., AINSCOUGH R., CONSELL M., COPSEY T., COULSON A.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., COULSON A.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., FOULD A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGER B., O'CALLAGHAN M.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGER B., SHOWNKEEN R.

PARSONS J., PERCY C., MCMURRAY A., SAUNDERS D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WATERSTON R.,

THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZK265.8 PROTEIN.
   LENNARD N. Submitted
                                                                                                                                                                     "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOBSON
                                                                                                                                                Nature 368:32-38(1994).
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ysArgGluAlaAspArgSerAspTyrGluIleAspValAlaThrSerGlu 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTG 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuSerGluAlaSerGlyAspGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leu.....LeuValleuAspProAlaAspArgGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alileArgArgGlnAsnHisLysLysGluLeuAspIleMetGlnSer 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuileLeuileThrileValSerLeuThrValVal.SerThrAlaLeuV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..AlaProSerProPheCysValProArgLeuLeuLeuProValLeuPro 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGCATGTCACCATTTGGCTTCTCAATGTTTATG.....GGTTTAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....AsnArgThrL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATCAGAAGG......CATAAAAATAATGTTAGAATCATCGAAGCA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTCC 466
       (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334
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alignment_block:
US-09-323-427-2/rev x Q93967
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DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q93967 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 281143; CAB03520.1;
EMBL; 275713; CAB03520.1;
EMBL; 275713; CAB00057.1;
EMBL; 281143; CAB00057.1;
SEQUENCE 440 AA; 49299 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1557 TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1607 ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1507 CTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTT 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1407
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                                                                                                                                                                                                                                                  1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eSer {\tt IleAspAsnGluIleIleGlyGluProAspIleGluCysLeuGluA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrAlaLysGlyArgAlaGluLeuGluAspCysTyrLysAspAspPheGl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt spGluIleArgIleTrpValLysThrArgLysIlePheAlaGlyArgIle}
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCCTGC 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyMetLysSerLeuArgSerValAspProArgGlyMetTyrTyrGlyIle 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG
                                                                                                                                                                                                                                                                                                                  ATGCCAGTATGCCGTTATGAAATT......TTGGA 1138
                                                                                                                                                                                                                                                                                                                                                                                                                          aTyrHisValLysCysPhePheGluGluAlaAsnLysGlyLeuThrAlaG
                                                                                                    GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA 991
                                                                                                                                                                           CAGTTTATCATAAATGGACATGCGATTCTGAAAACCGTTGATACTTTCTGC 1041
                                                                                                                                                                                                              TGGTGGA...CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC 1091
                                                                                                                                                                                                                                                                                 luLeuGlyValSerMetIleProThrThrGluLeuGluAlaArgHisGly 153
                                                                                                                                                                                                                                                                                                                                                                                       AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG 1167
                                                                                                                                        rgValLeuHisGlnTrpHisCysAsnAspGln......MetTyrGly
pValIleAspAspLysGlyCysProIleAspProIleLeuIleThrGlyI
                                  AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT 941
                                                                     ValLeuIleAsnAsnCysTyrValThrAspGlyPheGlyLysLysAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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2.296
65.000
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MW; 3F2BBBA2 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1217
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Seq_documentation_block:
ID 022680;
AC 022680;
PRELIMINARY;
AC 022680;
DT 01-NOV-1996 (TrEMBLrel 01
DT 01-NOV-1996 (TrEMBLrel 01
DT 01-NOV-1999 (TrEMBLrel 12
DE 722C8.7 PROTEIN.
CC CHARYOTE METAZOS: Nemato 02
Rhabditins; Rhabditoidea; Rhabditins; Rhabditoidea; Rhabditins; Rhabditoidea; RI 1
RP SEQUENCE FROM N.A.
RA THOMAS K.;
RL SUBMITTED (APR-1995) to the RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE; 94150718
RA MILSON R., AINSCOUGH R., A BONFIELD J., BURTON J., CO CRANTON M., DEAR S., DU Z. RA GARDNER A., GREEN P., HAWK RA JONES M., KERSHAW J., KIRS RA LIGHTNING J., LLOYD C., MC RA PARSONS J., PERCY C., RIFK RA SMALDON N., SMITH A., SONN RA THIERRY-MIEG J., THOMAS K.
RA WATSON A., WEINSTOCK L., W RT "2.2 Mb of contiguous nucl RT elegans.";
RA LNST; P03000; 1TIF.
SQ SEQUENCE 609 AA; 68882
                                                                                                                                                         alignment_block:
US-09-323-427-2/rev x Q22680
                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                    Align seg 1/1 to: Q22680 from: 1 to: 609
                                                                                                                                                                                                                                                                                   Percent Similarity:
1611 GATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATT 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAYELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
NELLES COLORS OF THE CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
EMBL; Z49071; CAA88879.1; -.
HSSP; P03000; lTIF.
SEQUENCE 609 AA; 68882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999) (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 rProLysPro 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 TGCAGAACCG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843 CATTAAAGAACCAAATAGCGAATGT.....GTTCGACCACAATGT. 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 LysPheAlaAspLysProGlyValTrpPhePheCysGlnValGlnMetCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sMetLysLys...HisGlyMetCysAspGlyIleThrProProSerCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
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                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                               453.50
2.399
65.854
                                                                                                                                                                                                                                                          Gaps: 11
Percent Identity: 37.282
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                                                 snGlyCysGluGlyIleSerProProIleCysArgProMetAspLeuGly
                                                                                                     ATAGC...GAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGA 783
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ProlleLys 287

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47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT

KEYWORDS		ACCESSION	DEFINITION		CEF22B5
HTG; Cuticulin; Elongation factor; GTP-binding ADP-ribosylation	Z50044.1 GI:899234	250044	d F22B5, complete segi	CEF22B5 25823 bp DNA INV 02-SEP-1999	

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REFERENCE
AUTHORS
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Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F22B5.

IMPORTANT: This sequence is not the entire insert of clone F22B5.

INFORTANT: This sequence is not the entire overlapping sections once, or longer because we arrange for a small overlap between
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1 (bases 1 to 25823)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor; Phenylalanyl-tRNA synthetase; RNA binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-JUL-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2 Mb of contiguous nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R., Ainscough, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368 (6466), 32-38 (1994) 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bin/display?db=wormace&class=Sequence &object=F22B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 266523.

The true left end of clone M05D6 is at 25723 in this sequence. The true right end of clone F14E5 is at 4610 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence Z66522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 25823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              true right end of clone F22B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           true left end of clone F22B5 is at 24607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end of this sequence (25723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z66523
                                                                                                                                                                                                                gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                      /protein_id="CAA90354.1"
/db_xref="GI:3876226"
                                                                                                                                                                                                                                                                                                                                                                    join(411 .462,584. .663,745. .1127,1216. .1471)
/gene="F22B5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F22B5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="II"
/db_xref="SWISS-PROT:Q19706"
                                                                                                                                                                                                                                                                                                                              /note="similar to RNA binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="F22B5"
                                                                                                                                                         codon_start=
                                                                                                                                                                                                                                                                       from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                             CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is at 16002 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .25823) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans"
                                                                                                                                                                                                                                                                                             EST
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                                                                                                                                                                                                                                                                                        yk499d6.3 comes
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                                                                                                                                                                                                                                                                                                                                              CDNA EST yk390d8.5
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/translation="MAPAPEVVSWAEAVEQDNAPHIQEGADGTRTETAFTEVDGVRWK VVTQFKVINRRVPKVVADRKKKWVKFGSCKGEPAGPQVATTYVAEEVDMQFTRNRAGEQ ILDVQEDKQTAKTTSREHCRHCKGNDHWSTHCPYKVMYQLDEEADADKDTEKDRMAMG MRPDGRQIDRNRSDENTCRVTNLPQEMNEDELKDLFGKIGRVIRIFIARDKVTGLPKG FAFVTFESRDDAARAIAELNDIRMYHMVLKVEWTRPSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from this gene; cDNA EST CEEXY90RB comes from this gene; cDNA EST eMBL:T00412 comes from this gene; cDNA EST yk38667.3 comes from this gene; cDNA EST yk38667.5 comes from this gene; cDNA EST yk504b12.3 comes from this gene; cDNA EST yk504b12.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk652b8.3 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(2833. .3042,3088. .3700,3823.
4273. .4393))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2833. .4393)
/gene="F22B5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPTLGFDIKTVHFKDFOLNLMDVGGOKSLRSYWKNYFESTDALIWVVDSSDREBLLQC
SEELKKLLGEERLAGASLLVLANKSDLPGAIDVNSIAQVIOMSSVYTSEKKCFLVLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA90353.1"
/db_xref="GI:3876225"
/db_xref="SWISS-PROT:Q19705"
/translation="MGFLKILEKQRAEBREMRILILGLDNAGKTTLMKKFLDEPTDTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(1870. .2158,2209.
/gene="F22B5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F22B5.1"
join(1870. .215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSIKSHHWKIFSCCALSGDRLVQAMTWLCDDVGSRLFILD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to GTP-binding ADP-ribosylation factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="marySLGLGLCLLVASVSAIPVDNNVEGEPEVECGPTSITVNFN
/translation="marySLGLGLCLLVASVSAIPVDNNVEGEPEVECGPTSITVNFN
TRNAPEGHVYVKGLEPQQECRNDEGGRQVAGIELPFDTCNVARTRSLNPKGVEVTTTV
VVSFHPQFVTKVDRAYRVQCFYMEADKTVSTQ1EVSDLTTAFQTQVVPMPICKYEILN
GGPTGEPVQFATIGQQVYHKWTCDSETYDTFCAVVHSCTVDDGGDTVQILDENGCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F22B5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to cuticulin; cDNA EST EMBL:T01970 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9691. .10234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REIGEDSFROELCISSFHISVVTVFLGLTVFVAIFITYMIVSRMMVPSDKMQSAC"
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FGAVKQANQTAQFFRVLKKRSAPVMENILDVRAELTTLEVLEGNLPSSLTQAQALVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q19707"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA90355.1"
/db_xref="GI:3876227"
                                                                                                                                                                                                                                                                                                                       complement(join(10849. .10984,11033. .11343,11397. .11521, 11578. .11832,11917. .12154))
/gene="f2285.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="Sptrembl:Q19708"
/db_xref="Sptrembl:Q19708"
/translation="mSLSKAPRKTMFREVLSRNASTSNVPSPARIQLKKPAEAGHFQY
/translation="mSLSKAPRKTMFREVLSRNASTSNVPSPARIQLKKPAEAGHFQY
SRNWSRDPRFVKVAIQKGDTPYQFLVBRLGHAYEVYPLFVLTAAWFVLFCSASYWSFG
SRNWSRDPRFVKVAIQKGDTPYQFLVBRLGHAYEVYPLFVAFAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="cDNA EST yk304c8.3 comes yk304c8.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA90356.1"
/db_xref="GI:3876228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F22B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(9691.
                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10849. .12154)
/gene="F22B5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAEIWLDRSNSKAPWDWERLRDTYWKMPTVAFDLDGRTRKRCELMEQLQDEMLEAAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F22B5_4"
                                                       SDSTYLSGTQSITYKSLNRSIPDEQTFĞLSYQPDNTYNLLPHLMHEMATDFKSYKMNS
GGCVDSKYAAVWRKVLHTKVRGPTYYVSHYKPDEVFNPELEPDDVVKFSDVPVEHVVK
YDNSIFPYERKEYILAKFKNGVGRVAYNKSGEVIGIGLVSTESSGNCEIGPIYCDNKN
                                                                                                                                               /translation="MNGCKQSASKVFKLVGGFNKASSRCFSSEKLIPKDLKIVKNPTS
EQIKQFQKLVGDFNDIKLLKETMKDNYQLYLLCHKAKWSIAALCYNFNLNSNVMSIYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
AAQAIFQSIIQDLPMKDLKDVLVRCSDKFEDSATWIRPFLRRSHEMTPFAHIKFNRVI
PDGLNFSKVFVSSNPSNAPC"
                                                                                                                                                                                                      /db_xref="SPTREMBL:Q19709"
                                                                                                                                                                                                                                     /protein_id="CAA90357.1"
/db_xref="GI:3876229"
                                                                                                                                                                                                                                                                                                  codon_start=i
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CDNA
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DNA EST
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Best Local :
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                                                                                                                                                                                                                           CTGAGCAGTTTGGTTAGCTTGC---
                                                                                                                                                                                                                                                       agctgcaggcttttgctgcggcaccacctgtttttaacagctccgaatccttgtggttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acgtaaatcaactggcaaagcttgattatcatcgctaatttcaagggtgttgatatcagt 680
  TTGATAGAAAAGTTGAGAACGATCAGCGTATTTGTAGACGTGAGCCTCTTGTCCAGCCAT
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/gene="F2285.7"
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DNERLSTKASTAELIGHLOWVLAKDANINCQALAAKGIGKFATGURAKESSFAGPLLP
VIFEKMKEKKEMLREPLYDCSNEVGRTWOSLEFGQEDIILAALAKPNPOIKKOGTALFVA
ROLDLVPAKOPKGFIKAVVPVFGKLTGDADQDVREASLQGLGAVQRIIGDKNVKNLL
GDASSDEGKMKKIGETAEKSTASFAEEGAKNAPVAFTSSTESASASGDSGGTAATA
VVSSGAPVAEADPWDELDAFDVLSKWDDGFDTWIESKKWOERKEALEGLULITANFA
LDPKANYGALVERLOKVLEKDANINVAALAANCITGIANGLRTKFQPFAVSVTPIIFE
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LAQYHIIHESSNIISWNMLNSSRGKIVNENATNTHFGLTCVTTAFLCILTSLIIVDIL
EKTHFTFRYVVFMNIAVVACGLFVTGYLLGHIVEIWFAKMSTIYSCRQLGIQTYLITS
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/gene="F22B5.6"
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/db_xref="GI:3876230"
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בייים איטנום; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi 1 (bases 1 to 34831)
                                                            Caenorhabditis elegans.
                                                                                                    HTG; Cuticulin; Fork head.
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Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Therry, Mieg, J., Thomas, K., Vaudin, M., Staden, R., Sulston, J., Therry, Mieg, J., Thomas, K., Vaudin, M.,

Caenorhabditis.

Vaughan, K., Waterston, R., Wilkinson-Sproat, J. and W

Wohldman, P Watson, A.,

Weinstock, L.,

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COMMENT
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current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. Exceptions are indicated by an explicit note the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-APR-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elegans
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IMPORMANT: This sequence is not the entire insert of clone C47G2.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 249912.

The true left end of clone T24F1 is at 34731 in this sequence. The true right end of clone T05B9 is at 12750 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions. The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ittp://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 34831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end of this sequence (34731. .34831) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"similar to cuticulin; cDNA EST EMBL:C10444 comes /note-"similar to cuticulin; cDNA EST EMBL:C12078 comes from this gene; cDNA EST yk262c12.3 comes from this gene; cDNA EST yk265c13.5 comes from this gene; cDNA EST yk265n3.5 comes from this gene; cDNA EST yk265n3.5 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.5 comes from this gene; cDNA EST yk479g8.5 comes from this gene; cDNA EST yk499g8.3 comes from this gene; cDNA EST yk49ge8.5 comes from this gene; cDNA EST yk49ge8.5 comes from this gene; cDNA EST yk48gc11.3 comes from this gene; cDNA EST yk583c11.3 comes from this gene; cDNA EST yk380a11.5 comes from this gene; cDNA EST yk380a11.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z499
                                                                                                                                                                           /trainslation="MMWKPIICLAALVLSASAIPVDNNVEGEPEVECGPNSITVNFNT /trainslation="MMWKPIICLAALVLSASAIPVDNNVEGEPEVECGPNSITVNFNT RNPFEGHYVKGLYDQAGCRSDEGGRQVAGIELPTOSCONTARTRSLNPKGVEYGTTVV ISFHDQEVTKVDRAYRIQCEYMESDKTWSTQIEVSDLTTAGTQVPMPCKXFEILDG GPSGQPIQFATIGQQVHKWNTCDSETTDTFGAVHSCTVDDGNGDTVQILNEEGCALD GPSGQPIQFATIGQQVHKWNTCDSETTDTFGAVHSCTVDDGNGDTVQTHNEEGCALD KFILNNLEYFTDLMAGCEAHVXXYADRSOLFYQCOISITIKDPGSECARPTGSEPQGF KFILNNLEYFTDLMAGAAAAPQAGVEEVQAAFVAAAAAPVAAAAAAAPAVPRATLAQLRL GAVKQAGAGGAHAAAAPQAGVEEVQAAFVAAAAAPVAAAAAAAPAVPRATLAQLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(2562. 2679,2992. .3217,3898. .4636,4687. .4878)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
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15433. .17108
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IGFASFLGIGTIVATALSATIFYVARPTSHKH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="C47G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=.
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gene CDS

/note="cDNA EST CEMSB75F comes from this gene; cDNA EST MBL:C13621 comes from this gene; cDNA EST yk227d8.5 comes from this gene; cDNA EST yk257e7.5 comes from this gene; cDNA EST yk319c4.5 comes from this gene; cDNA EST yk319c4.5 comes from this gene; cDNA EST yk331d4.5 comes from this gene; cDNA EST yk335b12.5 comes from this gene; cDNA EST yk385b12.5 comes

comes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="C47G2.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(24417. .24975,25043. .25176,25237. 25668. .25907,25967. .26054,26106. .26227,26277. ... 26681. .26785,26846. .26914))
//gene="C47G2.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:Q18694"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEYYKEKFPAWQNSIRHNLSLNDCFVKYARGPGNPGKGNYWALDPNCEDMFDNGSFLR
RRKRYKKNSDTYHEMMSHHPMPFPPFLPQGMPFPPRMMHPMANIPMLGHPMNPRAVPN
MPAFFIPQNIDSQKLLSMMASSIMPMDAPVSSGQKRTSSSSSPNENGSSAVSDKLSA"
                                                                                                                                                                                                                                                                                                                       SLIFSAILCALTY YVERACUED RORTLINTTSTPADVPECELPGGYVPDDVLFULW
RVVYWSAQLLTWLILPLLQSYVTAGNETILGK IRAAVINNALY XAIY SLCELAILIYA
RVVYWSAQLLTWLILPLLQSYVTAGNETILGK IRAAVINNALY XAIY SLCELAILIYA
RKGVSINIENLKVIVVSASNIWGLELLVVLLGHGLVELPRSLWHHGNRHYRLRKTYF
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SRQVIDMAHLDESGPCSEAKLISLHKKTIYAVQTLNNATAQWKVLVDRALFLENLAPS
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ENSILFSAILLCRLTPPTCLNFFLGMIHMDSHISMAKSFGIETQFTKLMGHLDVIPILA
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SIKRSNDRSQFTQNWTNSFGSSNAGNGSTTSKFKRSNKNDEERPMLEDDDEEVEESST
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32639. .32935,32998. .33215,33263. .33651,33802. .34049)
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                                                                                                                                                                                                                                               30076. .34049
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CDS gene

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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                         DEFINITION
ACCESSION
                      REFERENCE
                                                                                                                                                                                                                    CELCUT1/c
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      AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                        w
                N C.elegans cuticlin I (cut-1) gene, 3' end.
M55997
M55997.1 GI:156271
Cuticle protein; cuticlin I.
C.elegans DNA.
C.elegans DNA.
C.elegans DNA.
Clenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditina; Rhabditoidea; Rhabditidae; Pelode:
1 (bases 1 to 2310)
                                                                                                                                                                                                                                                                                                                                                                                              tctgtgcactaactgttttatcagcttccatgtaaaagcattgtactcgatatgcacgat 1273
                                                                                                                                                                                                                                                                                               AAATTTTAGAA 3883
                                                                                                                                                                                                                                                                                                                                 caactttggta 1284
                                                                                                                                                                                                                                                                                                                                                                      TCTGTGTGGACACAGTCTTGTCGGACTCCATGTAGAAGCATTGGATACGGTAGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99catactggcatcgggacaatttgagtttgaaaagcagttgtgatttcagatacctcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caaccgcgcagaaagtatcaacggtttcagaatcgcatgtccatttatgataaactggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCTTCGTTAAGAATCTGAACGGTGTCGCCATTACCATCATCGACAGTGCAAGAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catcagcatttagaatttccacagtatcaccgttaccatcatcgacaaagcaggaatgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cagccattaaatctgttggatattccaaaattatttagcaaatatttatcaagagcacatc 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGGCATTGATAGAAGAGTTGGGAGCGATCGGCATATTTGTAGACGTGAGCTTCTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tctggcattgatagaaaagctgtgatcgatccgcatatttgtatacgtgagcttcttggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGCTCTGAGCAAGTTGGACGGGCACATTCGCTTCCTGGGTCCTTGATGGTGATGGAGA 4314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGAGCAGCGGCGTGATGAGCTCCTCCGGCACCAGCTTGTTTGACGGCTCCGAATCCTT 4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gttgcgcagctgcaggttttgctgcggcaccacctgttttaacagctccgaatcctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCGATGGTGGCGAACTGGATTGGTTGTCCGGATGGTCCTCCGTCAAGGATCTCGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACGCCCAGAAGGTGTCAGTCGTCTCAGAATCGCAAGTCCATTTGTGATAGACTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCCATCAAGTCAGTTGGGTACTCCAAGTTATTGAGCAAGAACTTGTCAAGAGCACATC
                                                                                                                                                                                                CELCUT1
      Sebastano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10589
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MDETLIAKIADNLIVEEGCPAEELVKKSALISASAKILEAFIKUFYSNAPAQOLEEI
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MADDFSSFFISFTAANASSSSSDAWPGSDIHLQGEASDWPLNNSHESKASDPVMVG
LAASISHPGDSSEA*
                                                                                                                                                                                                2310
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74.2%;
  Lassandro, F.
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                                                                                                                                                                           n bp
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              φ
  and
Bazzicalupo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 34;
                                      Peloderinae;
                                                        Rhabditia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34831;
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                                                        Rhabditida;
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                                GTCCGATGGTGGCGAACTGGATTGGTTCCGGATGGTCCTCCGTCAAGGATCTCGTATT
                                                gaccaatgatagcaaattgaactggttgaccggttggtccaccatccaaaatttcataac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="rlpypcfymesdktvstqtevsdlttafqtqvvpmpvckyetld
GGPSGQPIQFATIGQQVYHKWTCDSETTDTFCAVVHSCTVDDGNGDTVQILNEEGCAL
DKFLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKDPGSECARPTCSEPQG
FGAVKQAGAGGAHAAAAPQAGYEEYQAAPVGAAPVAARAAAAAPAVPRATLAQLRL
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567 c 433 g
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/protein_id="AAA27995.1"
/db_xref="GI:156272"
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join(1186. .1920,1971.
/gene="cut-1"
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AF125580.1
                                                                                                                                          AAGTGTAAAACCGGTTATTGACATACATATACCTTGTGTCATTGTTGCAACAACTTACCGG
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  attatcatcgctaatttcaagggtgttgatatcagttcgtacatcaatgatattctccgg
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                                                  ATGACCATTCTCATGTGCTAACAATGATGATCGATGACGTAGCGCATTTGGTAATGAGGT
                                                                                        ttgtccattatgttg-----cagaagtgcacggtgacgtaaatcaactggcaaagcttg
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Eukaryota; Metazoa; Nematoda; Secernentea;
Filarioidea; Onchocercidae; Wuchereria.
1 (bases 1 to 724)
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Submitted (03-FEB-1999) Research & Training Center
Submitted (03-FEB-1999) Research & Training Center
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/protein_id="AAD28743.1"
/db_xref="GI:4741875".1"
/db_xref="GI:4741875".1"
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/translation="TVDTFCAVVHSCEVDGNGDKVELLNADGCALDKFLLNNLEYPT
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1 bancrofti
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/db_xref="taxon:6293"
/dev_stage="L3 larvae"
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Location/Qualifiers
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Pred. No. 6.3e-36; 
0; Mismatches 261;
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U73005
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Gene 193 (1), 81-87
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Timinouni, M. and Bazzicalupo,
                                                                                                                                                                                                                                                                                                                                                                               Timinouni, M. and Bazzicalupo, P
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                              Ascaris lumbricoides
                                                                                                                                                                                                                                                                                 Submitted (01-OCT-1996) GA3, I.I.G. NA 80125, Italy
                                                                                                                                                                                                                                                                                                          Direct Submission
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lumbricoides
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/variety="suum"
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join(766. .954,2851.
                                                                                                                                                                                                                                                                     ocation/Qualifiers
/codon_start=1
/product="CUT-1-like cuticlin protein
                        /note="cuticlin gene; ASCUT-
proteins of other nematodes"
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                                                                                                                                                                                                                                                                                                                                                                    GCAAGTCCACTTGTGGTATACTTGCTGACCGATGGTTGCGAACTGTATCGGCTGTCCCGT
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X96677
X96677.1 GI:2648040
              cuticle protein; cuticlin 1; Mtcut-1 gene.
Meloidogyne artiellia.
Meloidogyne artiellia
Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria;
Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;
    Meloidogyninae;
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/db_xref="G1:1657625"
/db_xref="G1:1657625"
/translation="McRAVSFLALFGLAAAIPVDNGVEGEPEIECGPTSITVNFNTRN
PFEGHAYWGLYDQEGCRSDEGGRQVAGISLPPDSCRNARTRSLNPRGIFVTTTVVIS
FHELFITKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQTQIVPMPVCRYEILDGGP
TGQPIQFATIGQOYYHKWTCDSETVDTFCAVVHSCFVDDGSGDTIQILNEEGCALDKY
LLNLEYFTDLMAGQEAHYYKVADRSQLFYQCQITITIKEBNGECPROTECSEPQGFG
LLNLEYFYGDLMAGGCAHYYKVADRSQLFYQCQITITIKEBNGECPROTECSEPQGFG
VRPGGSIAPKQRRCQLRLIKKSGGDYDNTLDVRTDFSALDISDRDEALPMDLRHRAR
HARGQOVILSPAREGICMSPFGFSIFMGLAVALAAAVVVVVSEKLRPQQKA"
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Pred. No. 1.4e-33;
0; Mismatches 150;
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GGCATTGGTAGAAGAGTTGAGAGCGATCCGCGTATTTGTAGACGTGAGCCTCTTGGCCGG
                  ggcattgatagaaaagctgtgatcgatccgcatatttgtatacgtgagcttcttggccag
                                                                     GCTCAGCACACTTTGGACGAGCACACTCACTGTGGCCTCCTTGATGGTTATACTGATCT 1428
                                                                                        GCGGTGGGGCACCGGCACCACCTCCACCGGCGCCCACTTTGACGGCGTTGAAGCCGCTTG 1488
                                                                                                                                                                       gcgcagctgcaggttttgctgcggcaccacctgttttaacagctccgaatccttgtg
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De Giorgi,C.
Direct Submission
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
Biologia Molecolare, Via Orabona 4, 70126, Bari, ITALY
2 (bases 1 to 2584)
De Giorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
Modulation of expression at the level of splicing of cut-1 RNA ir
the infective second-stage juvenile of the plant parasitic nemate
Meloidogyne articlila
Meloidogyne articlilia
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/translation="MRKLLFAIGVFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV
/translation="MRKLLFAIGVFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV
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LEGAALGQP1QFAITAQQVYTSGTCDSETIDTFCAVVHSCVVDGNGDTVQILNEGSC
ALDKFLLNNLEYPTDLTAGQEAHVYKYADRSQLFYQQCJSTIKEPHSECARFXCAEK
SGFNAVKVGAGGAGAGAPPAAAAATPPPAAAAPPAPIAPAIPARVQRLRTRGULTLKE
KRAAPPEQVLDVRTEENALDISDKPFNLPAHIRHHHLLMENLSAEPQRRFIYOGGGQV
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/gene="Mtcut-1"
467. .2052</pre>
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/gene="Mtcut-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="cuticlin-1"
/protein_id="CAA65452.1"
/db_xref="GI:2648041"
                                                                                                                                                                                                                                                                                                                                                                                                                    /number=2
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/db_xref="taxon:42426"
/clone_lib="lambda7-2(1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=
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/codon_start=1
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                                                                                                                                            GAAGCTCAATTCCCCGCCACTTGTCGGCCGTGCTCATCCGAACGGCATCCGGCCTGGTCAA 651
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                             BMA012617 637 bp DN

Brugia malayi cut-1 gene, F

AJ012617

AJ012617.1 GI:3858954

cut-1 gene; cuticlin.
                                                                                                            CA 529
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Brugia malayi.
Brugia malayi
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Brugia.
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              Spirurida;
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                                                                                                                     agcaaattgaactggttgaccggttggtccaccatccaaaat---
                                                                                               TCAAAAAATTCAAAAAGACATGCCTCGTATCGACAAACAGGCATGGGGACAATTTGAGTT 130
                                               Devaney.E. cut-1-like genes are present in the filarial nematodes, pahangi and Brugia malayi, and, as in other nematodes, components of the cuticle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 637)
Lewis, E., Hunter, S.J., Tetley, L., Nunes, C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-NOV-1998) Devaney E., Veterinary University of Glasgow, Bearsden Road, Glasgow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devaney, E.
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/number=2
a 136 c 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="Sptrembl:096775"
/db_xref="Sptrembl:096775"
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QIVPMEVCRYEILDGGPTGQPTQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
GDTVEILSADGCALDKYLLNNLEYP"
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join(<2. .164,266.
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/db_xref="taxon:6279"
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/protein_id="CAA10074.1"
/db_xref="GI:3858955"
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               ttcataacggcatactggcatcgggacaatttgagtt 1182
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Pred. No. 1.6e-23;
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G61 1QH, UK
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AJ012618
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Filarioidea; Onchocercidae; Brugia.
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/number=2
a 64 c
                                                                                                                                                                                                            /protein_id="CAA10075.1"
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                                                                                                                                                                                                    LNADGCALDKYLLNNLEYPTDL'
                                                                                                                                                                                                                                                                                        join(<1. .191,350. .>356)
/gene="cut-1"
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                                      Score 156.6; DB
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                                                                                                                         overlap between neighbouring submissions. This sequence is the entire insert of clone F3FI. The true right end of clone M04G12 is at 21759 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence Z81103. The end of this sequence (39379. .39478) overlaps with the start of
                                                                                                                                                                                                                                                                                                          Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (21-OCT-1996) Louis, MO 63110, U
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from
                                                                                                                                                                                                                                               IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a sma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda, Secernentea; Rhabditia; Rhabditida;
Rhabditina, Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                      sequence AL021448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available information.
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                                                     1. .39478
/db_xref="taxon:6239"
                        /organism="Caenorhabditis elegans"
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                                                               /yere-predicted using Genefinder; similar to cuticlin;
/note-predicted using Genefinder; similar to cuticlin;
/note-predicted using Genefinder; similar to cuticlin;
/note-predicted using Genefinder; cDNA EST EMBL:C1739
EMBL:D74799 comes from this gene; cDNA EST EMBL:C11739
comes from this gene; cDNA EST EMBL:C12451 comes from this
gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST yk506b3.3 comes
EMBL:C10682 comes from this gene; cDNA EST yk506b3.3 comes
from this gene; cDNA EST yk437e9.3 comes from this
gene; cDNA EST yk437e9.5 comes from this gene; cDNA EST
yk311h10.3 comes from this gene; cDNA EST yk31hh10.5 comes
from this gene; cDNA EST yk341f6.3 comes from this
gene; cDNA EST yk341f6.5 comes
from this gene; cDNA EST yk300g2.5 comes
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AVNPVPIQNSLYGDVQVECDSRTISVQIKTEKPFVGVIFVKDFASEEYCTSRCGTGRLS
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ANNISVDEISTISYNVLTIMPFCTYQLLSGGPFGEPVEFGLIGQQVYNGWKCDNDKGM
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YKFADRDALFFQCQISITVKEEDQGECVRPICEDVEGGGAPVVGPPPYGMISKNLVNIW
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TAGYRMEDTAKYLNEKELGEALKILLPKHGLSRSDVFLITSKEPESENCREACRGFV

ERSLOGTDYLDMYLVHYPKPNDSDNDDVNNAEYRKTAYEVLEBAKAAGKVESIGVS

RYSIVHLEELKTYYAKVPECANQLEYHPHFARIPLQKYCKEKNIFFQAFSSLARHEPKL

IEDPVYVELAKKHNTSYPLVLAWALRQNVGIVPKSVTPSRIVENFKVIDIALTPEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(14923. .16486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB03124.1"
/db_xref="GI:3877456"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="predicted using Genefinder; similar to cuticlin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F53F1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comes from this gene; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKNSFLTFFKSPYMYVVGITNYHNKAIQKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18339. .18524)
/gene="F53F1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/translation="MSIKLNTGYDCPLIGLTTKMPPNTVENVKKLVDESLSLLKTSYID
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MYLHYPKSTOYDCDQDPMNKTLRIATMYNDEXCKNAGKIRSVGVSSFEITTRLAEK
GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEITTRLAEK
GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEITTRLAEK
GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEITTRLAEK
YYNPKTTYLLSWATSQKVGIIPKSTNPERLAQNLKTVLLEEEEVKKICNLNLDKHYVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(18714. .18887,18935. .19056,19113.
19919. .20008,20072. .20251)
/gene="F53F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSLTALDRGQHYIRCTGWLVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to aldehyde reductase; cDNA EST yk473d8.3 comes from this gene; cDNA EST yk473d8.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F53F1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F53F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21582. .22009
/gene="F53F1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to aldehyde reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(21582. .21670,21781. .22009)
/gene="F53F1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGWLVL"
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MEDLINE
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15074 GCTCCACCGCCTTCTACATCTTCACATATTGGTCTCACGCATTCCTGGTCTGGCTCTTTG 15133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 gctccgaatccttgtggttctgaacattgtggtcgaacacattcgctatttggttcttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aagcaggaatggacaaccgcgcagaaagtatcaacgg 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACACGTGTGAACTACCATGCAGAATGAGTCTTCTG 15350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAATTGAGCACCCATTCGAGTCTATGAGAAATGAGGTTTCACCTCGTCCATCGTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcaagagcacatccatcagcatttagaatttccacagtatcaccgttaccatcatcgaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGCTTCTTGCCCAGCGAGTAAGTTTCCCCGGATACTCAAGGTTCGACAATAGAAACTTA 15253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgagcttcttggccagccattaaatctgttggatattccaaattatttagcaaatattta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGGTAATTGATATCTGACACTGGAAGAAAAGAGCATCTCGATCAGCAAACTTATACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Morthmore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vandin, M., Wataron P., Wataron A., Wainstock, I., Vaudin, M., Vandin, M., Wataron D., Wataron A., Wainstock, I., Vaudin, M., Vandin, M., Vandin, M., Wataron A., Wainstock, I., Vandin, M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-007-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                    IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small
                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; Cuticlin-like protein.
Caenorhabditis elegans.
Caenorhabditis elegans
                                    overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence &object=E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McMurray,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson, R., Ainscough, R., Anderson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 31536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEE04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 31536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a graphical representation of this sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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    is not the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E04D5, complete sequence.
entire insert of clone E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baynes, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1999
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CDS

complement(join(8619. .8761,8813. 10089. .10283,10330. .10614,10730.

.8988,9895. .1 . .10935,11582.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neighbouring submissions. The true left end of clone E04D5 is at 1 in this sequence. The true right end of clone E04D5 is at 2110 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The end of this sequence (31437. .31536) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence Z48585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="EUAUD:1"
//note="EUAUD:1"
//note="EUAUD:1]
//note=
complement(8619. .11718)
/gene="E04D5.2"
                                                                                                                                                                                                                                   NGREFAVCYGYMPAKVTFYNPRGVPIFDTIEGPRNDVFYNAFGNIVLICGFGNIAKGK
MEFWDVETKKEIISIEVPNTTLFDWAPDGQHFVTCTTAPRLRIDNSYRFWHYTGRMLA
                                                                                                                                                                                                                                                                                                                                                                   CDNQVTRVFEIATNKEILCVELKRTRKILFSPKDNFLLTFEPWAVYGPKTAENQKPEP
NVRVYSLADGKHVSTFSAPKEASWEPQFSDDESLAARMVGSEVFFYTNMSFDRYDHKL
VEKCATNFALSPGPAPNHVANYVPAVGSTPARVRVHRVSESFPVVGNRTFFKSDKAVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QINKMGDNLVYAVRSSEGFYLKRGLGKDAVTVFEQNKTSRDVACNVFAYSNNGQLFAY
                                                                                        EQERKAFQLKKKVEEIKVLKQRVANGDQLQPNQMEKIQRENEYLSELSKLTI"
                                                                                                                                                                                           ETHFESPKELWEVRWRPMTGYNKFAIKELTKTDKMAAGLPIRKKDASHPLNNVPAGAV
                                                                                                                                                                                                                                                                                                                                      TWNQRGQSLLILASVEVDKTNQSYYGEQSLYLINIQSGESVVVPLEKKGPIYAAKWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:Q19052"
/translation="MPAPNTTPSRDSNEFVISSSESNELLLPEKEKTESEERLSQTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA91279.1"
/db_xref="GI:3875451"
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/db_xref="taxon:6239"
/chromosome="II"
                                                                                                                                     RQAGAYIPPHLRKPLGGGGSAGPPSAAAPTPGNQNQRPAQPRANGNGNAPQPFRPQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(6082. .6250,6307. .6379,6432. .6509,6564. .
6750. .6930,7003. .7283,7337. .8179,8228. .8326)
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/gene="E04D5.1"
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gene

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27801 AGGTGATCCACCGGCTTCA 27783

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27861 AAGTTCAGCAACGCAAGTCCATTTGTGATAGACTTGATCTCCGATTCGAGCGTACTTAAT 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                             819 acattogotatttggttotttaatggtaatactgatctggcattgatagaaaagctgtga 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                  AAGATTCTGAAGGATCACCCCATCTACAGAACATCCATTGGCATCAATGACAGTTACTGG 27922
                                                                                                                                                                                                                                                                                                                                         TTTGTCAGCAAATTTGAAGACTGGTGCGAGTTTTCCAGCTGTCAAGGTCAGAGGTGTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATCCATAATTTACGTCTTTGATTGTTAATTGAATTTGACAATTGAAATAAAGCCCAGC
                                                                                         ggtttcagaatcgcatgtccatttatgataaactggctgaccaatgatagcaaattgaac 1115
                                                                                                                                                         TGGTCCACCTTGTCCATCATAAACCGTACATGAGTGAACTTTCATACAGTACACATTCTC 27862
                                                                                                                                                                                   agtatcaccgttaccatcatcgacaaagcaggaatggacaaccgcgcgcagaaagtatcaac 1055
                                                                                                                                                                                                                                                                                          casattatttagcaaatatttatcaagagcacatccat---cagcatttagaatttccac 995
                                                                                                                                                                                                                                                                                                                                                                                 togatococatatttgtatacoctgagottottggccagocattaaatctgttggatattc 938
tggttgaccggttggtcca 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179;
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/gene="B04D5.3"
/join(25834. .25873,27277. .27512,27582. .27
join(25834. .25873,27277. .27512,27582. .27
28158. .28410,28491. .28811,29092. .29213)
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YDFHVITAIOMMFPFVVLLLLNLTIIKRLVAEKRENMYPILRGAGTTTEVKKASFVQG
NLPENYVLLQVAADVIKESLIHRSSRSKRSQLRNAIYTMLAIVTSYLVCNGVHLELTI
LEREDPSYLLESTDRMQSSTFYIVLSDTVSICYMASSAIRIFIYAKCNPKLRQEITDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MFGENLFYADIHSTIPFKCEKLKIRVFLSENAQKHLFGFFLKYP
INFQLLMAVFRRSLPSSIFLATLATCDMLICLTYTLLFGVDAGIWYRKNTTLFFLYHR
YIVPVFFIAKVVQFAIPFILILITFERYLWTCTERKRFGITFQVLTLSLSFRKAFSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSEPSCMTVGDGKTGHRFEVRHDSCGVRRQREINGVVISATVIISFHSIFITKIDRAY RVSCFYVEGTKKVHNHYDISALTTQLLESETQLPVCRYEILNEAGGSPIKYARIGDQV YHKWTCVAELENVYCMKVHSCTVYDGQGGPPVTVIDANGCSVDGVILQNLEYTSDLTA GKLAPVFKFADKAGLYFNCQIQLTIKDVNYGCSNTQPQCPTSQYVVEBAQKTTETAEP YPYDSHESGYPTRPANYPVASSRYPIPTTQAPASYPSSPAPPPGADIDNGYPEPQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA91282.1"
/db_xref="GI:3875454"
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/codon_start=1
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/tbanslation="MMSINLTVHIILLVTFSVSHVVTTAVTKATGETTVRGAGQDLGD
/translation="MMSINLTVHIILLVTFSVSHVVTTAVTKATGETGVGAGQDLGD
VSSSFFYETTTASTCADDPNTDCTQYTFLCSNAKYTPLLQQFCAKTCGFCGSGSTAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTVCDIDLÞERGILVFGLEENEDGETTNAGDHGATRALREARNSOEKTCFSTSRMYFT
LILLCLLFATTVVVFIVIVQKQRQILAOTAFFKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA91280.1"
/db_xref="GI:3875452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to cuticlin like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKREKSIETNSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VACVDTSTQ"
5592 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // 29840,31127.
// 29ene="E04D5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIAETPENAYDGIVGFNDTEQPFTTSAAYTEDGVYSRLIKRNVVESTEQINASNKKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MPSRLAMKELKGGGEPEVVCETASISLLFKTRNSFNGKVFVKGY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q19053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA91281.1"
/db_xref="GI:3875453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="E04D5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5636 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ore 83.8; DB 34;
ed. No. 1.6e-05;
Mismatches 137;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
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ORIGIN

Matches Query Match BASE COUNT

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/gene="F53B6.1"

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Current sequence finishing criteria for the C. elegans genome current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced sequencing consortium are that all bases are either sequenced sequencing consortium are that all bases are either sequenced ye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

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Exceptions are indicated by an explicit note only sequence is nowneed the specified clone. It may be shorter because we only sequence we arrange for a small overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap between sections once, or longer because we arrange for a small overlap between
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Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Culson, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans cosmid F53B6, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 32412)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor associated protein; Thrombospondin like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z81086.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368 (6466), 32-38 (1994)
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                                                                                                                                                                                                                                                                                                                                    The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neighbouring submissions.
The true left end of clone F53B6 is at 1 in this sequence. The true
right end of clone F53B6 is at 5116 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94150718
                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                The end of this sequence (32306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence Z81523.
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                                                                            /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="F53B6"
                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                    .105) overlaps with the end of sequence
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for a small
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                                                                                comes from this gene; cDNA EST yk193h3.5 comes from gene; cDNA EST yk411f5.3 comes from this gene; cDNA yk411f5.5 comes from this gene"
                                                                                                                                                                                                                                                 complement(join(20516. .20602,20648.
21609. .21818))
                                                                                                                                                                                                                                                                                                                                                                                    GGYYQSNYWGKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(19892. .20022,20241.
/gene="F53B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCRFTNGTSVDIQHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRLLSCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIKIKCPAKKFDKKKIYWKKNGKKIKNDAHIKVSANGNLRVFHARMEDAGVYECFTDR
LQGNVTLNFKYRDFPASRVDLAPKPQIPSTKNRQRVQVSKEDVLREQASVLHKMNVSL
LEALLTAPNDEKAREGLRKYGNELVARNDIGHMSECRQKTCHVAGYQARGISCKVTFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OWRYGDWTQCSASCLGGKQKAALKCIQVSTGKSVQWSQCDARRRPPEKSRPCNOHPCP
PFWLTSKYSDCSMSCGSGTARRSVKCAQTVSKTDGADAHIVLRDDRCHFKKPQETETC
NVVACPATWVSSLNKRHNKIKLNKLKTAQWTECSRSCDSGERRRQVWCEIRDSRGKTQ
RRPDVECDANTKPQTVEVCSFGSCSRPELLSNRVFEQNAEQKKLTLGIGGVATLYQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTRPAAEENCVSTSCGRWEAGKWSKCTASCGOGVRRRHVACVGGSDCDEGGRPRQE
TTCYAGIPCSIATNSLDWNDRAYLDGNTFGSMDNHNDWQAPRLVAGEWSTCSSTCGTG
VMSRTVECVAVNPISSAPIKLPMSECQDQEQPKLFESCEVRSCPLQEDSKLSEDEAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQLRRCLTSKCSGESVRFKVCAQKTCESKSRLARDTICGGEEIVSRGQCEVVCRSRLTGANFLWRVDDGTPCQAATSRAVCSKGSCQIVGCDGLISSSFRFDACGVCGGRGDTCDNGANFLWRVSEEYTACASKCDDIVDWSGACRSIASTSQPIVVCVNALTGRVVPEKLCADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"predicted using Genefinder; similar to thrombospondin like; CDNA EST EMBL: 214404 comes from this gene; CDNA EST EMBL: 21571 comes from this gene; CDNA EST yk195c9.5 comes from this gene; cDNA EST yk195c9.5 comes from this gene; cDNA EST yk26g7.3 comes from this gene; cDNA EST yk28g7.5 comes from this gene; cDNA EST yk28g7.5 comes from this gene; cDNA EST yk28g7.5 comes from this gene; cDNA EST yk39a.5 comes from this gene; cDNA EST yk39a.5 comes from this gene; cDNA EST yk35ahl.3 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(1480. 3205. .330
                                                                                                                                                                                                                                                                                                                                            complement(20516. .21818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(19892. .20283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEIRNVDNSICESLASVRPPETRPCHREDCPRWEASQWSECSSQRCVSSMLAQKRRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(4270. .4339,4493. .4547,5071. .5295, 5368. .5662,5891. .6148,6204. .6752,6818. .7287,7546. .76:8104. .8184,12576. .12775,13246. .13384,13931. .14122, 14183. .14294,14341. .14457,14994. .15155,15198. .15311))
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SKWYWHQRAPKLLIPESCCIPSEIERCRSNPFDQDAPPPYYTSTCYEPLQNDLLHVMN
VASWLCITNAIVQVIFVSLKTIKLNFILLKT"
                                                                                                                                                                                                                   /gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                 /gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                     translation="MDFGILLVFLMAVAGTFAGISVSFSHSHEFPRHGLLGGGGFNPY/
                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB54255.1"
/db_xref="GI:5824510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F53B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL: P90884"
/translation="MKCSYTVVFLLFYLLIASFHVDALSWAAWSPWSSCTKTCGGGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4270. .15311)
/gene="F53B6.2"
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RKIKNVDQQDSrLfSLLEKYIFHSLSINLTIYLKALHFQTRVFPFKSFPHFNTLKFTF
QLKMGALGDSAYGARGRLIKFSYIVTALISILFSISCICYGIWLLARRSQYAELVSPS
                    /protein_id="CAB03117.1"
                                                                                                                                                                           /note="predicted using Genefinder; cDNA EST yk193h3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIKLFHSCDSLEVRQKCCSTCTFVERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRPKVEARPCPMLICPSRWMAADWTECVPHCGEGTRKREVYCVQTAHNVTVHVPDTFC
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/db_xref="GI:4008366"
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/gene="F53B6.2"
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/db_xref="GI:3877452"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80. .1638,1707. .
3308,3430. .3649)
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                                                                                                                                                                                                                                                                            .20953,20999.
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Best Local Similarity
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                                                                             29678
                                                                                                                                                                                                                                                     1174 atttgagtttgaaaagcagttgtgatttcagatacctcaatctgtgcactaactgtttta 1233
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1294 ggatgaaacgaaatgacaacagttgttgttacaaaaataccacgtggattcagagatcgt 1353
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                                                               ATTGACTCGAGGAAGAACATCGAATACTGAATGCTCGATCCATTCCCGTCACAAAGAAT 29737
                                                                                                                                                                                               AATTGATTTAATACTTCAGAGTTAACATACCCAACATCAATTTCCGCGTTCAATCCTTTA 29677
                                                                                                                                                                                                                                                                                                                                  127;
                                                                                                                                                                                                                                                                                                                                     Conservative
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gene

0;

Mismatches

Indels Length

0;

Gaps

0,

.00055; DB 87; 34;

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/protein_id="CAB03116.1"
/db_xref="G1:3877448"
/db_xref="G1:3877448"
/translation="MNLSLFIVKTVYTEYWVVLEKVQLHSFKQYVVALRFESVQFKNP
FILLLLIYNRIFLQSITILILLSTSSCFEIQNGVVGKPEVFCGIDTIRVKVNTEHPFN
GRIYVDGESDKQHCVQHSADAHSSPQEFTIPIGACNMRRQRTLHPRGISFSFTMITSF
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(27666. .27862,27919. .27959,28076. .2877
28905. .29001,29330. .29417,29467. .29606,29648. .29915,
30107. .30201,30478. .30589))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(27666. .30589)
/gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="msrespyslaqlverettnlkvrgssplvshaesmglifpnwvr
VCYRRGPMEYHPYDMNMPPKLVPRPPLHYKFDPPLTERGQIVSETYGRGLLNAGIRPF
EVFCSPDMKSYQTAAFLIKGLGLSYTTINIDPALLSYRQMLPTNFQEMLLSPKAFFNM
GYPINIQYLPSQGFIRAENIEDYNLRIQAFFKKNIAKIEQKQVVVISDNVMVDLTRNE
                                                                                        PQIEYEHGAISAYTNAHVFKYADKVQLYFTCTVQLCYKHDGGCEGITPPQCSGHSHGI
                                                                                                                     HPFFVTGMDRAFSIRCFFLESIKGLNAEIDVGTLAPQHVDQEYSLPVCAYHLKDGIEG
HVLRFAQVGQKVTHVWRCDQDASHVYGILIHSCYADDGHGNKFELVDDRGCSTDPFLL
                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F53B6.tl"
/note="TTT Lys K-tRNA; predicted using tRNAscan-SE-1.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVETVDDILQCIKKPTCQMNFISLKKGEAQIMDSPILPLTKSLYLVKPFYWTDVPLQL
SVPNHPELNQN"
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GQSIAQCRIFIEKTVPIVKGGEQARKDENEIYAIETFGSTGKGYFHDDMETSHYMKNF
ELADEKIPLRLQKSKGLLNLIDKNFATLAFCRCWIDRLGETKYLMALKGKCSYSTASR
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VPLTAIVTTSLPMVAAIAFCAKNRKTVHAKNKNKNKSSKSAKSSKSTRGASKSGKSRR
SSKAAHSKRSSKSSKKGTSGKGGKGSKRGGKSSKSKKKVKTATTSGSQVSTVSAA
                                                                                                                                                                                                                                                                                                                                                                     /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="F53B6.tl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB03118.1"
/db_xref="GI:3877450"
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/db_xref="GI:3877451"
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23555. .24160
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QVGHSLAEEVNSIKHSKEMNVAPAKLQYQTLGGVNQIELKNTSNERKAYKIKCSDNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(26258. .26342,26501. .26802,26846. .26926,26974. .27107.
27153. .27288,27334. .27459)
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4.2%;
59.3%;
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Score 74.8;
Pred. No. 0.
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CEY111B2_0/c
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CEY111B2_4
CEY111B2_5
CEY111B2_6
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CEY11182_1
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                                                                            73348 TGAAAAAATGTAAACAAAAAAAGAAAAATGAAAGAAAAATGAGAAAAAAATGAGAAA 73289
                                                                                                                                                                                      73408
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                                                                                                            taagtgaattgtttacagaataggaaatgatgcccataaaaattgggcaatacaaggtat 120
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Direct Submission

Submitted (27-OCT-1999) Nematode Sequencing Project, Sanger Centre, Submitted (27-OCT-1999) Wand Department of Genetics, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Season of University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditoidea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 614429)
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                                                                                                                                                                                                                                                                                                164;
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be
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NOTE: This is a 'working draft' sequence.

This record will be updated with the finished sequence will sequence will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis
/db_xref="taxon:6239"
/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        Score 71.6; DB 32;
Pred. No. 0.0017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 atgataataacaaacgaaactattcatggcctaatgatgaaacatttacaatagtatgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTCGTGGCGAAACCAC 73091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Bonfield, J., Burton, J., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hiller, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Lister, N., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Lister, N., Mortimore, B., Latreille, P., Lightning, J., Lloyd, C., Rifken, L., Roopra, A., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thiomas, K., Vaudin, M., Valdin, M., Valdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                            bin/display?db=wormacesclass=Sequence &object=Y18D10A
Current sequence finishing criteria for the C. elegans genome
current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
Exceptions are indicated by an explicit note of
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-DEC-1998) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, predictions from Genefinder (P. Green, U. Washington), and ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL034393.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.2 Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans
                                                                                                                         neighbouring submissions.

The true left end of clone F08A8 is at 152766 in this sequence. The strue right end of clone B0019 is at 105 in this sequence. The softhis sequence (1...105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is not the entire insert of clone Y18D10A It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://webace.sanger.ac.uk/cgi-
The end of this sequence (152766. of sequence 299710.
                                                                               AL008866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 152878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 152878)
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                                                      .152878) overlaps with the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete sequence
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/gene="Y1
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KWPEGIHKPTEKDSFGLLNSTKIHRNOPPTSDFETIAQATAEBEKALLGAQGAAGASE
PGSSSSIHGKKGKTVRELQTEMMKGESVKEKAARMRAEASAGRSQAPGPAPAPARSEL
QDPPQDFGLSMSDPGSDSETEEHGVQDEKHIPAMVTRRSARLSALPVTPKKASSSSKMP
PPPSPSPSTEGRRFRTLSTMSMEPAAAAVTPAPRGRPRSRSAAKVSENTEPLSEA
PSAPVKRGRGRPRSRSTMSITEDDSEPSTSSTAAKRSKAESDEEEQDLKLTMKSPEK
PKKPSKTTEETVGDVLKKRLRDTAKTTATVIHTPGPPLTRKMERMRAPTAVTSSKKE
KPKNAGSADSSINEEEHBDETMILEEQTIDLFQQTSQQEPRISGGSELLDEQFDASEE
KPKNAGSADSSINEEEHBDETMIEEQTIDLFQQTSQQEPRISGGSELLDEATPTALEF
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(29879. .35351)
/gene="Y18D10A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(26502. .26573,27346. .27405,27490. .27580,
27624. .27788,28732. .29006))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(26502. .29006)
/gene="Y18D10A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WOONVERGGKKVNKIKTHLRQALDLKIPFEELKRPMEEKGIKLGDSIPLTPSDAVDYM
MEFLRETSAADMWAUNRORIDANLKPLMNKEEENFLOYSVTLMEHDQOLLEVFISRI
IFELCARESIGSNEGGRLIRLPCHAVERSESAENPDDYTSPVYOKKSTWIRRLFOIL
LNHPNQIGKSTCYILMSDVAKYCRFLVVEEMDKDHMGSEFHLAFRVLMHKDSEQASAV
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KRAAPPAVQKSISSTTGQAPPTSVQAPPTSCSAAPPVDDLLSEILSGAKTKTTKT
KRAAPPAVQKSISSTTGQAPPTSVQAPPTSCSAAPPVDDLLSEILSGAKTKTTKTK
MPPUDQKISSEAPPISDSAPTSVHQOTPKSPKQILMSKYGLDISDSEDEEEEEEER
MEIVEEEEEAPPISDSLQASEPSSTATVKPEKVVAVVKIFSPEIDSTSVEAPPEASVP
EKAPAATKIDMQLASEPSPKAKTLPIAKKIPPKIKISJEDDLMS
DILAGAKTTKTKPKAPPTRVALGAVKRKASPFTPAGTTAPKRQYIKKSIDS
DILAGAKTTKTTKPKAPPTRVALGAVKRKASPFTPAGTTAPKRQYIKKSIDS
ULPPSSSSSTEPPSAPDSASTTSSMKKGGGAIMIEAVPCRPGGKAIKREQKPIGMKEM
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                                                                                                                                         /protein_id="caa22319.1"
/db_xref="GI:3979940"
/translation="MDGSGEKAIGFLIQFSLNARFWTDKQLLATDEPFSSENYQMVRR
/translation="MDGSGEKAIGFLIQFSLNARFWTDKQLLATDEPFSSENYQMVRR
FRIISEKRPKSVDKLYKTGEIPARGRGNKVGGRVFSKMPISKSMELSLVKLKQTPIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWLLNAKFDVAYVAPPTSNDVTEACINAHKQCIDDDDVTPSLLKKSIFLAKTAAPEVL
NVAFDFLRQKMDLIGEQFLKPKEMEKEPKRITAFSVPTVVTKMTKSEAEMLKKESKWQ
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ECEVLRMKLVSTDAAYRESVQREAEAINAKEIAEASLKQGQYDSEFYKKKSASLQEQA
DDAEKHKDQANYWRNKYDSVCALTERLEANNIDIKSKYESTVKLLETAGKRMTSLDNQ
   GWDVELGAPSGNDDDVIHPHSVISLTLPKLCMKNWTGPHFLGGRFVPKSLVDEHELLM
                                     {	t TSSIPITATLPTNLQAFPLIVDALFGFSFHPPTREPFTEMLKTVRASGIHVFSIDVPS
                                                                   QFYMKNGKKSTMVHIISKKTVSFIGQKLAAQIDEQLFTKYGFKVEQLMELAGLAAAQA
LAAHYPKSNVAVLCGPGNNGGDGFVCARHLQQFGFTPSIVYPKESRNELMKSLVVQCE
                                                                                                                                                                                                                                                                                                                                                                                               complement(join(29879. .30346,31220. .31296,31346. .31522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNDENSYRYNVAPHSAWLPWIQVNGERNRNAEFKLKDFSSVFRLFFEVFLQKCLKRS]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRCPDTSKFTHNQLVPFYQNYKGNLSDGLKLDFHAVPTGGHQVDGKYVNRCLHGALEC
ALNKLQMCSKKHTKQDWLVTAGCTQGKTAYSAGLKCLPDTEEGKTVQNCAESEEGEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA22309.1"
/db_xref="GI:3979930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNLVDLISIYTNFPLKPTTLPPSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNVLRVMIDNPFSSHSHAIFAALKQISPQVSQLREIIESSEINQYVEMTGEDAIRDAV
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LFFNSQPWKNSLSTSDPSISATEAEASEDPEHLDDVITEPAPPIGEQTLSDDEEEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA22308.1"
/db_xref="GI:3979929"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Y18D10A.1"
complement/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MQMNPNKSPPISINFPLFTMSKFLLFISISAVATASDLVEVFGI/
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                                                                                                                                                                                                                                                                                                                        .34852,35323. .35351))
r18D10A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Qualifiers
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9. .16655,17748.
9. .20807,22205.
0. .26130,26236.
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. .23127,
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/db_xref="GI:3979941"
/tdb_xref="GI:3979941"
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TSGIMRRALKTALSICIFLLIFQTVDSDSSDSSASAVVSGAVKSEDTVVAVNKTDVL
GEAIDANATSLEQHGAAIVGNVSEEKKRSLAIFFILFVIMLATLVVHMLIVSKIHWMP
                                                                                                                                                                                                                                                                                                                                                                                                                  join(54375. 54405,54825. 54924,54984. 55168,55357. 5
56162. 56529,56606. 57056,57123. 57193,57641. 57905,
58630. 58995,89841. 59066,59124. 59210,59257. 59373,
59630. 59775,61492. 61610,61724. 61783,61846. 61959,
62188. 62409,62843. 62943)
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FVPILTFAIFGTTISAWVIGAGLYILGAIGLIFEFTFFECFAFAMISAVDPVGTLAI
FQAVKVESLLXMLVFGESMLMDAVSIVLAAFALKHARKFSHUSLPASEIITSAFVFTEE
MFFFSACLGVGIGLLSALLFKHVDLRKTPSLEFALLLIFSYIPYGFAEALDLSGIMAI
LFCGISMSQFTRHVS9IAQITFRHTFRTISFVAETSYFAYIGMFFTIKLNFAPWLI
FWSVVLCLLGARCNVFPLAYLVNOGRRDVQISWAGTSYFAYIGMFFTAKLHFAFWLI
DKEKKSILLTTVLFLILFTTIFLGGSALPFISFINRCYPNERQRKRRRTPRNKESTGN
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//gene="Y18010A.5"
                                                                   DYDGHVENASAWLTLYQLKNEKWQLSRDFEDGLAEKTQSGEAPSELLNLYYFHSATFD
                                                                                                /translation="MSQNHIILLPDSFKNSMIISKIRAAPLEQPWANIVAKYCLFVAK
YPWFFIIPLITICLSMGIILNFKIYMGVNYLYAPLMATWKTBEAVFGENWAKDDDH
YYPGKDILRFQGIYLIVMAKDGGNULRQEYAQDFLKILDMILMVKLLSSAGRIFTYKD
VCLHFQNDCFSNPHAKLLANIYSKNHQNSMFNITYPIYRSTYATEPIDISKVLGNVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTKRALASDQMTDSDDVEFGGGGGVGGGGRMKDDVTPTRGRSGSRNSSDVIISAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLPTLEMDGPMGTGEVSTTSGDVAGPSA"
47525. .53224
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DVWSAGTVMAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIQSMNPNYKEFKFPQI
KAHPWNKVFRVHTPAEAIDLISKIIEYTPTSRPTPQAACQHAFFDELRNPDARLPSGR
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/db_xref="GI:397932"
/taanslation="MNKQLESCSLKSGKQVTMVVASVATDGVDQQVEISYYDQKVIGN
/translation="MNKQLESCSLKSGKQVTMVVASVATDGVDQQVEISYYDQKVIGN
GSFGVVFLAKLSTTNEMVAIKKVLQDKRFKNRELQIMRKLNHPNIVKLKYFFYSSGEK
                                                                                                                                                                                                                                                  /protein_id="CAA22312.1"
/db_xref="GI:3979933"
                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                        /gene="Y18D10A.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSALMMSKTQEMSFFGSDDWGPKKSALDATSSAGRIMRQLFVRKFTAIERLENRDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(47525..47593,48112..48208,48610..48751,49616..5
50501..50818,51553..51971,52106..52364,52847..53224)
/gene="Y18D10A.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Y18D10A.6"
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                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Genefinder"
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/db_xref="GI:3979931"
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Score 68.8;
DB
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                                                                      source
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                                                                                                                                                                                              Submitted (07-SEP-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: Jes@sanger.ac.uk or rw@nematode.wustl.edu on Nov 21, 1998 this sequence version replaced gi:3873430. On Nov 21, 1998 this sequence version replaced gi:3873430. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
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                                                                                                                         NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence as soon as it is available and the accession number wi
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                                                                                                          preserved
               /chromosome="I"
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                                                                                         Location/Qualifiers
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Best Local S
Matches 205
                              AUTHORS
TITLE
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                                                                                                                         Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Coopper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Collson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
C'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Meg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
Wilkinson-Sproat, J. and Wohldman, P.
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 Submitted (12-NOV-1999) Louis, MO 63110, USA. jes@sanger.ac.uk or rw@nematode.wustl.edu
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jes@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a sma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone Y111B2D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence_&object=Y111B2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QARKKLKTLLTKLGEPLKIGKETRKSNSFTQPFAPGKIGRKSYGKYQTGKQTGANSRE
IFKFRVKKMTFYMTKSRNSESGGNLDFDIINTLDSSEKNGGGGQDANDLICERSEN
FHFSSIYIKLIRKTLELQFADLPEIFNSGTSPUCCREFSISEICRFAVKFTSKIYAGLE
EILNSDNLPVCRNFLLYPICLFDGIFHSGTLPIPKHERSRKARMFLHQWVYLSRKFLE
                                                           DHSFDILKEAEKDAHIIPTKSIKAEPLDVQKPLSAFEKLASLRGRTQSADMRRGGDST
EMPNVTQQYQAEQNHLAQSSNNSQYNAPSTSSQPQHFPTEPSIRQPPPQQSYNSNQML
QNPRQQPQNQIVQNFQSAPQRHPHQNPQIATSSSSGGVNQFYNNGGAAPPVVEQQAAN
                                                                                                                                                                                                                           TOKTONKOCLTONDYOLLFDYFGKFEKALEORKAKKËEAERLKKLEËKLKKEKEKOAE
KDRIEAKKFEERMKKOOEKOEKEEKEREKKEKKEEKEE LEIMERKKREEDDRIAA
KLOIAQOLEMDRKMERAEESARKETEERRAKMETEAANALOGLEEDLLMDJDIDTMYOOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB60887.1"
/db_xref="GI:6434388"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(12998. .13081,13735. .14229,15626. .15715,16386. .1
16940. .17225,17597. .17869,21574. .21764,21915. .22057,
22109. .22243,23083. .23146)
/gene="Y111B2D.b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQLPKLKHHSPPVEGLAKKQVIAANAIKEGVRKQISLFENKKDRLPGDPVYVFQFTEP
VLTAVAPYLEDLVDYALAAKKIELIVSGIDALHQSTDGKITIIQFYIEICRRLQKLSF
LAVEEPMKSRLKEANEQIMKHQVVQIPKYQLKWPDGQAEPSLKGLNRELYEFDKSILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTASTPKKEEIGTLETFLKNIFANLDAKGKLYQEKKLKTFDTETLKEITTFIDVMKHH
KTEKVNMEPLIYSLAKSFGMTTQEVMKQVEQEISSKKATTPKPSTNAVLSTISSQKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Y11182D.a"

/gene="Y11182D.a"

/gin(<616. .1221,2288. .2593,3842. .4122,6454. .6687,

/gin(<616. .1221,2288. .2593,3842. .4122,6454. .1226,6454. .6687,

/gin(<616. .1221,2288. .2593,3842. .4122,6454. .1226,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227,6454. .1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVQAKKPRHFEIFWWKLVKNGLISTKFCVKNHKSKKITIFTPRPISDSPRPLFNQSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVAAKPSAPATPKASSSTALRPSTSSTPSQQQSTSTAKAMTSSSTSAEDAKRLLAMNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKNAADWKLTQTDLPTMGEKDIQMLTTIVRSWKSKKEISNSMVTGWLKDVNQLKMNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEIILIDDNAPAAKKQPESAQKGSTTVTMSAKKICKQQEEIAKQKPSSSSVTPSKPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPRKPSPPPAVEPTRSVEIIEKPEKTEKPAEKRKTAATTSALEPAEKKKKPDSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKVKIRKIKEKSGEKSSKSSDSSSSSSSSDAAGPPRMTGAPPSIRMVSSSSSLKKL
RRSSFTMSHSVQQHQSPLQQQFPINSYQSPSHHNNSSSMSNSSLMQTPHSNSSMIARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted using Genefinder; preliminary prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12998. .23146
/gene="Y111B2D.b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITPRPISDSLRPLFNQSDEVGGARRWETRENICSRPAIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="VDDEPTTSKKGGFYVGKGDVKDSNDEDEEEEEETDVEESIQEVP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB60886.1"
/db_xref="GI:6434387"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="Y111B2D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11604)
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for a small
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                           CDS
                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59651. .59820))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45598. .58081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=
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60241. .69488
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join(60241. .60280,60336. .60490,60543...60683,61748. .6:
50in(60241. .60280,60336. .66250,68651. .68748,69285. .69488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKIKKGKIVPKKVSKLDNPDHLLVASAGQDTYVRLMAIEPETDEKSENIREDSSTTP PDELTSANLFSINYTEYRCSSHAVMGHDDWYHSTWSNDRFYLLTASSDKTCIIWK EIDNLWADDVRLGIVGGAAGFFAAVESSELDLKDSGEKNAEMVVISSSESYEGGLEGW KSTDEQKTFWTALPMTGGHVGEVRDVDMHRSDDGDSGFLMSVGQDQTTRVFAKNGRQQ SYVELARPQVHGHDMQCLSFVNRSIFVSGAEEKVFRAFRAFKSVKSLEAISGVDTEK SFGSSDLAEFGACVPALGLSNNEMVEGETVDGEHWEEDAFRAAFVVLTSSPTEDTIOQ NTLWPEQHYLYGHGYEVYAVTANPTGNVLATACKSSHVEHSVVLLMSTSNWSKKSEII
                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB60891.1"
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GDAFAFVEFEDHRDAEDAVRARDGYEFDGRRIRVEFTRGVGPRGPAVAHSKTEVITAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(58932...59820)
/gene="Y111B2D.f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELIVLRFDSEGLHVIEKIGANRIPIDSAVLRLRFSKNGRKLAVATTDAKLRIFNVSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(45598. .45726,45775. .46085,46422. .46521,46742. .470
47048. .47125,49176. .49590,50604. .50829,52685. .53006,
55142. .55272,55631. .55811,57669. .58081)
/gene="Y111B2D.e"
/note="predicted using Genefinder; preliminary prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB60889.1"
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/db_xref="01:6434390"
/translation="MSIYPGVRPPMKRGPKPQSFFDDTPVASSDDPPDFESHIVLRVP
EDCVCRIEKIIQSDKHEEFSLNILNSDARNSTYRIGNQLLNGKILDLPTITEHKTLD
NKSLYKVADVSQILVCTHDSINSIASSSEDAAQKAAAAKAKQWQYPHGLTPPMKSARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPEAQMRRITEFLDIPWDDKVLHHEQLIGKDISLSNVERSSDQVVKPVNLDALIKWVG
TIPEDVVADMDSVAPMLRRLGYDPNANPPNYGKPDELVAKKTEDVHKNGAEWYKKAVQ
VVNDPGRVDKPIVDNEVSKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Protein_id="CAB60888.1"
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RATVNSIISRKVTITGFDLNDFRQCNTKWNAAIQIMVDQCESYGEKNCLKYYYBQLYL
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/gene="Y111B2D.c"
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/gene="Y111B2D.c"
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ISIQNSVLLAVGTSKRFVELYGESADKKSFSRLISVAGHTDWIHSIAFNEKKSVKMAK
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DSEVGVIKSTSERRHQKPITVLKRLKSSEIVADEFVTGGVDSRVVLWKLRGEHVEYVA
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/db_xref="GI:6434391"
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/gene="Y111B2D.d"
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Search completed: April 16, 2000, 04:52:00 Job time: 10929 sec
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// translation="MPNEIEEGSGLDVASRLAGKKWWTCSILLLVNLLNYMDRYTIV
// CHANGLAFFEDIDKGOGLCOYVFIVEYMFFAPLFGYLLGDRYNRKMLMTGGLGSTVANGV
VFASSFCGEGHYYLFLLCRGIVGIGEASYSTIAPTVLSDLFSGGLRSRVLMMFYPAIP
VGSGLGFISGSSISQARDSWOWGVRFSFIIGIACHMLLDEEVRGACDGARQNGD
VGSGLGFISGSSISQARDSWOWGVRFSFIIGNMWTPQYVGFSVAVHHNYFKYPET
ELTQINLIFGIITCMAGLLGVATGSILSRAWRDGSSIFRNHATEKADVYICALSMFVA
LPFIEFAIFIAEYSTNGCLILTYFAINSMCLNNSVNUDVLAMYVVYANRRATALAVQTM
VAHLFGDAASFYIIGVLSDMLRGDDASAVGHFFALQKALYVPTFMLVVAGAFYLAATF
FVEDDRKEALYVANGENFWKTELKDANWSESGRGESLIGRRVLSDFLTPDDIETLASV
DEDGINLEEDACTIKFDSIRRKNDDNSVENGQNAADLSDETDEWDVQRPDSGDDDP"
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/codon_start=1
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pred. No. 0.0078; 
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tgaataagctt 	ttcatggccta 	actgtt ATTTI	ggaaatgatgc TAAAATATGTA	tcacaaatga TTATAAAATA	; Score 67 ; Pred. No . 0; Misma	element gene the gene	ALIGNMENTS	x20248_04 x20249 C54656 T58640_4 v22733 v22733 Q53480 x52366 x52366 x52266 Q12515 Q125173 Q11710
ttcagaagctataa 	atgatgaaacattt ATTATAAAATATTT	agaataaa ATTATAAA	agaataggaaatgatgcccataaaaattgggcaatacaagg 	tacttttaat AATTATAAAT	; DB 1; Len . 3.1e-05; tches 205;	clone Rh32. rapy; vecto: t; apolipop: t; apolipop: t; apolipop: t; apolipop: ders ders ders attachment (T31531) re: distal 1212 nce. These n apol gene ule adapted etin (EPO) to an exprients. The EPO in stal	ENTS	
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CThis sequence corresponds to the genomic sequence encoding a Plasmodium CT rhis sequence corresponds to the genomic sequence encoding a Plasmodium CT rhis sequence corresponds to the genomic sequence encoding a CLSA-3) CC protein (W24790). The gene sequence was isolated by screening a CP - falciparum strain T9/96 library with the serum from a missionary CP - falciparum strain T9/96 library with the serum from a missionary CC - treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones CC isolated, clone 729s was used to screen a library generated from Thai CC strain K1. One clone contained a 6.85 kb insert including the sequence CC presented here. The gene organisation comprises a first exon, a short CC corresponding to a glycosyl-phosphatidylings a 1.8 kb region encoding CC corresponding to a glycosyl-phosphatidylingsitol membrane anchoring CC corresponding to a glycosyl-phosphatidylingsitol membrane anchoring CC corresponding to a glycosyl-phosphatidylingsitol membrane anchoring CC amino acids derived from the LSA-3 polypeptides of at least 10 CC amino acids derived from the LSA-3 polypeptides of at least 10 CC amino acids derived from the LSA-3 polypeptides of at least 10 CC and as vaccines for immunotherapy of malaria.
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plasmodium falciparum; pre-erythrocyte; liver stage antigen;
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derived from the liver stage antigen-3, useful for malaria vacc
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RESULT
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WO9640766-A2.
19-DEC-1996.
07-JUN-1996; U09508.
07-JUN-1995; US-4878
                                                claim 4; Page 56-61; 96pp; English.

Claim 4; Page 56-61; 96pp; English.

This sequence represents the var-7 gene of plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and stalic acid binding protein (SABP) conserved regions (see T72889 and T72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention The compositions are for the treatment and prevention of malaria, and
                                                                                                                                                                                                                                                                     Chitnis C,
Wellems TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBL gene family; SABP; sialic acid binding protein; vaccine; therapy Duffy binding like gene; Duffy antigen binding protein; erythrocyte: DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune respons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5898
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comprise
                                                                                                                                                                                                               binding domains homologous
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 either a
                                                                                                                                                                                                                                                                                      Miller
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                                      WO9641877-A2.
27-DEC-1996.
12-JUN-1996; F
13-JUN-1995; F
                                                                                                                                                                                                                                                                       prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob
glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;
vaccine; immunotherapy; malaria; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to Plasmodium merozoites (especially Plasmodium falciparum or Plasmodium vivax).

Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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08-OCT-1997
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Daubersies P, Dr
WPI; 97-065464/06
                     (INSP ) INST PASTEUR
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falciparum liver stage antigen-3 genomic sequence.
falciparum; pre-erythrocyte; liver stage antigen;
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Similarity 47.1%;
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                                                                                                                                                                                                            stage antigen-3
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RESULT 5
Q11710/c
ID Q11710 standard; D
AC Q11710;
DT 30-JUL-1991 (firs
DT 30-JUL-1991 repli
DE Dictyostelium plass
KW slime mould; repli
OS Dictyostelium disc
FH f Key
FT cds
FT cds
FT cds
FT ds
FT PD W09106644-A.
PD 16-MAY-1991.
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PS Claim 20; Fig IA-E; 69pp; French.

CC This sequence corresponds to the genomic sequence encoding a Plasmodium CC This sequence strain K1 pre-erythrocytic liver stage antigen-3 (LSA-3) CC protein (W24790). The gene sequence was isolated by screening a CC P. falciparum strain T9/96 library with the serum from a missionary CC treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones collected, clone 729s was used to screen a library generated from Thai CC strain K1. One clone contained a 6.85 kb insert including the sequence presented here. The gene organisation comprises a first exon, a short CC library and a 5 kb second exon containing a 1.8 kb region encoding CC plocks of 4 amino acid repeats and a 3 hydrophobic region encoding corresponding to a glycosyl-phosphatidylinositol membrane anchoring sequence. The invention relates to new polypeptides of at least 10 CC amino acid derived from the LSA-3 polypeptide with the exception of cc peptides W24791-4. The LSA-3 peptides can be used to raise antibodies can das vaccines for immunotherapy of malaria.
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                                                                                                                                (first entry)
um plasmid Ddp2
; replication; R
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                                                                            2378. .5041
                                        /product=
                                                                                            Location/Qualifiers
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47.0%;
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                                                                                                                                Rep gene;
                                        involved in
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1. No. 0.012;
1-ches 228;
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Chaim 15; Fig 1; 90pp; Pig 1; 90pp; Fig 1; 90pp; Pig 1; 90pp; 
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p-PSDB; R11988
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Flores MV, OSullivan WJ,
WPI; 94-200271/24.
P-PSDB; R55694.
Nucleic acid encoding carba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The CDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSII) of Plasmodium falciparum was determined. The CDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit of CPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSa and CPSb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated from Plasmodium falc
the treatment of malaria.
Disclosure: Page 6-16; 31pp:
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03-DEC-1992; AU-006206
16-DEC-1992; AU-006380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                     Malaria-specific DNA insert of clone DNA; malaria; clone 41-2; Plasmodium Plasmodium falciparum Ep-322712-A.
                                 (BEHW) Behringwerke.
Knapp B, Hundt E, Enders
WPI; 89-194071/27.
P-PSDB; P90417.
New antigenic proteins from Plasmodium acid sequences and derived antibodies, Claim 1; Table 17; 25pp; German.
                                                                                    20-DEC-1988; 121299.
30-DEC-1987; DE-831351.
                                                                                               05-JUL-1989.
20-DEC-1988;
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Best Local Similarity
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e 1052 BP; 394 A; 93 C; 88 G; 477 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                /transl_except=
5546. .5548
                                                                                                                          3461.
transl_except=
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                                                                                                                                                                                                                                                            /transl_except=
556. .658
                                                                                                                                                                                         transl_except=
2909. .2911
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Best Local Similarity
Matches 217; Conserv
                                                                                                                                                                                                                                                                                                                                      membrane protein 1 (PFEMP1) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1996; U05798.
27-APR-1995; US-430908.
(AFFY-) AFFYMAX TECHNOLOGIES
Baruch DI, Howard RJ, Pasid
WPI: 96-497376/49.
                                                                                                                                                                                                                                                                  alternative, truncated version of the coding sequence is given in T41853.

Sequence 9789 BP; 4061 A; 1393 C; 1837 G;
                                                                                                                                                                                                                                                                                                  immunoreactive with the PfEMP1 polypeptide or its fragments may used in diagnosis of malaria infection. This sequence encodes the pfEMP1 protein of the MC type of Plasmodium falciparum. An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Figure 12; 149pp; English. A polypeptide comprising a Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      develop products for the diagnosis, malaria parasite infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Plasmodium falciparum erythrocyte membrane develop products for the diagnosis, treatment c
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                                                  aactattcatggcctaatgatgaaacatttacaatagtatgcatataaaagattactgaa
                                                                        caaatgataaactgttagaataaaataggacaagttgataatgatgataataacaaacga
                                                                                                    AAAAAAAATTATTAATAAAAAAATAATG - ATTATAAAAAAATTTATTAGAAATAAAA
                                                                                                                                                                        tttttttcacaaatgaaatactttttaattgcaataatgcaaataagtgaattgtttaca
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/transl_except=
6257. .6259
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/transl_except=
6263. .6265
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7754..8478
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5269. .6271
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                                                                                                                                                                                                                                                                                                                                                                                                      PT Recombinant DNA molecule expressing mammalian erythropoietin
PT useful to transform cell lines, and for gene therapy, e.g. of
PT useful to transform cell lines, and for gene therapy, e.g. of
PT anaemia and other red blood cell disorders
PT anaemia and other red blood cell disorders
PS Claim 7; Page 59-60; 84pp; English.
CC Human apolipoprotein B (apoB) scaffold attachment region (SAR)
CC element clones Rh32 (731530) and Rh10 (731531) respectively carry
CC element clones Rh32 (731530) and Rh10 (731531) respectively carry
CC camp with the boundaries of the distal 1212 bp 5' human apoB
CC co-map with the boundaries of the human apoB gene chromatin
CC domain. A novel recombinant DNA molecule adapted for transfection
CC of a host cell comprises an erythropoietin (EPO) cDNA (731529) or
CC genomic clone (731532) operably linked to an expression control
CC sequence and to the 5' and 3' SAR elements. The SAR elements
CC increase expression of the recombinant EPO in stable, long-term
CC mammalian cell cultures.
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09619573-A1.
27-JUN-1996.
18-DEC-1995; CA0696.
19-DEC-1994; US-358918.
(CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            History 1936 (first entry)
Human 3' apolipoprotein B SAR element clone Rh32.
Erythropoletin; EPO; anaemia; gene therapy; vector
scaffold attachment region; SAR element; apolipop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delcuve G;
WPI; 96-309587/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T31530 standard; cDNA;
                  296
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                                                  AGATGAGGTAATTGTGTTTTTATAATTAAATATTTTATAATTAAAATATTTATAATTAAA 64
                                                                                                                  195;
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605 BP; 278 A;
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Pr binding proteins
Claim 4; Page 55-61; 96pp; English.
Claim 5; Page 5; Page 5; Page 6; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996. 009508. 07-JUN-1996; U09508. 07-JUN-1995; US-487826. 07-JUN-1995; US-487826. Chitnis C, Miller LH, Peterson DS, S:
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DBL gene family: SABP; sialic acid binding protein; vaccine; therapy;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-1997 (first entry)
Plasmodium var-7 gene.
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binding domains homologous
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Query Match
Best Local Similarity
Matches 180; Conserv

Conservative

0,

2.9%; 45.6%;

Score 51; DB pred. No. 0.1; Mismatches

1; 215;

Length 19124; Indels

0;

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RESULT 11
X20248_02
Continuation (3 of 10) o
WP Sequence split into 1
WP Fragment Name
WP X20248_01
WP X20248_01
WP X20248_03
WP X20248_03
WP X20248_04
WP X20248_05
WP X20248_06
WP X20248_06
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Local Similarity 44.8%;
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11-SEP-1984; AU-007066.
10-SEP-1985; AU-047326.
(HALL-) HALL INST MED RES.
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The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (M60472) or FIRA (M60473). RESA and FIRA antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.

Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p-pSDB; p60569.

DNA coding for Plasmodium falciparum poly:peptide(s) having antigenicity of the poly:peptide(s
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N60472;
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11-SEP-1984: AU-007067.
11-SEP-1984: AU-007066.
10-SEP-1985: AU-047326.
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Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
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PA (CORI) CORINA CORP.

PI Fridakis TN, Reed SG, Smith JM;

PI Fridakis TN, Reed SG, Smith JM;

PR WPI; 98-557473/47.

DR WPI; 98-557473/47.

Pr - and related vectors, transformed cells, proteins and antibodies, pr - and related vectors, transformed cells, proteins and antibodies, pr - useful for diagnosis, treatment and prevention of breast cancer PS Claim 1; Page 127; 173pp; English.

CC V68800 to V68998 represent nucleotide sequences which encode human companies of compass transfer periods. Detection or measurement of compass transfer periods and nucleotide sequences, or the corresponding RNA in a sample, is used for diagnosis and companies of breast cancer. Human breast tranour specific polypeptides and nucleotide sequences, and the vectors containing the DNAs, are also cuseful in vaccines for inhibiting development (for prevention or containing the polypeptides may also be used to craise monoclonal antibodies, used as immunoassay reagents.

SQ Sequence 715 BP; 183 A; 131 C; 86 G; 294 T;
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Best Local Similarity
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09-APR-1997; US-838762.
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lecule encoding a breast tumour specific polypeptide #169.
breast cancer; breast tumour tissue; diagnosis; treatment
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22-FEB-1990.
10-AUG-1989;
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/note="Alelle II, skips 3098. .3136."
485. .2526
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241. .245
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Best Local Similarity
Matches 173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding SERA antigen of Plasmodium falciparum - also DNA encoding signal and regulatory sequences of SERA gene, for diagnosis, prevention and treatment of malaria.

Disclosure; p: English.

Sequence allows for production of antigenic malarial proteins, useful in diagnosis, prevention and treatment of the disease. The sequence may be used in an expression vector, and signal and regulatory sequences may be used to stimulate production of other products.

Sequence 6124 BP; 2567 A; 602 C; 801 G; 2137 T; 17 Others;
 2389
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Pred. No. 0.19;
D; Mismatches 188
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       Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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US-08-883-795A-3
US-08-883-795A-3
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US-08-8232-463-1
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G. C.		
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OB-083-795A-36/c equence 36, Application atent No. 5985607 general information: APPLICANT: Delcuve, APPLICANT: Ontario COUNTRY: Granda ZIP: W5H3y2 COMPUTER READABLE FOR MEDIUM TYPE: Flopp COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentin CURRENT APPLICATION NUMBER: FILING DATE: 27-JU CLASSIFICATION UNBER: FILING DATE: 27-JU CLASSIFICATION UNBER: FILING DATE: 27-JU CLASSIFICATION UNBER: FILECOMMUNICATION UNBER REFERENCE/DOCKET NU TELEFAX: (416) 351 INFORMATION FOR SEQ ID SEQUENCE CHARACTERIS SECUENCE CHARACTERIS LENGTH: 665 base p. TYPE: nucleic acid STORLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE: ORGANISM: Homo Sap IMMEDIATE SOURCE: CLONE: Rh 32 08-883-795A-36	42.6 42.6 42.6 42.1.6 42.1.6 42.1.6 42.1.6 42.1.6 42.1.6 42.1.6 42.1.6 43.1.6 4	
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en Activator	Patent No. 5340934 Sequence 2, Appli Sequence 4, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 41, Appli Sequence 41, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli	

Query Match
Best Local Similarity
Matches 217; Conserv

Conservative

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3.6%;

Score 64; DB 4; Le Pred. No. 4.5e-06; n. Mismatches 235;

Length 665; Indels

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US-09-056-075-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRAL
ZIP: 53701-2115
COMPUTER READABLE FORM:
COMPUTER: FLOPPY disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TANDITER: TBM PC COMPATIBLE
TO COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 2731
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 TAATTATAAAATATTTAATTATAATATTTTAAT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 atataaaagattactgaataatgaataagcttttcagaagctataaaagcgatagaagaa
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                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STRANDEDNESS:
                                                            LENGTH:
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1 South Pinckney Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnson, Eric A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradshaw, Marite
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OTHER INFORMATION: plasmid RP4"
US-09-056-075-1
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US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Miller, Louis H. APPLICANT: Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 tatcacaaatgataaactgttagaataaaaataggacaagttgataatgatgataataaca 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                COUNTRY: U
ZIP: 92660
                                                                                                                                                                                                                           CITY: Newport Beach
STATE: California
                                                         CLASSIFICATION:
                                                                            FILING DATE:
                                                                                                                                                                                                                                                          STREET:
REFERENCE/DOCKET NUMBER:
               REGISTRATION NUMBER:
                                                                                         APPLICATION NUMBER: US/08/487,826E
                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agttattagaaggatgataagaagaaacgaatatatatggcagttttattattgctt 429
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                             Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08487826B
                                                                                                                                                                                                                                                       E: Knobbe Martens Olson & Bear 620 Newport Center Drive 16th
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PE: DNA
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Wellems, Thom
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3770..4013
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                                                                                                                                                                                                                                                                                                                    BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                                                  Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                               Chetan
               29,655
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                                                                                                                                                                                                                                                               16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6243;
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RESULT 4
US-07-867-106-2/c
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                                                                                                                                                                                                                        Sequence 2, Application US/07867106
Patent NO. 5389526
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Sline Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
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INFORMATION FOR SEQ ID NO:
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            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1471
                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & STREET: One Liberty Place 46th Floor
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                             COUNTRY:
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nes 170; Conserv
APPLICATION NUMBER:
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US-08-446-855A-1/c
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Best Local Similarity
Matches 214; Conserv
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ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                                    1619 AAAGTAATTATAACTAGGTTAGTTTTTTATAATTTTT 1583
                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                      1979 ATAGAAAAAAGTTGGTTAAACTACATTAGTTTTTATAGTTTTTGCATATTTAAAAAATAA 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                           ANTI-SENSE:
                                                                    412 gcagttttattattgcttcgatgattctaacattatt 448
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LOCATION:
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APPLICATION NUMBER: PCT/AU90/00530
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Sequence 1, Application US/08446855A Patent No. 5849573
GENERAL INFORMATION:

APPLICANT: APPLICANT:

Stewart, Thomas Flores, Maria

Thomas Maria V

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RESULT 6
US-08-883-795A-36
; Sequence 36, Application US/08883795A
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ZIP: 22201-4714
COMPOTER READABLE FORM:
COMPOTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: POPOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 3.0%;
Local Similarity 47.6%;
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STATE: Virginia
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                                                                                                                aatttgtgatattatcacaaatgataaactgttagaataaaataggacaagttgataatg 180
                                                                                           ttttgatgaaaatatcacttattgtattacagtaattatttcctacatactatatttg
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Best Local
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APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
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ORIGINAL SOURCE:
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NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
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APPLICATION NUMBER: US,
FILING DATE: 27-JUN-199
CLASSIFICATION: 435
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ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
                                                                                                                             247 agattactgaataatgaataagcttttcagaagctataaaagcgatagaagttttga 306
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CITY: Toronto
STATE: Ontario
367 aaaattagttattagaaggatgataagaagaaacgaatatata--tggcagttttattat 424
                                      316 TACATATTTTATAATTAAAATGTTTATAATTACATATTTTATAATTAAAATGTTTATAAT
                                                                   307 tgaaaatatcacttattgtattacagtaattatttcctacatactatatatttgttagct
                                                                                                                                                                              189 aacaaacgaaactattcatggcctaatgatgaaacattt--acaatagtatgcatataaa
                                                                                                         256 TAAATATTTTATAATTAAAATGTTTATAATTAAATATTTTATAAATTAAAATGTTTATAAT 315
                                                                                                                                                                                                                                                                    129 atattatcacaaatgataaactgttagaataaaataggacaagttgataatgatgataat 188
                                                                                                                                                                                                                                                                                                                                                                                                           17 ttttttttcacaaatgaaatactttttaattgcaataatgcaaataagtgaattgtttac
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                    77 agaataggaaatgatgcccataaaaattgggcaatacaaggta-----taatttgtg 128
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US-08-487-826B-13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AUGUST. Ned NAME: Israelsen, Ned REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: NIH1: TELECOMMUNICATION INFORMATION: 701.PDHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                    MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING STATEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                  178
                                                                                       118 tataatttgtgatattatcacaaatgataaactgttagaataaaataggacaagttgata 177
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                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 10-SEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                          aaataagtgaattgtttacagaataggaaatgatgcccataaaaattgggcaatacaagg 117
atgatgataataacaaacgaaactattcatggcctaatgatgaaacatttacaatagtat 237
                                                                   180;
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Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitnis, Chetan
Miller, Louis H
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                        Score 51; DB 4; Length 19124; Pred. No. 0.01; 0; Mismatches 215; Indels
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US-08-232-463-14
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14,
   Matches
                             Query Match
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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y Match 2.8%; Score 49.6; DB 1; Local Similarity 4.3%; Pred. No. 0.016; hes 16; Conservative 204; Mismatches 148;
                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                  NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 91 114 300.6
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Query Match
Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                         * TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stewar, APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
APPLICANT: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
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                                                                                MOLECULE TYPE:
                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                              STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Nixon & Vanderhye PC STREET: 1100 No. 5849573th Glebe Road, 8th Floor
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                                                                                                                                                                                                                                                                     Mitchard, Leonard
                                                                                                                             nucleic acid
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2.78;
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Score 48.6; DB Pred. No. 0.028;
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              Length 8920;
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US-07-638-431-1/c
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                                                                                                                                                                                                                      TELEFAX: (301) 295-403
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              NAME: Spevack, Avrom D. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: protective m
TITLE OF INVENTION: immunogen an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hoffman, Stephen I
APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
                                                                                  ANTI-SENSE: N
ORIGINAL SOURCE:
                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Spevack, Avrom D.
                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 tataaaagattactg 255
                 DEVELOPMENTAL STAGE: erythrocytic stage TISSUE TYPE: Blood
                                                                                                                                                                                    TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US FILING DATE: 19910110
   CELL TYPE:
                TISSUE TYPE:
                                                   STRAIN:
                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Bethesda
                                                                  ORGANISM:
                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                  17X(NL)
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NMRDC Building 1 T-12 National Naval
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erythrocytic stage
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; NAME/KEY: CDS
; LOCATION: 718..3195
; OTHER INFORMATION:
US-07-638-431-1
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PCT-US92-00018-1/c
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Best Local Similarity
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APPLICANT:
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                           NAME: Spevack, Avram D. TELECOMMUNICATION:
                                         ATTORNEY/AGENT INFORMATION: NAME: Spevack, Avram D.
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19920103
                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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LIBRARY: Py-la
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TELEPHONE:
                                                                      CLASSIFICATION:
                                                                                                                               SOFTWARE:
                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20814-5044
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Hedstrom, Richard
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Rogers IV, William O.
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 (301)
                                                                                                                                PatentIn Release #1.24
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             (301)
                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                              David Spevack
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             295-6759
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Sequence 15, App...
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Best Local
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                                                                                APPLICANT:
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                         APPLICANT: GAVIN, Kimberly TITLE OF INVENTION: ORIGIN NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                             3321
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               CORRESPONDENCE ADDRESS
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                                                                     APPLICANT:
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Local Similarity 48.1%;
es 165; Conservation
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LOCATION:
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NUCLEIC ACID
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                                                                                                                                                                                                                          Application US/08484105
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                                                                                                         RINE, Jasper
FOSS, Margit
MCNALLY, Francis
                                                                     LI, Joachim J
                                                                                LAURENSON, Patricia HERSKOWITZ, Ira
                                                                                                                                                   KOBAYASHI, Ryuji
                                                                                                                                                                 BELL, Stephen P
                                                                                                                                                                                STILLMAN, Bruce
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                                         REPLICATION COMPLEX GENES
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ALBRITTON & HERBERT
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Best Local :
                                                                                                                                                                                                                                                                                                      Patent No.
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                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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LENGTH: 2504 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 494-877
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                       CORRESPONDENCE ADDRESS
                                                    TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES NUMBER OF SEQUENCES: 24
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TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEX: 910 277299
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ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-5903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                            APPLICANT:
                                                                                                             APPLICANT:
                                                                                                                                 APPLICANT:
                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 2.6%; Score 47; DB 1; Local Similarity 45.5%; Pred. No. 0.044; hes 95; Conservative 17; Mismatches
                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    5, Application US/08484106
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                                                                                          GAVIN, Kimberly
                                                                                                                                                                      MCNALLY, Francis J
                                                                                                                                                                                      RINE, Jasper
FOSS, Margit
                                                                                                                                                                                                                         BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                               HERSKOWITZ, Ira
                                                                                                                                               LAURENSON, Patricia
                                                                                                                                                                                                                                                                STILLMAN, Bruce
FLEHR, HOHBACH, TES
Embarcadero Center,
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IBM PC compatible
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                                                                                                           Joachim J
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US-08-484-106-15
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REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELERAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08323170B Patent No. 5733772
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      STREET: TWO CITY: San Francisco
STATE: California
                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           APPLICANT: Williamson, Kim C. APPLICANT: Kaslow, David C. TITLE OF INVENTION: Cloning at TITLE OF INVENTION: falicipar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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NAME: Osman Ph.D., Richard
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STRANDEDNESS: double
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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California
                                                                                                                                                              Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                             6828
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7008 CTAAAGATGTTATT 7021
                                                                                                                                     6888 TTGCTATATTTCCACAAGCATGTTTTAGTAATGTTTTATTAGAATATTATAAAAGTGATT
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                                                                                                                                                                     435 attotaacatt--atttttatgccttctgatttggacgaaatttaaacgaaatggtaata 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/010,409 FILING DATE: 29-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 9636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                    ttattagaaggatgataagaaggaaatatataggcagttttattattgcttcgatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGAAAAAATGAAGTATCTATTAGTTTAGCTTTGAAAGGGGTTTATGGAAATCGAATT 6589
                           atgcagattccatt 566
                                                                    ATGAAGATAGTGAACATATTAATTATTATATTCATAAAGATAAAAAATATTAAAAAC
                                                                                                  atgacggcagcaatcaatgcaatgcttaaacccataaacattgagaagccaaatggtgac
                                                                                                                                                                                                            AAAAGTGCACTGTTAAAATTAAAAAAGGAGATATTTTTGGATTGAAATGTCCTAAAGGTT
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                                                                                                                                                                                                                                                                                                                tcacttattgtattacagtaattatttcctacatactatatatttgttagctaaaattag
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20-MAR-1991 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION UNIMBER: US 08/075,783
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
3060 AAAATAGGTATCATT 3046
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APPLICATION NUMBER:
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                            190 acaaacgaaactatt 204
                                                                                                                                              70 tgtttacagaataggaaatgatgcccataaaaattgggcaatacaaggtataatttgtga 129
                                                                                                                                                                                                         10 ttttttttttttttcacaaatgaaatactttttaattgcaataatgcaaataagtgaat 69
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TELEX: 425066 CURTMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 09-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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                                                                                   tattatcacaaatgataaactgttagaataaaataggacaagttgataatgatgataata 189
                                                            TTCGGTCAAACCTGTAATTACTTTTGAATTAGATTTTACGAATTGTTTGATATCATCATT
                                                                                                                          New York
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                                                                                                                                                                                                                                                        Conservative
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Search completed: April 16, 2000, 04:36:19 Job time: 9753 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
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1 tttttttttttttttttttt.....caaacttgggtaattaaacc 1779
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SUMMARIES

Result Query No. Score Match Length DB ID
. Score
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. G
% Query Match
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Description

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
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VERSION
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                           Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae Unpublished (1997) on Sep 12, 1996 this sequence version Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIIII196 665 bp mRNA EST 31-AUG-1998 SWOV3MCA1232SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1232 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AI111196
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
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AA625044 SWOV3MCA1

AA625044 SWOV3MCAN

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/lab_host="XL1-Blue
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VERSION
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                                                                                               ggtttcagaatcgcatgtccatttatgata--aactggctgaccaatgatagcaaattga 1113
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWOV3MCA1144SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1
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                                                                                                                                                                                                                                                                                                                           /note="Wector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3; were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome@smith.edu
                                                                                                                                                                                                                                                                                          slustigm@nybc.org)."
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/clone_lib="Onchocerca volvulus molting
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/db_xref="taxon:6282"
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/lab_host="XL1-Blue MRF'"
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                                                                                                                                                                                                                           Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
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On Jan 14, 1998 th
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                                                                                                                                                                                Email: genome@smith.edu
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                                                                                         /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/note="Vector: Lambda Uni-ZAP
               /lab_host="XL1-Blue MRF'"
                              /dev_stage="molting L3"
                                              (SL96MLW-OvmL3)
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                                                                          /clone="SWOv3MCAM12G08"
                                                                                                                       /organism="Onchocerca volvulus"
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130 c 121 g 191 t
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Pred. No. 3.2e-64;
                              mRNA
     volvulus
molting L3 larva cDNA
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1231 ttatcagcttccatgtaaaagcattgtactcgatatgcacgatcaacttttggtaacaaat 1290
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO1879 5', mRNA sequence. AA618895
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On Sep 12, 1996 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Filarioidea; Onchocercidae; Onchocerca. 1 (bases 1 to 672)
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Onchocerca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lizotte-Waniewski in the Laboratory of Dr. S. A. William The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

132 C 129 g 202 t 11 others
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
On Oct 30, 1997 his sequence version replaced gi:2 Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science Center, College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWOV3MCAM02C01SK Onchocerca volvulus molting L3 larva cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
AA668071
AA668071.1 GI:2629570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onchocerca volvulus.
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                                                                                                                                                                                                                                                                                                                                                                                                      il: genome@smith.edu
primer: pBluescript
(SL96MLW-OVMLJ)
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% ECS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
                                                                                                                                                                                                                                                                                                                                                                                                                                               4135853786
                                                                                                                                                                                                                                                               /clone="SWOv3MCAM02C01"
/clone_lib="Onchocerca volvulus
                                                                                                                                                                                                                                                                                                        /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                             /organism="Onchocerca volvulus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGTATCGACACAGGCATTGGTACCACTTGTGTCTGGAATGCTGTGGTCATTTCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                 AAGACACCTCGAGGATTTAAGGACCGTGATCGTTCAACATTACATGAATCCATCTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA585626 776 bp mRNA
SW3D9CA349SK Brugia malayi L3 molting-day 9 larva
(SAW97MLW-BmL3d9) Brugia malayi cDNA clone SW3D9C/
Brugia malayi.
Brugia malayi
Brugia malayi
Eukaryota, Metazoa, Nematoda, Secen
Filarioidea, Onchocercidae, Brugia
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                                                                                      AA585626.1
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                                                                                                                      sequence.
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a 106 c 138 g 178 t 1 others
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0; Mismatches 158;
                Secernentea;
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                                                                                                                                                  ctggcaaagcttgattatcatcgctaatttcaagggtgttgatatcagttcgtacatcaa
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                                                                                                                   CTGGTAGAGCTTGATTATCTTCGCTGATTTCAAGGGCGCTAATATCAGTCCTCACGTCGA
                                                                                                                                                                                                                                         CTGCGGCGAGTACCACTGGTTGTCCACCGAGATGCAAACGTGCACGATGACGTAAGTCAA
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Location/Qualifiers
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/lab_host="E coli XLI-Blue MRF'"
/note="vector: LambdaZap II (UniZAP XR); Site_1: Eco RI
/note="vector: LambdaZap II (UniZAP XR); Site_1: Eco RI
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi
isolated from the peritoneal cavity of jirds nine days
after infection. The mRNA was converted to double
stranded cDNA using reverse transcriptase and oligo (dT)
followed by Rnase H and DNApol I. The library was
constructed by Michelle Lizotte-Waniewski. The library is
available from the Filarial Genome Project Resource
Center: contact Dr. S.A. Williams, Clark Science Center,
Contact Dr. S.A. Williams, Clark Science Center,
Contact Dr. S.A. Williams, Clark Science Center,
Contact Dr. S.A. Williams, Clark Science Center,
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Contact Dr. S.A. Williams, Cl
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(SAW97MLW-BmL3d9)"
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Pred. No. 8.7e-58;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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On May 9, 1995 thi
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Williams, S.A., Lizotte-Waniewski, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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SWOV3MCAM0ZA04SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM0ZA04 5',
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//lab_most="XLI-Blue MRE'"
//note="Vector: Lambda Uni-Zap XR; Site_1: Eco RI; Site_2:
//note="Vector: Lambda Uni-Zap XR; Site_1: Fhird-stage
Larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDN+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of 0. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNAse H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
                       157
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                The library is available from slustigm@nybc.org)."

102 c 106 g 172 t
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(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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L3 larvae of Onchocerca volvulus
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Query Match

Best Local Similarity

17.7%; 78.9%;

Score 314; DB 37; Pred. No. 3.7e-53;

Length 537;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATATCGGCATACAGGCATCGGTACAATTTGTGTTGCAAATGCAGTTGTCATTTCGGAA 478
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1. SWOV3MCAM12A04SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM12. mRNA sequence.
                                                                                                                                                                                                                                                                                  Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797124.
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AI322068.1 GI:4056219
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                                                                                   /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
             /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                         /clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
                                                                     /clone="SWOv3MCAM12A04"
                                                                                                               /organism="Onchocerca volvulus"
                                                                                                                                        Location/Qualifiers
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mRNA sequence.
AI317885
AI317885.1 GI:4033152
                                                                                                AI317885 615 bp mRNA EST 17-I
SWOV3MCAM06H12SK Onchocerca volvulus molting L3 larva
                                                                   (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone
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3. USE C. 111 g. 181 t.
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EST. Onchocerca Onchocerca

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TITLE
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TTTCGGCATCCTGCCTGATCGTATAAGCCTTTCACGTATACATGTCCTTCAAATGGATTA 199
                    ttacggcaaccttcttgatcataaagacctttcacataaacatgtccttcgaatgcatta 1479
                                                                                                          gcaacattgcatgaatcaaatggaagtgaaattccggcaacttgacgtccaccttcatca 1419
                                                                                                                                                                                                acgaaatgacaac-agttgttgttacaaaaataccacgtggattcagagatcgtgtacgc 1359
                                                                                                                                                                                                                                                                                      ccatgtaaaagcattgtactcgatatgcacgatcaactttggtaacaaataatggatgaa 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams, S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately d000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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124 c 123 g 189 t 7
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/clone_lib="Onchocerca volvulus molting
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/db_xref="taxon:6282"
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Pred. No. 1.3e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
On Jan 19, 1998 this sequence version replaced
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams,S.A., Lizotte-Waniewski,M., Laney,S., Lustigman,S.,
Hillier,L., Allen,M., Bowles,L., Geisel,S., Jost,S., Kucaba,T.,
Martin,J., Steptoe,M., Theising,B., White,Y., Wylie,T.,
Chappell,J., Person,B., Gibbons,M., Harvey,N., Pape,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 531) Williams, S.A., Lizo
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Eukaryota; Metazoa; Nematoda;
Filarioidea; Onchocercidae; Or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            slustigm@nybc.org When requesting this clone please reference the Williams lab clone id -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S.A.Williams. The Library is available from Dr. Sara Lustigman email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Underwood, K. and Marra, M. Molecular Parasitology OvmL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: -40ml3 fwd. ET from Amersham quality sequence stop: 484.
                                                                    /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, 13, were isolated from infected black files in cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately do nolting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture.
in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda
                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                        /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                               /clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                     /clone="onch17"
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RESULT 11
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                                                    Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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1 (bases 1 to 363)
Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S
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(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO691 5', mRNA
                                   College, Northampton, MA, Tel: 4135853826
                                                                                                                           On May 9, 1995 this sequence Contact: Steven A. Williams
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genome@smith.edu
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                                                                                                                                        1995 this sequence version replaced gi:802401
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                                                                          AA625024 466 bp mRNA EST 12-NO SWOV3MCA758SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO7
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a 71 c 77 g 110 t 1 others
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/lab_host="XL1-Blue MRF'"
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85.4%;
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                 accttcttgatcataaagacctttcacataaacatgtccttcgaatgcattacgtgtat
                                                                                                   tgcatgaatcaaatggaagtgaaattccggcaacttgacgtccaccttcatcattacggc 1426
                                                                                                                                                                                   tgacaacagttgttgttacaaaaataccacgtggattcagagatcgtgtacgcgcaacat 1366
                                                                             TACAGGAATCAANCGGAAGGTCAATTCCGGCNACCTGACGTCCACCTTCATCATTTCGGC
                                                                                                                                                               TGACAACAACTGATGTGACAACAATACCACGTGGANNTAACGAACGTGTACGTGCTACAT
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On May 9, 1995 this sequence version replaced gi:802407
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
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Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The library is available from Dr. slustigm@nybc.org)."

91 c 93 g 144 t 12
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/db_xref="taxon:6282"
/clone="SWmL3C0758"
/clone_lib="Onchocerca volvulus molting L3
(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams
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75.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can be viewed at http://www.sanger.ac.uk/brugia/3D6/MB3D6AA4G10T3.html
Seq primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Jan 19, 1998 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +44 131 650 6760 Fax: +44 131 670 5450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes expressed in day six
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blaxter, M.L., Waterfall, M., Daub, J.,
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AA841200.1 GI:2922536
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          105
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The library was constructed by Michelle Lizotte-Waniewski. The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, M 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email genome@smith.edu."

81 c 84 g 84 t
                                                                                                                                                      /note="vector: lambdaZapII (UniZap XR); Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. mRNA was prepared from third stage larvae of Brugia malayi isolated from the peritoneal cavity of jirds six days after infection. The mRNA was converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 2 x 10E5 independent recombinants and average insert size was 900 base pairs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Brugia malayi day
larvae SAW96MLW-BmL3d6"
                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="third stage larvae, six days after infection"
/lab_host="E. coli XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="3D6AA4G10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brugia malayi"
/strain="TRS Labs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:6279"
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Matches 301; Conser
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                                                                                                                                                                                                                                                                                                                                                           AA618952 459 bp mRNA EST 12-NOV SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C020
                                                                                                                                                                                                                                                                                                                                                         College, Northampton, Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Sep 12, 1996 this sequence version replaced gi:1405277. Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 459)
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                                                                                                                                                                                                                                                                                                                       genome@smith.edu
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by
                                                                                                                                                  /clone="SWmL3CO2020"
/clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
                                                                                                               /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                       /db_xref="taxon:6282"
                                                                                                                                                                                                                            /strain="Kumba, Cameroons"
                                                                                                                                                                                                                                            /organism="Onchocerca volvulus"
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85.0%;
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                                                                                                                                                                                                                 Onchocerca volvuius
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Onchocerca.
College, Northampton, Tel: 4135853826 Fax: 4135853786
                                    Smith College Department of Biological Sciences Department of Biological Sciences, Clark Scienc College, Northampton, MA, 01063, USA
                                                                                                               Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:802391
Contact: Steven A. Williams
                                                                                                                                                                  1 (bases 1 to 395) Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca
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EST.
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SWOVJMCA318SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO318 5',
                                                                                             Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    slustigm@nybc.org)."
a 85 c 91 g
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Pred. No. 2.7e-43;
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Seq primer: pBluescript
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Search completed: April 16, 2000, 03:09:09 Job time: 6193 sec

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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
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Human protein tyrosine phospha
Human protein tyrosine phospha
Mouse protease activated recept
pli0. Recombinant polypeptide
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Asparaginyl-tRNA synthetase from
S. aureus asparaginyl tRNA synt
Asparaginyl-tRNA synthetase from
S. aureus asparaginyl tRNA synt
Alpha-facto profibrolase from S
H. pylori transporter protein,
H. pylori protein,
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Expression plasmid pUCPICI799 r
C-terminal prepro-C-terminal al
Peptidyl C-terminal alpha-amida
                                           Alpha-Trichosanthin encoded by Ribosome inactivating protein Mouse SRY-related protein. Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by sequence whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Type B alpha-amidating enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Type A alpha-amidating enzyme.
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                          BAR1 gene product.
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A_Geneseq_36:R99462
A_Geneseq_36:R97208
A_Geneseq_36:R97210
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08-JAN-1992.
27-MAY-1991;
01-JUN-1990;
10-AUG-1990;
30-NOV-1990;
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                                                   .SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
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seq_documentation_block:
ID R20112 standard; Pr
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                                                                                                                                                                                                                                                                                                                    US-09-323-427-3 x R20112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel DNA encoding peptidyl hydroxy:glycine N-C lyase (PHL) - used to prepare PHL which can be used in the amidation of peptide(s) e.g. human calcitonin.

Claim 4; Page 18; 28pp; English.

The sequence was deduced from a CDNA insert from pAE-III-202-4 (PERM BP-3172). The vector serves as source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyOH -> R-NH2. It can be used to produce peptides with amidated C-termini, e.g. calcitonin, growth hormone, LH-RH. Sequence 935 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE-III (peptidylhydroxyglycine N-C lyase precursor). Amidation; PHL.
                                                                                                                                                          147 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
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AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                              ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                   lAlaAspGlyTyr.....
                                                                                                                                                                                               {\tt CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVal}
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! Blosynthetic enzyme of icos 
! Blosynthetic sensor protei 
! Human calcium sensor protei 
! Human kidney calcium sensor
                                       Cys
                                                                                                                                                          196
  291
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563

291

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1077 CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 854 CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
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                                                                                                                                                                                                                                                                                                                                                                                GCA...............GAACCGGAGAATATCATT...GATGTACGAAC
                                                                                                                     GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT
                                                                      ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
                                                                                                                                                                                                                                                             aGlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG
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                                                                                                                                                                 lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     756
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US-09-323-427-3 x P94856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: P94856 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence encodes a derivative of the mature C-terminal alpha-amidating enzyme from plasmid pXX799.

The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.

Although pXX799 is similar to pXA457 at the N-terminus, it has an are hydrophobic elements suggesting a membrane function.

See also N93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno WPI; 89-017279/03.
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                                                                                                                                                                                                                   247
                                                                                                                                                                                                                                                                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-amidating; pAX799; alpha
                                              545 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                    491 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-1987; JP-306867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-1990 (first entry) 
Expression plasmid pUCPlCI799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        823 lSerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI
            334 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
                                                                                                                                                                                                                   AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                     ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                    lAlaAspGlyTyr...
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                                                                                 ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
                                                                                                                nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI
                                                                                                                                               Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                                                                    .....Cys
                                                                                                                                                                                                                                                                                                                                                 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leAlaIleAlaIlePheIleArg
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JP-177184.
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0.945
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Length: 232
Gaps: 12
Percent Identity: 21.552
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-09-323-427-3 x P94854
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                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                documentation_block:
                                                                                                                                                                                                                                                                                                   Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.

Plasmid pXA799 contains a sequence derived from Xenopus laevis.

The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.

Although the gene product is similar to that of pXA457 at the N-terminus, lithas an area of hydrophobic elements suggesting a membrane function.
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Obsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno
WPI; 89-017279/03.
N-PSDB; N90791
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15-JUL-1988; 306508.
17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-terminal prepro-C-terminal alpha-amidating enzyme of pXA799. alpha-amidating; pAX799; alpha amide; ds.
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                                 97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 593
CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gly......ValLeuTyrAlaValAsnGlyLysProTyrTy 611
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                                                                       to: P94854
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0.945
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seq_documentation_block:

ID R73053 standard; Protein; 87
AC R73053,

DT 06-NOV-1995 (first entry)
DE Peptidyl C-terminal alpha-an
KW Peptidyl C-terminal alpha-an
KW trichostatin; CHO.

OS Not specified. Location/Qua
FH Key
FT peptide 1.39
FT peptide 1.39
FT peptide 1.39
FT PO 26-APR-1995.

PD 26-APR-1995.
PF 07-SEP-1994; 306587.
PR (SUNR) SUNTORY LTD.
PA (SUNR) SUNTORY LTD.
PI FURUKAWA K, Ohsuye K, Sugi
                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: A_Geneseq_36:R73053
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                                                                                                                                                                                                                                                                    06-NOV-1995 (first entry)
Peptidyl C-terminal alpha-amidating
Peptidyl C-terminal alpha-amidating
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-323-427-3 x R73053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing protein prodn. from cultured animal cells - by adding a trichostatin to the medium, effective at low concn. and not injurious to host cells
Disclosure; Page 10-15; 19pp; English.
3mu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alpha-amidase enzyme (AE)) were suspended in F-12 medium to which aliquots of trichostatin were added. Cells were cultured for 3 days at 37 deg and then assayed for AE. Without trichostatin, AE productivity was 708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities were respectively 866, 1897, 1894 and 3359 U/ml.
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                                                                                                                                                                                                           GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 530
                                                                                                                                                                                                                                                     laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                                                                                                              AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
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                                       TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 630
                                                                                                                       TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                            Gly.....
                                                                                                                                                                                                                                                                                              AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
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seq_documentation_block:
ID R88469 standard; Prot
AC R88469;
DT 14-AUG-1996 (first e
DE Feline infectious per
KW Feline infectious per
KW Feline infectious per
KW Feline infectious per
KW Feline infectious per
PN J07327683-A.
19-DEC-1995:
19-DEC-1995:
19-DEC-1995:
19-DEC-1994; JP-12930
PR 10-JUN-1994; JP-12930
PR 10-JUN-1994; JP-12930
PR (KITA) KITASATO KENK
DR WPI; 96-072341/08.
DR N-PSDB: T10166.
DR N-PSDB: T10166.
DR N-PSDB: T10166
DR N-PSDB: T0166
CG Taim 1; Page 14-17;
CC This sequence represe
CC (FIPV-I) spike protest
CC infection. The spike
CC cell with the spike
CC that the spike protest
CC that the spike protest
CC cell with the spike
CC that the spike protest
CC Sequence 1464 AA;
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US-09-323-427-3 x R88469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding feline infectious peritonitis I virus spike protein used in a vaccine for prevention and treatment of FIPV-I infection Claim 1; Page 14-17; 23pp; Japanese.
This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host cell with the spike protein DNA and expressing the sequence such sequence 1464 AA;
                                                                                                                                                                                                                                                                             789
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(KITA) KITASATO KENKYUSHO WPI; 96-072341/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          679
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                                                                                                                                                                                                                                                                                                                                ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT
                                                                                                                                                                                                                                                                                                                                                                                   alAsnGlnThrAspLeuPheGluPheValAsnAsnThrGlnAlaArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCACTTCCA.....GTTGCATTCATGCAAT......GTTGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAsnSerThrThrGlyGluIlePheThrValValProCysAspLeuTh
TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 458
                                                snCys.....ThrSerAlaIleThrTyr 825
                                                                                                                                                              oGlnPheTyr.....TyrIleThrLysTrpAsnAsnAspThrSerSerA
                                                                                                                                                                                                                                                                          SerArgSerSerThrProAsn.....PheValThrSerTyrThrMetPr
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                                                                                                        AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA
                                                                                                                                                                                                                 TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGCTGATGGATGTCTTTGATAAATATTTG.....CTAAATAATTT 674
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O antigen; Olll antigen; wbdM gene; colitose transferase; glucose transferase; diarrhoea; haemorrhagic colitis; diagnosis Escherichia coli.

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seq_name:
W88310;
26-APR-1999 (first entry)
E. coli colitose or -
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coli colitose or glucose transferase
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                                                                                                                                                                                      TT.....CGTTTAAATTTCGTCCAAATCAGA 1156
                                                                                                                                                                                                                                                    IleGlyGlyMetAlaLeuGlySerIleThrSerAlaValAlaVal.ProP
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alignment_block:
US-09-323-427-3 x W88310
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12-NOV-1998.
01-MAY-1998; AU0315.
22-JUL-1997; AU-008162.
01-MAY-1997; AU-006545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology with TrsE of Yersinia enterochalitica, and is predicted to be a colitose or glucose transferase. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within 0 antigen gene clusters improves the specificity of methods for the detection and identification of 0 antigens, e.g. in testing food- or faecal-derived samples, or samples from patients. The 0 antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            faeces or patient samples
Disclosure; Fig 7; 165pp; English.
This is the amino acid sequence of the protein encoded by the wbdM
gene of a gene cluster (see x06748) involved in the biosynthesis of
the Escherichia coli 0111 0 antigen. The protein shows high
the Escherichia coli 0111 0 antigen.
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Reeves PR, Wang L;
WPI; 99-059669/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. for
                                                                                                                                                                                                       303
                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 111
                                                                                                                                                                                                                                                                                                                                                                      GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT
                                                                                                                                                                                                                                                                                      GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGT 302
                                                                                                                                                                                                                                                                                                                                                                                                              erPhePheArgAlaLeuPheGlnValLysLysIleIleValAlaLeuLys
gLeu....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAACAATCAATTTTAATACACGTAATGCATTCGAAGGAC.....A 152
                                                                             ThrAlaHisAsnLysAsnGluGlyGlyAsnAlaArgMetPheCysTyrAr
                                                                                                                                                                                                     TGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG...ATCGTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGAT 449
                                                                                                                     ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAG 399
                                                                                                                                                            lePheSerArgPheIleArgMetLeuIleProAlaValProLeuIleCys
                                                                                                                                                                                                                                                                                                                               ProAspIle.....IleHisSerHisMetPheHisAlaAsn..
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Ratio:
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0.533
46.281
.SerAspPheLeuAlaSerIleThrThrAsnValS 138
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Seq. ID AC DT DE DE KW KW KW OS PN PD PF PR PR PR PR
                                                                                                                                                                                                                                                                                                                                                                                     seq_name: A_Geneseq_36:W13825
                                                                                                                                                                                                                                                                                                                                          _documentation_block:
                 Yeast transcription regulatory factor SRBB.

Transcription regulatory factor; suppressor of RNA polymerase SRBB; RNA polymerase II; holoenzyme; SWI/SNF.

Saccharomyces cerevisiae.

W09708301-A1.

06-MAR-1997.
28-AUG-1995; U14192.
28-AUG-1995; U14192.
31-AUG-1995; US-521872.
11-OCT-1995; US-521872.
11-OCT-1995; US-540804.
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(WHED)
                                                                                                                                                                                                                                                               04-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                 W13825 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 lValGlyProHisAsnAspValIleProValSerAsnHisIleLeuLeuA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    IleIleGlyMetLysAsnArgGluTyrIleValSerAsn 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....LeuValCysGlnLeuAsnLeuValAspLysValPhePheLe
WHITEHEAD INST BIOMEDICAL RES
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alignment_block:
US-09-323-427-3 x W13825
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polymerase B proteins or SWI/SNF proteins
claim 11; Fig 10a-b; 154pp; English.
Claim 12; Fig 10a-b; 154pp; English.
Claim 13; Fig 10a-b; 154pp; English.
Claim 14; Fig 10a-b; 154pp; English.
Claim 15; Fig 10a-b; 154pp; English.
Claim 16; Fig 10a-b; 164pp; 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: W13825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 AACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 eIleLysValProThrTyrIleArgLysLeuIle......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTT
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GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 503
                                                                                                                                                 CTGAAATCACAACTGCTTTTC....AAACTCAAATTGTCCCGATGCCA
                                                                                                                                                                                                                                                                                                                                                                                    nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL
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                                                                    LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh
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Seq ID AC AC DT DE KW KW KW PD PR PR PR PR PR PR PR PR PR
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26-JUL-1990.
17-JAN-1999; JO0042.
17-JAN-1989; JP-005878.
(SUNR ) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka S
WPI; 90-254034/33.
N-PSDB; Q05631.
                                                                                                                                                                                                                                                          documentation_block:
R06400 standard; pr
                                                                                                                              Homo sapiens.
WO9008190-A.
                                                                                                                                                                                   C-terminal alpha amidating
                                                                                                                                                                                               17-DEC-1990 (first entry)
Lambda gt10ch2 encoded C-t
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                                                                                                                                                                    lambda gt10ch2.
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metSerIlePheLeuLysArgLysAspPheThrAsnLysAsnLeuIleG1
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                                                                                                                                                                                                                                                                                                                                                      lyLeuGluTyrIleIleArgLeu
                                                                                                                                                                                                                                                                                                                                                                                         AATTAGCGATGATAATCAAGCTT 976
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                                                                                                                                                                                                                                                                                                                                                                                                                           nLeuIleSerLeuLysLeuLeuThrPheGluValThrGlnAsnValLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTT.....TACTCAAGAAAAGATCTGCAGAACCGGAGAATA....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAA......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ys \verb|ValTyrSerMetIleAsnAsnSerAsnGlnAlaValGlyGlnThrTrp|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hrSerPheMetProPheTrpLysPhePheMetLysAsnPheProPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTGCTA.....TCATTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....TCATTGATGTACGAACTGATATCAACACCCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AACCTGCTGCAGCTGCGCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \verb|nSerGluIleIleAspThrAsnThrSerLysGlnPheGlnLysAlaArgA| \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...ATAGCGAATGTTCGACCACAATGTTCAG.....AACCACAAGGA 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pGluLysLeuLysThrGluLysLeuLysAsnAspLysSerGluValLeuL
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                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                  terminal alpha amidating genzyme; human thyroid g
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: R06400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-323-427-3 x R06400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA in lambda gtll and gtl0. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtl0 library, including gtl0chT2. Restriction analysis indicated that gtl0chT2 encoded a different type of enzyme to one of the other two clones. The DNA can be inserted into vectors for expression in E.coli or (more efficient)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The enzyme is useful for prodn. of physiologically active alphamanidated peptides from their C-glycyl precursors. See also Q05630 and Q05632. Sequence 776 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 CysGlnProThrAspValAlaValAspProGlyThr.......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nTrpGlyGluGluSerSerGlySerSerProLeuProGlyGlnPheThrV
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CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT 636
                                                                                                                                                                                                                                                                                                                                                                                             AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alProHisSerLeuAlaLeuValProLeuLeuGlyGlnLeuCysValAla
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                                                                                                                                                                                                ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
                                                                                            ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT
                                                                                                                                                                                                                                                                                            AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA 486
                                                                                                                                                                                                                                                                                                                                             eValArgGluIleLysHisSerSerPheGlyArgAsnValPheAlaIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
                                              .........AspGlnGluProValGlnGlyPhe.......
                                                                                                                                       .....GlyLeuLeuPheAlaValAsnGlyLysProHisPheGly..
                                                                                                                                                                                                                                           erTyrIlePro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                              AspArgGluAsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TT.....GTCATTTCGTTTCATCCATTATTT.....GTTACCAAAGTT
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seq_name: A_Geneseq_36:R06379
                                                                                                                                                                                                                                                                                                   17-JAN-1990; J00042.
17-JAN-1989; JP-005878.
(SUNR) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka S
WPI; 90-254034/33.
                                                                       COGLING Sequence: Disclosure: pp; English.

Disclosure: pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA cDNA libraries were prepared from the grobes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gt10 library, including gt100chT01.

Restriction analysis indicated that gt10chT101 encodes a different type of enzyme to one of the other two clones. The DNA can be increased into vectors for expression in E.coli or (more efficiently)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block:
See also
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620
                                                       The
                                                                                                                                                                                                                               coding sequences.
                                                                                                                                                                                                                                               C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
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                                                                                                                                                                                                                                                                                      N-PSDB; Q05632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lambda gt10ch101 encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R06379 standard; protein; 866
                                                                    in animal cells.
                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                               lambda gt10ch101.
            enzymes are useful for prodn. of physiologically dated peptides from their C-glycyl precursors. also 005630 and 005631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTTGATTTACGTC 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt saspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
   AA;
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                                                                                                                                                                                                                                                                                                                         s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme; human thyroid gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                      (more efficiently)
                                                     active
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alignment_scores

Quality:

87.00

Length:

322

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alignment_block:
US-09-323-427-3 x R06379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: R06379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nTrpGlyGluGluSerSerGlySerSerProLeuProGlyGlnPheThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
TAAAACAGGTGGCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                         ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
                                                                                  AGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                            hrAsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer
                                                                                                                                                                     CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
                                                                                                                                                                                                             sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT
                                                                                                                                                                                                                                                      AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT
                                                                                                                                                                                                                                                                                               .....LysProValArgLysHisPheAspMetProHi
                                                                                                                                                                                                                                                                                                                                         GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AspGlnGluProValGlnGlyPhe.......
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Percent Identity: 18.944
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alignment_block:
US-09-323-427-3 x R06399
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                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: R06399
                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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CDNA libraries were prepared from human thyroid gland poly(A) RNA cDNA libraries were prepared from human thyroid gland poly(A) RNA cDNA gril and gtl0. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtl0 library, including gtl0chT201.

Restriction analysis indicated that gtl0chT201 encodes a different type of enzyme to the other two clones. The DNA can be inserted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-1990 (first entry)
Lambda gtlOch201 encoded C-terminal alpha amidating enzyme.
C-terminal alpha amidating enzyme; human thyroid gland;
Lambda gtlOch201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This enzyme is useful for prodn. of physiologically amidated peptides from their C-glycyl precursors. See also Q05631 and Q05632.
Sequence 974 AA;
                                                   197
                                                                                                                                                                                             631 CysGlnProThrAspValAlaValAspProGlyThr......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q05630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUNR ) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka
WPI; 90-254034/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9008190-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R06399 standard; protein; 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       into vectors for expression in E.coli or (more efficiently) in
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                                                                                                                            AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
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                                                                                               .GlyAlaIleTyrValSerAspGlyTyr.
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0.592
45.652
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Percent Identity: 18.944
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                                                                                                                                                                    CGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCC 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
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                                                    AGTTGATTTACGTC 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT 736
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leAlaIlePheIle
                                                                                                            .ValLeuIleThrThrLeuLeuValIleProValValValLeuLeuAlaI 883
                                                                                                                                                                                                                      etGlnGluLysGlnLysLeuTleLysGluProGlySerGlyValProVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspArgGluAsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh
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887
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seq_documentation_block:
ID R74171 standard; Pr
AC R74171;

Protein;

3038

seq_name: A_Geneseq_36:R74171

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alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                          alignment_block:
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                                                                                                                                           US-09-323-427-3 x R74171
                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1995.
28-OCT-1994; U12423.
28-OCT-1993; US-148132.
QZ-NOV-1993; US-148132.
(MERI ) MERCK & CO INC.
Conder MJ, Davis CR, He
Reeves CD, Vinci VA;
WPI; 95-193816/25.
N-PSDB; Q92323.
 1188
                                                      Claim 12; Figure 2; 107pp; English.

The full-length TPKS-encoding DNA in plasmid pLOA was designated pTPKS100. Splicing of the introns from the DNA sequence and translation of the 9114 nt ORF results in a protein of 3038 AAs (R74171) with a mol. wt. of 269,090 daltons. Inspection of the TPKS AA sequence for active site residues and motifs known to be associated with polyketide synthases and fatty acid synthase (FAS) activities resulted in the identification of candidates for expected sites (see FT). Except for the presence of a methyl transferase, not present in FAS, the succession of activities on the most present in FAS, the succession of activities on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel DNA encoding triol poly-ketide synthase - used to isolate and identify homologues of triol poly-ketide synthase, and in the treatment of hyper-cholesterolaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
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region
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Aspergillus terreus triol polyketide synthase.
Triol polyketide synthase; TPKS; HMG-COA reductase inhibitor;
hypercholesterolaemia; LDL- cholesterol.
                                                                                                                                                                                                                                                                                       protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus terreus
                             66
                                                                                      16
                                                                                   ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA 65
                          CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT.....GGACCAACTT 109
                                                                                                                                                                                                                                                                                                   protein is the same
                                                                                                                to:
                                                                                                                                                                                                                                                                         3038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= dehydratase motif
1446. .1450
/label= methyl transferase motif
1932. .1937
/label= enoyl reductase motif
2164. .2169
                                                                                                                R74171
                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2521. .2535
/label= misc feature
                                                                                                                                                                                     87.00
0.481
38.347
.GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1603. .1612
/label= misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1450. .1460
/label= misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= keto reductase motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label keto-acyl synthase motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= acyl carrier protein motif 32. .288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 658
                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hendrickson LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acetyl/malonyl transferase motif
                                                                                                                                                                                                                                                                                                    as that observed for the rat FAS
                                                                                                                                                                                Length: 472
Gaps: 24
Percent Identity: 19.703
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6
                                                                                                                3038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcada PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rambosek
                                                      1187
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-	CAATA	14
115	isvalaspargliernriedvalproserledcysledalarnralagid	пκ
1217	SerGlyCysGluLysValAlaPheAsnThrIleAsnThrTyrAspLysGl	1233
15	3 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTA	193
123	3 yAspTyrLeuSerGlyAspIleValValPheAspAlaGlu	1246
194	ATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT	240
1247	GlnThrThrLeuPheGlnValGluAsnTleThrPheLysProPheSer	1262
241	TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT	288
126	3 ProProAspAlaSerThrAspHisAlaMetPheAlaArgTrpSerTrpGl	1279
28	9GTAACAACAACTGTTGTCATTCGTTTCATCCATTATTTGTTACCA	334
127	9 yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA	1296
ω	5 AAGTTGATCGTGCATATCGAGTACAATGCTTTTAC	369
129	6 laGlnAspLysGluAlaIleProIleIleGluArgIleValTyrPheTyr	1312
37	0 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC	419
1313	IleArgSerPheLeuSerGlnLeuThrLeuGluGluArgGl	1326
42	CTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCC	460
132	6 nGlnAlaAlaPheHisLeuGlnLysGlnIleGluTrpLeuGlu	1340
46	1 GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT	510
1341	GlnValLeuAlaSerAlaLysGluGlyArg	1350
511	ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT	560
135	1HisLeuTrpTyrAspProGlyTrpGluAs	1360
56	1 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT	603
136	0 nAspThrGluAlaGlnIleGluHisLeuCysThrAlaAsnSerTyrHisP	1377
603		603
137	7 roHisValArgLeuValGlnArgValGlyGlnHisLeuLeuProThrVal	1393
604	GGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	650
1394	ArgSerAsnGlyAsnProPheAspLeuLeuAspHisAspGlyLeuLe	1409
65:	1 TGATAAATATTTGCTAAATAATTTGGAATA	582
1409	uThrGluPheTyrThrAsnThrLeuSerPheGl	1426
68:	3 CAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGG	132
142	6 laArgGluLeuValAlaGlnIleAlaHisArgTyrGlnSerMetAsp	1441
73:	3 CGATCACAGC	182
144:	2 IleLeuGluIle 1	445
78:	33 AAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG 8	332
144	6GlyAlaGl	448

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alignment_block:
                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: A_Geneseq_36:R06427
                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1463 GlyPheAsnSerTyrThrTyrThrAspIleSerThrGlyPhePheGluGl 1479
                                                                                                                                            expression vector. The AEE encoded is used as a catalyst in the conversion of a peptidyl substrate to a corresp. peptidyl amide. This can be used for making a protein biologically active, e.g. calcitonin or growth hormone releasing factor. See also Q05637. Sequence 944 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1990; 301034.

06-FEB-1989; US-307366.

(UNIG-) UNIGENE LAB INC.

Betelsen AH, Mehta NM, Beaudry GA;

WPI; 90-248308/33.
                                                                                                                                                                                                                            The corrsp. DNA sequence hybridises, under stringent conditions, with a DNA sequence (I) which encodes an alpha amidating enzyme (AEE) and is foreign to the host cell into which it is transformed. (I) is connected to a promoter and is contained in an expression vector. The AEE encoded is used as a catalyst in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha amidating enzyme.
Alpha amidating enzyme; peptidyl amide EP-382403-A.
                                                                                                                                                                                                                                                                                                                               N-PSDB; Q05636.

Prodn. of alpha amidating enzyme - using prokaryotic eukaryotic expression vectors having transcriptional claim 3; page 19; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-1990 (first entry) Protein encoded by sequence which hybridises with DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R06427 standard; protein; 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrAspLeuIleIleAlaSerAsnValLeuHisAlaThrProAsp....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nAlaArgGluGlnPheAlaProPheGluAspArgMetValPheGluProL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gCysThrGluProPhe 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheIlePheGlyLeuPheAlaAspTrpTrpAlaGlyValAspAspGlyAr 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyGlnMetValIleLeuGluIleThrHisLysGluHisThrArgLeuGly 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACAACCTGTAATACTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ....LeuGluLysThrMetAlaHisAlaArgSerLeuLeuLysProGlyG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTTTGCCAGTTGATTTACGTCAC...CGTGCACTTCTGCAACATAATG 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euAspIleArgArgSerProAlaGluGlnGlyPheGluPro...HisAla 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......GCTGCAGTACAAAATGGAAT 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....CGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ThrGlyGlyAlaThrLysTyrValLeuAlaThrProGlnLeu 1462
                                                                          Quality:
                                                         Ratio:
                                   86.50
0.588
43.363
                                     Gaps:
Percent Identity:
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14
17.994
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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671 nTrpGlyGluGluSerSerGlySerSerProArgProGlyGlnPheSerV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 AGGACATGTTTATGTGAAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                         836 lGluProLysValGluAsnLysProThrSerSerGluLeuGln.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA 486
GAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAAC
                                                                                                                                 ValLysLysAlaGlyIleGluValGlnGluIleLysAlaGluAlaValVa
                                                                                                                                                                              ....CAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTT..
                                                                                                                                                                                                                            hr {\tt AsnThrValTrpLysPheThrLeuThrGluLysMetGluHisArgSer}
                                                                                                                                                                                                                                                                        .....AAATATGCGGATCGATCACAGCTTTTCTATCAATGC
                                                                                                                                                                                                                                                                                                                         sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT
                                                                                                                                                                                                                                                                                                                                                                   AGATTTAATGGCTGGCCAAGAAGCTCACGTATAC........
                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGATGTGCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ValMetAsnPheSerSerGlyGluIleIleAspValPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AspGlnGluProValGlnGlyPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....GlyPheLeuPheAlaValAsnGlyLysProTyrPheGly..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: R06427
                                                                                        .... CGACCACAATGTTCAGAACCACAAGGATTCG
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879
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	980 CAGTTGATTTACGTC 994	
884	68 1.ValLeuIleThrThrLeuLeuValIleProValLeuValLeuLeuAla	
979	GATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGC	
929 868	880 CTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGT :::::: ::::::::::::::::::::::::	
851	Lys	
879	830 GAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAA	
850		
829	AATGTTCAGAACCACAAGGATTCG	
ũ	20 ValLysLysAlaGlyIleGluValGlnGluIleLysAlaGluAlaValVa	
798	.CAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTT	
819	AsnThrValTrpLysPheThrLeuThrGluLysMetGluHisArgSer	
756	AAATATGCGGATCGATCACAGCTTTTCTATCAATGC	
803	eGlyAspAlaHisT	
720	ATTTAATGGCTGGCCAAGAAGCTCACGTATAC	
786	roHi	
686	TATTTGCTAAATAATTTGGAATATCCAAC	
775	763ValMetAsnPheSerSerGlyGluIleIleAspValPhe	
636	GATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT	
762	ValGlnGlyPhe	
586	CTTTCTGCGCGGTTGTCCATT	
754	742GlyPheLeuPheAlaValAsnGlyLysProTyrPheGly	
536	CAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA	
741	ro	
486	AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA	
738	gGluIleLysHisAlaSerPheGlyArgAsnValPheAlaIleS	
436	TGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC	
721		
386	ATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAAC	
704	OHisSerLeuAlaLeuValProHisLeuAspGlnLeuCysValAla	
339	ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT	
889	lyGluGluSerSerGlySerSerProArgProGlyGlnPheSerV	
297		
671	nSerArgIleValGlnPheSerProSerGlyLysPheValThrGl	
296	GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC	
655		
246	197 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC	

885 IleValMetPheIle 889

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alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: A_Geneseq_36:W13009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-323-427-3 x W13009
                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
DE19531033-A1.
27-FEB-1997.
23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods are as a therapeutic to deliver agents, e.g. other Ab or toxins, to target cells. The Ab provides rapid and reliable detection of metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, useful for diagnosis and treatment of carcinoma micrometastases claim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab)
                                                                                                                                     349
                                                                                                                                                                          163
                                                                                                                                                                                                                332
                                                                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                        315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W13009 standard; protein; 560 AA.
                                                                                                                                                                                                                                                                                                                                                           299 LeuAspPheSerValIleValAlaAsnLysAlaAlaPheHisAspSerIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1997
                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                    43
TTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity:
                                                          nIleIleGlyAsnPheGlnAlaPheAspGluAspThrGlyLeuProAlaH
                                                                                                                                 SerGluSerMetAsp.....
                                                                                                                                                                      AAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCA
                                                                                                                                                                                                          snValLysGluGlyIleHisPheLysSerSerValIleSerIleTyrVal
                                                                                                                                                                                                                                             ATGCATTCGAAGGA.....CATGTTTATGTG 162
                                                                                                                                                                                                                                                                                  eArgSerLysTyrLysProThrProIleProIleLysValLysValLysA
                                                                                                                                                                                                                                                                                                                        T.....GAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTA 136
                                                                                                                                                                                                                                                                                                                                                                                              TTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAAT
                                                                                              AGTTGCCGGAATTTCACTTCCATTTGATTCATGCAAT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                      to: W13009 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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0.822
51.232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                   .ArgSerSerLysGly.....Gl
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                                                                                                                                                                                                                                                                                                                                                                                                                                      560
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12
25.616
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alignment_block: US-09-323-427-3 x R20026

Percent Similarity:

Align seg 1/1

to: R20026

from: 1

to: 973

alignment_scores:

Quality: Ratio:

85.00 0.582 43.976

Gaps: 14
Percent Identity: 18.072

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seq_documentation_block:
ID R20026 standard; Protein; 973
                                                                                                                                                                                                                                                                                                                                                                                            seq_name: A_Geneseq_36:R20026
                                                                                                                                                                                                                                                                                                                                                                                                                       493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409
                                                                                                                                              N-PSDB; Q20198. cDNA sequence - coding for peptide C terminal amidation enzyme obtd. from horse.
                                                                                                                                                                                  14-MAR-1990; JP-063306.
(SHIS ) SHISEIDO KK.
WPI; 92-012701/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426
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                                                                                                                                                                                                                      22-NOV-1991.
14-MAR-1990;
                                                                                                                                                                                                                                                                                                                       C-terminal amidation enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                              532 CATAAATGG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 IleAsnAspAsnCysProThrLeuIleGluProValGlnThrIleCysHi
                                                                                                                                                                                                                                               J03262484-A.
                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                            Equus caballus.
                                                                                                                                                                                                                                                                                                          Horse
                                                                                                                                                                                                                                                                                                                                   08-APR-1992
                                                                                                                                                                                                                                                                                                                                               R20026;
                                                                                                                                                                                                                                                                                                                                                                                                                     GluLysTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snSerGlyProPheSerPheSerValIleAspLysProProGlyMetAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCA.....GTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sAspAlaGluTyrValAsnValThrAlaGluAspLeuAspGlyHisProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.....TATGAAATTTTGGATGGTGGACCAA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG...CCAGTATGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spTyrProArgLysThrIleThrGlyThrValLeuIleAsnValGluAsp 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AT.....AAAACAGTTAGTGCACAG.....ATTGAGGTATCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gTyrValGlnAsnGlyThrTyrThrValLysIleValAlaIleSerGluA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTT....GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt SerValThrSerGluIleLysLeuAlaLysLeuProAspPheGluSerAr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ... GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isAlaArgTyrValLysLeuGluAspArgAspAsnTrpIleSerValAsp 392
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                      063306
                                                                                                                                                                                                                                                                                                                                                                                                                       495
                                                                                                                                                                                                                                                                      829.
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                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                          deleted in R20027 and R20028"
                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                             of
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950	GCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCT	904
855	:::::: lnLysMetGlnGluLysGlnLysLeu	839
903	CCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT	857
839	uA	827
856	GTTCAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAG	807
827	sAlaGlyIleGluValGlnGluIleLy	815
806	CCATTAAAGAACCAAATAGCGAATGTGTTCGACCACA	757
814	rpLysPheThrSerThrGluArgValGluHisArg	799
756	AAATATGCGGATCGATCACAGCTTTTCTATCAATGC	721
799	::::::: luAspGlyThrValTyrValGlyAspAlaHisT	782
720	ATTTAATGGCTGGCCAAGAAGCTCACGTATAC	687
782	LysProValArgLysHisPheAspMetProHi	772
686	ATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTTGGAATATCCAAC	637
771	rSerGlyGluIleIleAspValPhe	759
636	CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAAATTCTAAATGCT	587
758	ysProValGlnGlyPhe	751
586	ATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT	537
750	GlyLeuPheAlaValAsnGlyLysProTyrPheGly	738
536	TCAATTTGCTATCATTAGTCAGCCAGTTTATCATAA	487
737		734
486	AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA	437
734	 	717
436	AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC	387
386 717	GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAAC	340 701
700	isSerLeuAlaLeuValProHisLeuGlyGlnLeuCysValAla	684
339	ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT	298
684	lyGluGluSerSerGluSerAsnProLysProGlyGlnPheArgV	667
297	Α	297
667	AsnSerArgIleValGlnPheSerProThrGlyArgPheIleThrGl	652
296	TGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTTGTAACAAC	247
651	Cys	651
246	ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC	197
650	::::: ::: 	642
196	AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG	147
641	CysGlnProThrAspValAlaValAspProAsnThr	630
146	TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA	9/

- ||||||| ::: ::: ||| |||||||:::||| 856 ||IeLysGluProGlySerGlyValProVal.ValLeuIleThrThrLeuL 872

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128.39

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database sequences: 133990
Database length: 13297546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM of: US-09-323-427-3 to: Issued_Patents_AA:*
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/cgn2_6/ptodata/1/1aa/6_COMB.pep:US-08-477-459-20 + 78.50 128.39 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database:
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/cgn2_6/ptodata/1/iaa/5B_COMB.
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-COOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-XGAPEXT=0.500 -DELEXT=7.000 -START=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .pep:US-08-325-071-65 +
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\(^3 + 81.50 110.13

\(^3 + 81.00 134.36

\(^3 + 81.00 122.48

\(^7 + 81.00 122.48

\(^7 + 80.50 132.59 0.8)

\(^4 80.50 132.59 0.8)

\(^4 80.00 126.53 1.2)

\(^7 + 79.00 126.08 1.4)

\(^7 + 79.00 126.08 1.4)

\(^7 + 79.00 126.08 1.4)

\(^7 + 79.00 126.08 1.4)

\(^7 + 79.00 126.08 1.4)

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\(^7 + 79.00 126.08 1.4)
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132.48 0.7161
122.48 1.25
22.48 1.25
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22.65 0.7643
12.65 0.8441
12.59 0.8464
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                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                           97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10532
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alignment_block:
US-09-323-427-3 x US-07-707-367-2
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 Align seg 1/1 to: US-07-707-367-2
                                                                                                                                                                                                                                                                                                 TELEFAX: (919)541-868 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/
FILING DATE: 19910530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 141
FILING DATE: 01-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 329911/90 FILING DATE: 30-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 210535/90 FILING DATE: 10-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                              AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/07707367
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Kawahara, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kangawa, Kenj
                                                                                                                                                                                                                                                                                                                     (919)541-8689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimoi, Hiroko
Suzuki, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
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                                                                                     Length: 391
Gaps: 18
Percent Identity: 19.437
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to: 935
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GCA.....GAACCGGAGAATATCATT...GATGTACGAAC
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                                                                                                                                                             rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV
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seq_documentation_block:
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                     APPLICATION NUMBER: JP 2-205475
FILING DATE: 02-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
                                                                                                                                                                                                       FILING DATE: 15-AUG-1989
PRIOR APPLICATION UDBER: JP 1-18193:
FILING DATE: 31-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-76331
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: PATELICATION NUMBER: US/08/070,30: FILING DATE: 24-MAY-1991 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING NUMBER OF SEQUENCES: 21
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APPLICANT:
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                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 1-209687 FILING DATE: 15-AUG-1989
                                                                                                                               FILING DATE:
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
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5. 5871995
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Player, Willic
RATION NUMBER:
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YANAGI, Mitsuo
OKAMOTO, Hiroshi
KISHIMOTO, Jiro
IFUKU, Ohji
KATO, Ichiro
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KAMINUMA, Toshihiko
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                                                                                                                                                JP 2-106412
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alignment_block:
US-09-323-427-3 x US-08-070-301-16
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 989 amino acids
                                                                                                                                                                                                                                                                                                    431
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ORIGINAL SOURCE:
ORGANISM: Fro
                                                                    762
                                                                                                                                                               751
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
                     581 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 630
                                                                                                             531 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG 580
                                                                                                                                                                                                                                                  744 laValSerTyrAlaPro.....Gly 750
                                                                                                                                                                                                                                                                                                                                                                                       384 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                    713 AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA.... 291
                                                                                                                                                                                                                                                                                               AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 480
                                                                                                                                                                                                                                                                                                                                              uPheValLys...GlnTleLysHisGlnGluPheGlyArgGluValPheA 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 696
                                                                rGly......AspSerThrProValGlnGlyPhe.....
                                                                                                                                                        Gly......ValLeuTyrAlaValAsnGlyLysProTyrTy 762
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linear
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Gaps:
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alignment_block:
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                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-477-451-8 from: 1 to: 3200
                                                                                                                                                                                                                                                                                            US-09-323-427-3/rev x US-08-477-451-8
                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8,
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                         1050 ATTTTGTACTGCAGCAAGTAT......TACAGGTTGTCCATTATGTT 1010
                                                                                                                             1009 GCAGAAGTGCACGGTGACGTAAATCAACTGGCAAAGCTTGATTATCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 510-601-2708
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Covacci, TITLE OF INVENTION:
                                          959 CTAATTTCAAGGGTGTTGATATC.....AGTTCGTACATCAATGATATT 916
                                                                                  761 sLysThrCys......PheSerPheTyrArgLeuIleGluIleV 774
                                                                                                                                                                     745 IleValPheCysArgIlePheGluLeuValTyrArgLeuLeuIleAlaLy 761
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CORRESPONDENCE ADDRESS:
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774 alAsnPheLeuSerGlnPheLeuIleProLysProTyrLeuThrGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
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0.603
43.360
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Helicobacter Pylori Cagi Region
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Gaps: 20
Percent Identity: 22.764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        857 IleIleValIleGluIleSerLysPheCysIleGlnLeuPheLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           828 LeuSerValAsnGlyPhePheLysAlaSerCysLeuProCysPheLeuPh 844
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                                                 AAATTGATTGTTATTGAAGTTGGTCCACATTCAAT...TTCTGGCTCACC
                                                                                                                                                              CATAAAGACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrArgLeu.............IleGluIleIleAsnPheIleArg..
eIleGln..
                                                                                                                                                                                                                                                                         AATTCCGGCAACTTGACGTCCACCTTCATCATTACGGCAACCTTCTTGAT 176
                                                                                                                                                                                                                                                                                                                             heLysValAlaPheCysLeuArgTyrLeuAlaGluIle......
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                                                                                                                                                                                                            .....LeuIlePheAlaIlePheGluPh 989
                                                                                                                                                                                                                                                                                                                                                                                         GGATTCAGAGATCGTGTACGCGCAACATTGCATGAATCAAATGGAAGTGA
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                                                                                                          SerCysIleL
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alignment_block:
US-09-323-427-3 x US-07-906-349A-6
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Quality:
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                                                                                                                                                                                                       Align seg 1/1 to: US-07-906-349A-6
                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/07906349A Patent No. 5434064
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Skolnik, APPLICANT: Margolis, TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                    573 ThrThrAlaAlaAlaThrCysAlaCysThrGlyCysThrGlyCysThrCy
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PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/643,237
FILING DATE: 18-JAN-1991
TELECOMMUNICATION INFORMATION:
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589 sCysThrCysThrThrCysCysCysThrCysCysThrThr....
                                                                                866 CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG 915
                                                                                                                                                                 816 ACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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916 AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 965
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CORRESPONDENCE ADDRESS:
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ZIP: 20004
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Skolnik, Edward Y.
Margolis, Benjamin L.
MARGOLIS, Benjamin L.
NVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR NVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARN
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linear
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3.000
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; NAME/KEY:
; NAME/KEY:
US-08-415-751-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION UNMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Hana Dolezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 324-167
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CURRENT APPLICATION DATA:
APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE APPLICATION NOTICE
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ORIGINAL SOURCE:
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/415,751
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   Quality:
Ratio:
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NELSON, RICHARD, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette - 3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1995
N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRYPTOSPORIDIUM ANTIBODIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLYPEPTIDES BINDING ANTI-
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Suite 6
Length:
Gaps:
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alignment_block:
US-09-323-427-3 x US-08-415-751-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/08325071 Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: COBON,
APPLICANT: MOORE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1080 AATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCA 1129
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 n 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 .....TyrGly......CysCysCysCysCys***LeuTrpTyrAs 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 euPheTrpCysCysCysCysCysLeuAsnTrpThrLeuTrpTrp... 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 uCysCysCysGlyCysCysSerLysIleTrpAspAsnCysCysCysSerL 130
                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  APPLICANT: RIDING, George Alfred APPLICANT: RADD, Keith No. 5587311man TITLE OF INVENTION: DNA Encoding A Ce. TITLE OF INVENTION: Glycoprotein Of A
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           808 TGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGC 857
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   978 GCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACA.... 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         928 GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         884 GTTTACTCAAGAAAAGAT.....CTGCAGAACCGGAGAATATCATTGAT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            761 TCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCAC...AA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 *****LeuGlnPhe.AspLeuCysValLeu*******Trp***ArgLe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 lnThrIle***HisLeuLysAsnArgCysLysTyrGlnSerThrHisHis 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 yMetArgAsn***ProHisArgGluLeuLeuHisGluLeuValValLysG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 SerAsnLeuLeuGlnHisSerArgArgHisPhePheGluArgLeuGl 36
                                                                                                   STREET: 3000
GTTTY: Washington,
                                                                                                COUNTRY:
                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGluSerGlnIleAspPheLysLeuGlnAsnArgLeu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....LeuValGlu*****LeuGlnLeuArgLeuValValLeuLeu* 97
                                                                              20007-5109
                                                                                                                             E: Foley & Lardner 3000 K Street, N.W. ashington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                               COBON, Stewart Gary
MOORE, Joanna Terry
JOHNSON, Law Anthony York
                                                                                                                                                                                                                                                                                                                                                WILLADSEN, Peter
KEMP, David Harold
SRISKANTHA, Alagacone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.669
                                                                                                                                                                                                                             WAN Encoding A Cell Membrane Glycoprotein Of A Tick Gut 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 25.828
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alignment_scores:
Quality:
Ratio:
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US-09-323-427-3 x US-08-325-071-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-325-071-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-325-071-67 from: 1 to: 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: AU PH9196
FILING DATE: 27 NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 6004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS: LENGTH: 650 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
                                       294 ......TTCG 312
                                                                                                                                       261 ACGATCTCTGAATCCACGTGGTATTTTTGTAAC.........
                                                                                                                                                                                           173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI2570
FILING DATE: 19-UN-1987
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
200 yProAspGlyGlnCysLysAsnAlaCysArgThrLysGluAlaGlyPheV 217
                                                                                           187 ProProAlaAspSer......TyrCysSerProGlySerProLysGl 200
                                                                                                                                                                                                                                          211 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 260
                                                                                                                                                                                                                                                                                   163 sGluLysAsnLeuLeuGlnArgAsp......serA 173
                                                                                                                                                                                                                                                                                                                                  161 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 210
                                                                                                                                                                                                                                                                                                                                                                               147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163
                                                                                                                                                                                                                                                                                                                                                                                                                                138 TGCATTCGAAGGACATGT......TTATG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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TELEX: 904136
                                                                                                                                                                                   rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 186
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0.612
40.947
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Percent Identity: 21.727
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                                                                                                                                            293
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363 CTTTTTACATGGANGCTGATNAANACAGTTAGTGCACAGATTG 23 SPTOSETGLYSETTLYVALAGLUASPGLYLLETHICYSLYSSETILES 290 404 AGGTATCTGANATCACAACTGCTTTTCAAACTTCAATTGCTCCGATG 450 250 eTTYTTHYVALSETCYSTHTVALGLUGLUTYSGLITHICYSLYSETILES 290 251 CCAGTATGCCGTTATGAAATTTTGCATGCTGGACCACGG 491 252 CCAGTATGCCTTATGAAATTTTGCATGCTGGACCACGG 491 253 CCAGTATGCCTTATGAAATTTTGCATGCTGGACCACGG 491 264 CCAGTATGCCTTATGATACTTTCTCACAGTTCATACTTACATACTGA 541 275 CTACACCAGTTCAAATTTGCTTACATTCTTCACAGAGTTGATCATACTGA 541 276 TCAACCAGTTCAAATTTGCTATACTTTCTCGCGCGGTTGTCCATTCCTGC 591 277 TCAACCAGTTCTAAATTTCCTATACTTTCTCGCGCGGTTGTCCATTCCTGC 591 283 nGLnAACGGTGATACTGTTCAAAATTCGAAATTCGAATGGAT 643 290 hCCyS1leSerAsgCySullyValTyrMeLASAATTCGAAATTCGAATGGAT 643 290 hCCyS1leSerAsgCySullyValTyrMeLASAATTCTAAATGCTGATGGAT 643 290 hCCyS1leSerAsgCySullyValTyrMeLASAATTCTAAATTGCTGATGGAT 643 291 TTTGTCGATGATGATTTTCTTCTAAATTCTTAAATTCTTAAAATTCTTAAATTCGAAATTTCGAAATTCTTAAATTCGAAATTTCGAAATTTGCTAAATTCTAAATTTTGGAAATTTCTAAAATTTCGAAATTTCGAAATTTGCAAATTACCAAATACGATTTAATGGCTTGCAAATTCACAATTTACCAAATACAGTTTTTCTATCAAATACTCTCAAATTTACCAATACAAATTACGAAATTCACACTTAAATTACCAATAAATTACGAAATTACCAAATAAGCAAGATTTAATGGAATGTTCAAATACAATTACGAAATTACCAAATACAGTTTTCTATTCAAATTCAAACCTGCTGCAAAACCACAAAGCATTTAACTAAAATACAATTACGAAATACAAGTTGTTCTATCAAATACGCAAAAACCTGCCAAAAACCTGCACAAAACCACAAAGATTTAACGAATTAACCACAAAACCTGCTTCAAATTAACAATACAAGTTGTTCAAATACAAATACAAGTTGTTCAAATACAAATACAAGTTGTTCAAATACAAATACAAGTTGTTCAAATACAAATACAAGTTGTTCAAATACAAAAAAGATCTGCAAAACCACAAAACCACAAAGATTTACAAAAAAAGATCTGCAAAACCACAAAACCTGCAAAACCACAAAACCACAAAGATTACAAATACAAGTTGATAAAATACAAGTTGTACAAAAAAAGATCTGCAAAACCACAAAACCACAAAGATTACAAATACAACCTTTTCTATCAAATACAAAAAAAA	ם	<pre>seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-6</pre>
CTTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG SPIOSETGLYSETThrValalaGluAspGlylleThrCysLysSerIleS AGGTATCTGAAAATCACAACTCCTTTTCAACTCAAATTGTCCCGATG		51 yGlnAsnLysCysValLysValAsp 45
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG SPIOSETGLYSETThrValaGluaAspGly1leThrCysLySSET1leS AGGTATCTGAAATCACAAACTGCTTTTCAAACTCAAATTGTCCGATG :		63 TGATAATCAAGCTTTGCCAGTTGAT
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	5	35 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysG
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	962	13 GAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCG
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG		18 etTyrProLysLeuLeuIleLysLysAsnSerAlaThrGluI]
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG		TTACTCAAGAAAGATCTGCA
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG		lLeuArgLysLeuGlnAlaCysGluHisProIleGlyGluTrpCysMe
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG ::::::::::::::::::::::::::::::::::::	885	ACTTCGTACTTCGT
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	401	87IleLysAlaArgLeuIleAlaGluLysProLeuSerLysTyrV
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	878	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGC
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG ::::::::::::::::::::::::::::::::::::	386	5 alPheLysValGluIleLeuAsnCysThrGlnAsp
CTITTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG :::	N	AACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCAC
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG ::::::::::::::::::::::::::::::::::::	(4)	60 uAspArgValLeuGluAlaIleArgThrSerIleGl
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	~J	29 GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAÇC
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG SPTOSETGLYSETThrVallaGGUASpGLYIleThrCysLysSerIleS AGGTATCTGAAATCACAACTGCTTTTCAAACTTGTCCCGATG	σn	51 PheAspSerAspHisCysLysArgTyrG
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG ::::::::::::::::::::::::::::::::::::	728	79
CTTTTACATGGAAGCTGATAAACAGTTAGTGCACAGATTG :::		34 ysLeuLeuAsnGluTyrTyrTyrThrValSo
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	678	44 GTGCTCTTGATAAATATTTTGCTAAAT
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG :::	334	::: pLysSerArgLysProGlyProAsnVal
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG :::	643	07AACGGTGATACTGTGGA
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CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG :::	0	92 TTTGTCGATGATGGT
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG ::: SPIOSETGLYSETThrVallaGluAspGlyIleThrCysLysSerIleS AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG :: ::	(4)	90 hrCysIleSerAspCysValAspLysLysCysHisGluG
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	591	42 CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTG
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG :::		83
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG		
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG		67
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	491	51 CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCG
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG		50
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG ::: ::: ::! : sProSerGlySerThrValAlaGluAspGlyIleThrCysLysSerIleS	_	AGGTATCT
CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG		sProSerG
		ç
313 TTTCATCATTATTGTTACCAAAGTTGATCGTGCATATGGAGTACAATG 362		313 TTTCATCCATTATTGTTACCAAAAGTTGATCGACTACAATATCGACTACAATATGTACCAAAAGTTGATCGACTACAATATCGACTACAATATGTACATATATAT

seq_documentation_block:
 Sequence 61, Application US/08325071
 Patent No. 5587311

alignment_block: US-09-323-427-3 x US-08-325-071-61 alignment_scores: Quality: Ratio:

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AATGTGTTCGACCACAATGTTCAGAACCACAAGGAT ::: :: ::::: !uilebeuAsnCysThrGlnAsp	77 29
GGATCGATCACAGCTTTTCTATCAATGCC	,729 279
9 TATCCAACAGATTTAATGGCTGGCC ::: :: 0 PheAspSerAsp	67 27
4 GTGCTCTTGATAAATATTTTGCTAAAT ::::: 3 ysLeuLeuAsnGluTyrTyrTyrThrVa	64 25
AACGGTGATACTGTGGAAATTC	607 239
2 TTTGTCGATGATGGT ::: PheMetAspCysGlyValTyrMeta	59 22
CATGCGATTCTGAAACCGTTGATACTTTCTGCGCG	5 4 2 209
TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTT/:	492 202
.51 CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGG 491 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	451 186
4 AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTC ::	404 169
3 C	36 15
TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATAT 	313 136
yProAspGlyGlnCysIleAsnAlaCysLysMetLysGlu	297 119
1 ACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC :::::: ::::: f ProProAlaAspSerTyrCysSerProGlySerPr	26 10
CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCG	211 92
61 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTTGGACGT 210 ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	161 82
8 TGCATTCGA ::: 6 CysValPro	6

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913
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                                                                              APPLICATION NUMBER: AU PI
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/i
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RIDING, George Älfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Ceil Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    963 TGATAATCAAGCTTTGCCAGTTGAT 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 370
                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
FELECOMMUNICATION
                  NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                          APPLICATION NUMBER: AU PFILING DATE: 16-OCT-1987
                                                                                                                                                                         APPLICATION NUMBER: AU PI2570 FILING DATE: 19-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/325,071 FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/242,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  etTyrProLysLeuLeuIleLysLysAsnSerAlaThrGluIleGluGlu 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lLeuArgLysLeuGlnAlaCysGluHisProIleGlyGluTrpCysMetM 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Foley & Lardner 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOORE, Joanna Terry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRISKANTHA, Alagacone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEMP, David Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1993
INFORMATION:
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                                                                                                                                                                                                                                                                   AU PI4912
                                                                                                                                AU PH9196
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                    60042/111 BIAU
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alignment_block: us-09-323-427-3 \times us-08-325-071-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-325-071-63
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TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 63
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-325-071-63 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
                                                                                                                                                                                                                                                 542 CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC 591
                                                                                                                                                                                                                                                                                                283 nGln.........HisLeuValGlyAsp......T
                                                                                                                                                                                                                                                                                                                                                   492 TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 541
                                                                                                                                                                                                                                                                                                                                                                                                 267 GluAspCysArgValHisLysGlyThrValLeuCysGluCysProTrpAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 erHisThrValSerCysThrAlaGluGlnLysGlnThrCysArgProThr 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 alCysGluHisGlyCys.ArgSerThrAlaLysAlaTyrGluCysThrCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 sGluLysAsnLeuLeuGlnArgAsp......SerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 TGCATTCGAAGGACATGT.....TTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 sProArgGlyPheThrValAlaGluAspGlyIleThrCysLysSerIleS
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                                                                                                                                                  TTTGTCGATGATGGT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGTATGCCGTTATGAA.....ATTTTGGATGGTGGACCAACCGG 491
pLysSerArgLysProGlyProAsnVal.....AsnIleAsnGlyC
                                                                                            PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 320
                                                                                                                                                                                              hrCysIleSerAspCysValAspLysLysCys......HisGluGlu 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG
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                                           .....AACGGTGATACTGTGGAAATTCTAAATGCTGATGGAT 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTC...CCGATG
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0.614
40.390
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Gaps: 22
Percent Identity: 22.284
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  334
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Applic Patent No. 5744350
                                                                                                                                                                                           COUNTRY: USA
ZIP: 07065-0907
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                        ATTORNEY/AGENT INFORMATION:
NAME: CARTY CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT: CONDER, MICHAEL
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TELECOMMUNICATION INFORMATION:
                                                                                                                     APPLICATION NUMBER: US/08/450,332 FILING DATE: 25-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 126 I
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CHRISTINE E. CANAL
STREET: 126 E. LINCOLN AVENUE, P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysLeuLeuAsnGluTyrTyrTyrThrValSerPheThrProAsnIleSer 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yGlnAsnLysCysValLysValAsp 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....IleLysAlaArgLeuIleAlaGluLysProLeuSerAsnHisVa 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08450332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONDER, MICHAEL J. MCADA, PHYLLIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REEVES, CHRISTOPHER D. DAVIS, CHARLES R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA ENCODING TRIOL POLYKETIDE SYNTHASE
                        19076CA
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; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: TPKS Protei
US-08-450-332-2
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US-09-323-427-3 x US-08-450-332-2
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Percent Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3038 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1217 SerGlyCysGluLysValAlaPheAsnThrIleAsnThrTyrAspLysGl 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1175 ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro..... 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1263 ProProAspAlaSerThrAspHisAlaMetPheAlaArgTrpSerTrpGl 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1247 ..GlnThrThrLeuPheGlnValGluAsnIleThrPheLysProPheSer 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1233 yAspTyrLeuSerGlyAspIleValValPheAspAlaGlu..... 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1200 isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu 1216
1341 ....GlnValLeuAlaSerAlaLysGluGlyArg...
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1279 yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA 1296
                                                                                                                                                                                                                                                                                      370 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 419
                                                                                                                                                                                                                                                                                                                                                                                                     335 AAGTTGATCGT......GCATATCGAGTACAATGCTTTTAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 CAATA..... 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT.....GGACCAACTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                        GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT 510
                                                                                                                                                                    AACTGCT.....TTTCAAACTCAAATTGTCCCGATGCCAGTATGCC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT.. 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTT...CCATTTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTTATGTGAAAAGGT......CTTTATGATCAAGAAGGTTGCCGTA 193
                                                                                                                                                                                                                             Ile.....ArgSerPheLeuSerGlnLeuThrLeuGluGluArgGl 1326
                                                                                                                                                                                                                                                                                                                                               laGlnAspLysGluAlaIleProIleIleGluArgIleValTyrPheTyr 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....ACAATCAATTTAATACACGTAATGCATTCGAAGGACA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3038 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss: single
linear
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38.347
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Gaps: 24
Percent Identity: 19.703
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seq_documentation_block:
    Sequence 2, Application US/08637640
    Patent No. 5849541
                                                                                                                         seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-637-640-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT..... 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 560
                                                                                                                                                                                                                                                      CTGCATGTCACCATTT 1071
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                                                                                                                                                                                                                                                                                                                                                                         ......GCTGCAGTACAAAATGGAAT 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                           lyGlnMetValIleLeuGluIleThrHisLysGluHisThrArgLeuGly 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACAACCTGTAATACTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....LeuGluLysThrMetAlaHisAlaArgSerLeuLeuLysProGlyG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTTTGCCAGTTGATTTACGTCAC...CGTGCACTTCTGCAACATAATG 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCA 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG 832
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alignment_block:
US-09-323-427-3 x US-08-637-640-2
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                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATCONTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,640
FILING DATE: 23-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: VINCI, VICTOR A.
APPLICANT: CONDER, MICHAEL
APPLICANT: MCADA, PHYLLIS C
APPLICANT: REEVES, CHRISTOP
                                                                                                                 1188
                                                                                                                                                                                         1175 ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro..... 1187
                                        1200 isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/148,132

FILING DATE: 01-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: CARTY, CHRISTINE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: YOURGE: ORIGINAL SOURCE: ORGANISM: TPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 908-594-6734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                              66 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT.....GGACCAACTT 109
                                                                                                                                                                                                                              16 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA
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STREET: P.O. BOX 2000; 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: N.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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ZIP: 07065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
.....ACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 152
                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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MCADA, PHYLLIS C.
REEVES, CHRISTOPHER D.
DAVIS, CHARLES R.
HENDRICKSON, LEE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3038 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPKS Protein
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0.481
38.347
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Percent Identity: 19.703
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1479	GlyPheAsnSerTyrThrTyrThrAspIleSerThrGlyPhePheGluGl	1463
882		882
882 1462	CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGGCAACTT	833 1449
4	GlyAla	1446
832	GTTCGACCACAATGTTCAGAACCACAAGGATTCGG	783
782 1445	CGATCACGCTTCTATCAATGCCAGATCAGTATTACCATTAAAAGAACC ::::::::::::::::::::::::::::::	733 1442
4-	uLeuValAlaGlnIleAlaHisArgTyrGlnSerMe	1426
32	NATATGCGGA	683
682 1426	TGATAAATATTTGCTAAATAATTTGGAATATC	651 1409
1409	aAAATTCTAAATGCTGATGGATGTGCTCT ::::: :::	1394
ıω	HisValArgLeuValGlnArgValGlyGlnHisLeuLeuProThrVal	1377
603		603
603 1377	TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT :::	561 1360
1360	pGluAs	1351
560	SACATGCGATTCTGAAACCGT	511
510 1350	GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT ::::::	461 1341
1340	GInAlaAlaPheHisLeuGlnLysGlnTleGluTrpLeuGlu	1326
460	TTTCAAACTCAAATTGTCCCGATGCCAGTATGCC	420
419 1326	ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC::::::::::	370 1313
369 1312	AAGTTGATCGTGCATATCGAGTACAATGCTTTTAC ::	335 1296
33 4 1296	GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCA :::: yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA	289 1279
288 1279	TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT : : : : : : : : : : : : : : :	241 1263
240 1262	GAT ::: Ser	194 1247
193 1246	TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTA	153 1233
1233	$\verb alAlaPheAsnThrIleAsnThrTyrAspLysGl $	1217

882 1496 921 1511 971 1018 1018 1018 1055 1558 1575 2 2

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; LENGTH: 1226 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-540-804-12
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US-09-323-427-3 x US-08-540-804-12
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Ratio: 0.457
Percent Similarity: 47.949
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560 eIleTyrLysLysValLeuLysGluLysAspValProAlaTyrAsnValT 577
                                                                                                                     545
                                                                                                                                                                     521 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA.. 565
                                                                                                                                                                                                                                    528 luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe 544
                                                                                                                                                                                                                                                                                          504 ATTTGCTA.....TCATTGGTC 520
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                                                      ......CTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGA 602
                                                                                                                  SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh
                                                                                                                                                                                                                                                                                                                                                                                                             GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 503
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Gaps: 13
Percent Identity: 19.744
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	BER: W
	; NAME: Grananan, Patricia ; REGISTRATION NUMBER: 32,227
	EY/AGENT INFORMATION
	BER:
	ICATION DATA:
	SYSTEM: PC-DOS/MS-DOS
	IBM:
	DABLE
	; COUNTRY: US ; ZIP: 02173
	: MA
	Militia Drive ton
	RESSEE: Hamilton, Bro
	35
y sene Thereof	NO. 392238381 Factors which Modified Transcription and Methods of Use
,	aig M.
	CANT: Young, Richa
	TOFORMATION:
	ion_b Appl
2	seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-218-265-1
	727 euGluTyrIleIleArgLeu 733
	TAGCGATGAT
727	ValLeuGly
956	920TCATTGATGTACGAACTGATATCAACACCCCTTGAAAT
710	694 SerIlePheLeuLysArgLysAspPheThrAsnLysAsnLeuIleGlnLe
919	
693	677 snValMetLeuLeuIleAlaThrAsnLeuLysGluTyrIleLysPheMet
	*** COMMON TOTAL TERMINATION TO CONCOUNT TO CONTROL TO
877	GGAGCTGTTAAAACAGGTGGTGCCGCAGCA
677	660 rGluIleIleAspThrAsnThrSerLysGlnPheGlnLysAlaArgAsnA
827	812CAGAACCACAAGGATT
660	644 AsnPheProGluValPheGlnValAsnIleArgPheLeuLeuHisAsnSe
811	Ā
643	leAsnAsnSerAsnGl
784	GCCAGATCAGTATTACCATTAAAGAA
627	610 pGluLysLeuLysThrGluLysLeuLysAsnAspLysSerGluValLeuL
752	CTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATC
610	594 LeuLysValAspAsnAspLeuArgIleGluLeuGlnSerValTyrAsnAs
702	atttgctaaataatttggaatatccaacagatt
593	577 hrSerPheMetProPheTrpLysPhePheMetLysAsnPheProPheVal
652	

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alignment_block:
US-09-323-427-3 x US-08-218-265-12
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
     545
                                           521 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA..
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LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh
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                                                                                                                                                                                              ePheLysTrpIleGluPheIleValTyrHisGlnLeuLeuSerAspIleG
SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh
                                                                                              {\tt luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe}
                                                                                                                                           ATTTGCTA.....TCATTGGTC
                                                                                                                                                                                                                                                                                                                                                                                          euSerHisLeuCysSerGlyIleLeuSerSerValAsnArgThrValLeu 494
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5736139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS.
                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,604A
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   727
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FILING DATE:
                                                                                                                                                                                                 ZIP: 94104
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                       CITY: SAN FRANCISCO.
                                                                                                                                                                                                                                                                                              ADDRESSEE: MEDLEN & CARROLL, L
STREET: 220 MONTGOMERY STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGCGATGATAATCAAGCTT 976
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CLASSIFICATION:

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alignment_block:
US-09-323-427-3 x US-08-480-604A-6
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Percent Similarity:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/161,907
FILING DATE: U2-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/985,321
FILING DATE: 04-DEC-1992
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                                                                                                                                                                                                                                                                                                         679 TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC 728
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264 uAlaAlaAlaSerAspIleVal.....ArgLeuLeuAlaLeuLysA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/329,154
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APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027
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                           GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 878
                                                                                   GlnGluLeuLeuAsnIleTyrSerGlnGluLeuLeuAsnArgGlyAsnLe
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                                                                                                                              AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC
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seq_documentation_block:
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                                                                                                         TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
MOLECULE TYPE: protein
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                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDIEN & CARROLL, LI
STREET: 220 MONTGOMERY STREET,
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WILLIAMS, TITLE OF INVENTION: V
                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
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                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0' FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                        TOPOLOGY:
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                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                        'AGENT INFO.....
INGOLIA, DIANE E.
INGOLIA, 40,027
                                         amino acid
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                                                                                                                                                   (415) 705-8410
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                                                                                                                                 397-8338
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seq_documentation_block:
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                                                                                                                                                                                Patent No.
                                                                                                                                                           GENERAL INFORMATION:
                                                     APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                        APPLICANT:
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Ratio:
                                                                                                                                                                                5, Application US/08325071 5587311
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                                                                                           MOORE, Joanna Terry
JOHNSON, Law Anthony York
RIDING, George Alfred RAND, Keith No. 5587311man
                                      KEMP, David Harold
SRISKANTHA, Alagacone
                                                                          WILLADSEN, Peter
                                                                                                                                    COBON, Stewart Gary
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Gaps: 9
Percent Identity: 22.449
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alignment_block: US-09-323-427-3 \times US-08-325-071-65
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                                                                                                                                               Align seg 1/1 to: US-08-325-071-65 from: 1
                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-0UL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS: LENGTH: 620 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
APPLICATION NUMBER: AU P12570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 03
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DN
TITLE OF INVENTION: G1
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                     161 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 210
                                                                                                         138 TGCATTCGAAGGACATGT.....TTATG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
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NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-JUN-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
133 sGluLysAsnLeuLeuGlnArgAsp.....
                                                                      117 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 204136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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71	IleLysAlaArgLeuIleAlaGluLysProLeuSerLysTyrVa 37	57
78	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 87	129
56	alPheLysValGluIleLeuAsnCysThrGlnAsp 35	45
28	AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC 82	79
45	United to the control of the control	30
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78	GTGCTCTTGATAAATATTTGCTAAATAATTTGGAA 67	44
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290	PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 29	74
606	TTTGTCGATGATGGT	592
73	ysCysIleSerAspCysValAspLysLysCysHisGluGlu 27	960
91	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGC 59	142
60	nGln	253
41	TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 54	192
53	GluAspCysArgValGlnLysGlyThrValLeuCysGluCysProTrpAs 25	237
91	CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGG 49	51
36	:: :::	20
50	AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG 45	04
03	163 CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG 40	363 203
03	alCysLysHisGlyCys.ArgSerThrAspLysAlaTyrGluCysThrCy 20	.87
62	TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG 3	113
87	<pre>yProAspGlyGlnCysLysAsnAlaCysArgThrLysGluAlaGlyPheV</pre>	.70
312	AACAACTGTTGTCATTTCG 3:	294
70	:::::: ::: ProProAlaAspSerTyrCysSerProGlySerProLysGl 17	57
93	ACGATCTCTGAATCCACGTGGTATTTTTTGTAAC	61
56	::::::::::::::::::::::::::::::::::	43
0	CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 26	11

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405 GluAsnLeuCysAspSerLeuLeuLysAsnGlnGluAlaAlaTyrLysGl 421
963 TGATAATCAAGCTTTGCCAGTTGAT 987

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pir2:I57940
pir2:F71606
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-Q=/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.
-Q=/cgn2_1/USPTO_spool/US09323427/runat_14042000_170513_19903/app_query.fasta.
-DB=PIR_62 -QFMT=fastan -SUFFIX=backtrans.rpr -GAPOP=12.000
-GAPOXT=0.000 -MIMANTCH=0.100 -COOPCL=0.000 -LOOPEXT=0.000
-QGAPOXT=0.000 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -BELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER-US09323427 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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desmoglein 2 - human
probable integral membrane pro
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pir1:QXASRI
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cuticle protein cut-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C:Accession: A49772
R:Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
Dev. Biol. 146, 519-530, 1991
A;Title: cut-1 a Caenorhabditis elegans gene coding for a dauer-specific nor A:Reference number: A49772; MUID:91323673
A;Accession: A49772
A;Status: preliminary; not compared with conceptual translation
A:Accession: A49772
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A; Residues: 1-423 <SEB>
A; Cross-references: GB: M55997
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472 TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA
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    cuticlin 1 - Caenorhabditis elegans
    C;Species: Caenorhabditis elegans
    C;Date: 17-Apr-1993 #sequence_revision 17-Apr-199
    C;Accession: S27799
    R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
    submitted to the EMBL Data Library, July 1991
    A;Reference number: S27799
    A;Accession: S27799
    A;Accession: S27799
    A;Molecule type: DNA
                                                                                                                                                                                  seq_name: pir2:S27799
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alignment_block:
US-09-323-427-3 x S17855
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C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: oxidoreductase
F;131-342/Domain: peptidylglycine monooxygenase I homology <PGM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidylglycine monooxygenase (EC 1.14.17.3) - African clawed frog
N;Alternate names: peptidylhydroxyglycine N-C lyase
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: S17855
C;Dates: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: S17855
C;Accession: S17855
Eur. J. Biochem. 201, 551-559, 1991
A;Title: Purification and cDNA cloning of Xenopus laevis skin peptidylhydroxyglycine N-C
A;Reference number: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
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Quality:
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A; Residues: 1-935 < IWA>
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                  542
                                                    563 nTrpGlyGluGluThrSerSerAsnValProArgProGlyGlnPheArgI 580
                                                                                                                                                                    548
                                                                                                                                                                                                                   247 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                   547
                                                                                                                                                                                                                                                                                                                                     197 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
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....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 333
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0.541
47.315
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Gaps: 18
Percent Identity: 19.437
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1124	1077 823	1027 807	977 790	936 773	904 757	854 742	804 725	766 709	725 692	675 675	631 664	581 652	531 646	481 635	431 628	384 612	334 597	580
TTACCATTTCGTTTAAATTTCGT 1146	CTCAATGTTTATGGGTTTAAGCATTGCATTGCTGCCGTCATTA 1123 :: :::::::::::::::::::::::::::: SerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI 840	GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT 1076 ::::: :::::	TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT 1026 ::::::::::::::::::::::::::::::::::::	TGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTT 976 :::	GCAGAACCGGAGAATATCATTGATGTACGAAC 935	CAGCAAAACCTGCTGCAGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT 903 :: ::: :::	ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCG 853 ::: ::: :::	ATTACCATTAAAGAACCAAATAGCGAATGTGTTTCGACC 803 :::::: ::: ::::::::::::::::::::::::	ATGCGGATCACAGCTTTTCTATCAATGCCAGATCAGT	GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT 724 :::: ::: ::::: eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG 692	AATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTT 674 :::::	TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 630	TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTG 580	GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTTGGTCAGCCAGTTTA 530	AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 480 ::::::	AACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTC 430 : ::: ::: :: ::: nPheValLysGlnIleLysHisGlnGluPheGlyArgGluValPheA 628	AAAGTTGATCGTGCATATCGAGTACAATGCTTTTTACATGGAAGCTGATAA 383 ::::::::::	

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C:Accession: A40970
R:Just, M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripier, D.; Stein, H.; Schuppan, D.
J. Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular management of the fibronectin-tenascin family of extracellular management of the fibronectin-tenascin family of extracellular management of the fibronectin family of extracellular management of extracellular management of the fibronectin family of e
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
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                                                                         TTGTCCCGATG......CCAGTATGCCGTTATGAAATTTTGGATGGT 480
euThrProLeuThrGluTyrThrIleAlaIlePheSerIleTyrAspGlu
                                                                                                                                                          uIleAsnGluValGluValAspProIleThrThrPheProLeuLysGlyL 406
                                                                                                                                                                                                                                    TAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAA 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT
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0.578
53.086
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Gaps:
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A; Molecule type: mRNA
A; Residues: 12139-12167,'T',12169-13288 <EC3>
A; Cross-references: GB:M61883; NID:g454837; PID:g
R; Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.;
J. Biol. Chem. 263, 1081-1088, 1988
                                                                                                                                                                                  A;Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal domain A;Reference number: A40009; MUID:91236743
A;Accession: A40009
                                                                                                                                                                                                                                                                                R; Eckhardt, A.E.
J. Biol. Chem. 2
                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF005273; NID:g2581863; PID:g2581864 R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-13288 <ECK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 272, 33204-33210, 1997
A;Title: The complete cDNA sequence and structural polymorphism A;Reference number: Z14839; MUID:98070526
A;Accession: T03099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Sep-1999
C;Accession: T03099; A40009; A28528; B29789
R;Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-33210, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
mucin, submaxillary - pig
      A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names: apomucin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   577 lnPheArgValThrTyrMet 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 luValSerLeuLeuAlaValLeuAspAspGlySerGluSerGluVal.Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyGlnSer...GluProLeuIleGlyValPheThrThrGluGluValPr
Porcine submaxillary gland apomucin contains tandemly repeated, identical se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCGGAGAATATCATTGATG 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rThrSerSerLeuArgValLysTrpAspIleSerAspSerAspValGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGCTGCAGCTGCGC...AACTTCGTTTACTCAAGAAAAGATCTGCAGA 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgAsn.....LeuValValGlyAspGluTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAA 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lThrAlaValGlyThrThrLeuAspSerPheTrpThrGluProAlaThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A....AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .GluGlnAspSerHisValIleGluGlyLeuGluProGlyThrGluTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTCTTGATAAATATTTGCTAAATAATTTG.......GAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....AACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oAlaGlnGlnTyrLeuGluIleAspGluValThrThrAspSerPheArgV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCAACCGGTCAACCAGTT....CAATTTGCTATCATTGGTCAGCC
                                                                                                                                                                                                                                                                                E., Timpte, C.S.; Abe
266, 9678-9686, 1991
                                                                                       PID:g164374
                                                                Hill, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the polypeptide
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A;Cross-references: GB:J03512
A;Experimental source: submaxillary gland
A;Experimental source: submaxillary gland
R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr.,
J. Biol. Chem. 262, 11339-11344, 1987
A;Tittle: Structural properties of porcine submaxillary gland apomucin.
A;Reference number: A92606; MUID:87280230
A;Accession: B29789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: pig submaxillary
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1572-1607 <EC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 12139-12167, 'T', 12169-12641 <TIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A28528; MUID:88087170 A;Accession: A28528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-323-427-3 x T03099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13074 GlyGluGluLysSerProGlyAspValTrpThrAlaAsnCysHisLysCy 13090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13046 yAlaThrGluAspGlnGluAsnGluAsnLysThrGlyCysProAlaProL 13063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13030 LysGluIleThrAlaSerProLysValSerSerProGluThrThrAlaGl 13046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13124 AspThrCysCysGluIle......GlyHisCysGluLysArgThrCy 13137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 AAAACAGTTAGTGCACAGATTGAGGTATCTGAA...ATCACAACTGCTTT 428
                                                                                                                                                                                                                                                                                                                                                                                        GACATGC...GATTCTGAAACCGTTGAT.....ACTTTCTGCGCGG 577
                                                                              s...GlnAsnThrGlyPheThrAlaValValGlnAsnCysProLysGlnT 13178
                                                                                                                                   TTCAGAACCACAAGGATTCGGAGCTGTTAA.....
                                                                                                                                                                                                                                       ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATG 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                 erProProThrCysLysThrGlyGluArgLeuIleLysPheLysAlaAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACC 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAACTCAA.....A
                                                                                                                                                                                    ValGlySerSerPheAspAspProAsnAsnProCysValThrTyrSerCy 13162
                                                                                                                                                                                                                                                                                                                                                CTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATA 659
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1.089
40.724
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Gaps: 12
Percent Identity: 23.982
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                             ....AGCAAAACCTGCTGC...
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        =
                                                                                                                                   ....AACA
                                                                                                                                                                                                                                                                                          ....Glu
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    Quality:
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A; Experimental source: skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-875 < OHS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: URXLA2 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
584 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                        546 lAlaAspGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rAsnGlyCysThr 13215
                                                   ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
                                                                                                      nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
                                                                                                                                                                                                                                                       AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                     ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATTGATGTACG 932
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                                                                                                                                                                                                            SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
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0.945
43.103
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12
21.552
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567

291 551

291

600

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R;Ohsuye, K.; Kitano, K.; Wada, Y.; Fuchimura, K.; Tanaka, S.; Mizuno, K.; Matsuo, Biochem. Biophys. Res. Commun. 150, 1275-1281, 1988
A;Title: Cloning of cDNA encoding a new peptide C-terminal alpha-amidating enzyme A;Reference number: A27715; MUID:88134244
C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p le and dismutates to 91yoxyLate and the corresponding desglyvine peptide alpha-amide. hormones. The other enzyme is peptidyl alpha-amidating enzyme I.
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homo C;Keywords: copper; 91ycoprotein; monooxygenase; oxidoreductase; transmembrane protein; 1-24/Domain: signal sequence #status predicted <SIG>
F;24-39/Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptidylglycine monooxygenase (EC 1.14.17.3) II precursor - African clawed frog N;Alternate names: C-terminal alpha-amidating enzyme II (AE-II); peptidyl alpha-amida C;Species: Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13178 hrTrpCysAlaGluGluAspArgValTyrAspSerLysGlnCysCysTyr 13194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrCysLysSerSerCysLysProSerProValAsnValThrValArgTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATA 919
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hav

GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC

377

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R;Pauley, A.
submitted to the EMBL Data Library, June 1994
submitted to the sequence of C. elegans cosmid D1044
A;Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein D1044.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15881
                                                                                                                                                                                                                                             alignment_block:
US-09-323-427-3 x T15881
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: CESP:D1044.3
A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Restdues: 1-1995 <ADV
A;Cross-references: EMBL:U00065; NID:g495681; PID:g495684; PIDN:AAA50735.1; CESP:D1044
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z18423
A; Accession: T15881
                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:T15881
                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
1165 nAsnTyrArgLeuValTyrGlyTyrCysValProIleThrSerSerIleC
                                                                                          1149 GlnCysIleAspAsnSerValCysMetAsnGlnMetCysThrCysAsnAs
                                             296 CAAC......TGTTGTCATTTCGTTTCATCCATTATTT
                                                                                                                                          246 CAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632 laValSerTyrAlaPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 630
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DNA mismatch repair protein (mutL) homolog - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998 C; Accession: C70126 C. Accession: C70126 R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997 A.Authors: Smith, H.O.; Venter, J.C. A; Arathors: Smith, H.O.; Venter, J.C. A; Reference number: A70100; MUID:98065943 A.Accession: C70126
                                                                                                                                                                                                                                            A; Status, Francisco I A; Molecule type: DNA
A; Residues: 1-610 <KLE>
A; Cross-references: GB: AE001131; (
A; Cross-references: GB: AE001131; (
                            alignment_block:
                                                                                                                                                               alignment_scores:
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                                                                                                 ATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCA......
                                                                                                                                                                                   ACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCG
                                                                                                                                                                                                                                                                      CTGATGGATGTCTTGATAAATATTTGCTAAATAATTTGGAATATCCA
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alignment_block:
US-09-323-427-3 x Tl1616
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    Quality:
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C; Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z54328; NID:g1009451; PID:g1009456 A;Experimental source: strain 972h(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2244 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V. submitted to the EMBL Data Library, October 1995 A;Reference number: 217300 A;Accession: T11616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T11616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) - fission
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:T11616
                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: T11616 from: 1
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Percent Similarity:
                                                                                                                                                                                                   1012
1039 AlaValArgThrLeuArgAspArgGlyVal.....LysThrIleMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
                                                                                                                                                                                                                                          124 TTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 uArgArgTyrAsnSerIleIleGlnAsn.....ArgProThrLeuArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 GluAspValAsnGluProAsnLysAsnThrThrGlnSerAsnIleAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 958 AGCGATGATAATCAA......989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 luMetThrAsn.....Gln..ProGluAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
                                              256 CGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A...CGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATACTTG 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATTGATGTACGAACT...GATATC......AACACCCTTGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rGlnAspIleIleIleLysArgGlnLeuThrGluAspAspHisLeuIleG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuIleSerAspAsnIleAsnAsnPhePheAspLysAsnIleAsnAsnTy
                                                                                               lyValTyrArgIleGlySerSerValGluPheAspTrpCysAlaValArg
                                                                                                                                                GACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCG
                                                                                                                                                                                                 ...........AsnAspLysGlyValMetValLeuGlySerG
                                                                                                                                                                                                                                                                                             TyrThrThrTyrAsnAlaValGluHisAspIleHisPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    luAsnIleGlyAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATA
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0.544
46.301
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Gaps: 17
Percent Identity: 20.274
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1048 AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGT 1092
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                                                                                                                                                                                                                                                                                                           1282 eGlnPheIleAlaLysAspAsnGluIleLysValIleGluCysAsnValA 1299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1101 | aasnasnIlealaLeuProLeuHisargGluAsnValLysIleLeuGlyT | 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1171 SerTyrValLeuSerGlyAlaAlaMetAsnThrValTyrSerGlnSerAs 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1085 GluGlnGluSerSerGlyIleIleIleAlaMetGlyGlyGlnThrAl 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1266 AlaAlaAlaLysIleGlyGluAlaLeuAsnIleThrGlyProTyrAsnIl 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1249 alLeuProProGlnAspLeuAlaProThrThrIleGluArgIleValAsp 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1204 alValIleSerLysTyrIleGluAsnAlaLys................Glu 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1118 hrSerProGluMetIleAspGlyAlaGluAsnArgPheLysPheSerArg 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1052 tValAsnTyrAsnProGluThrValSerThrAspTyrAspGluAlaAspA 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           715 ....GTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 CGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 CCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATG 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCA.... 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pLeuHisSerTyrLeuGlnGlnAlaValAlaIleAsnLysAspHisProV 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGATGATGGTAACGGTGATACTGTG.....GAAATTCTAAATGCTGAT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetLeuAspAspIleGlyValAspGlnProLysTrpLysGluLeuThrSe 1151
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...GlyValAspMetIleSerMetAlaThrAspValIleMetGly 1325
                                                                                                                                                                                                                               GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA 1047
                                                                                                                                                                                                                                                                                                                                                                                       CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACC
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eSerGluHisValGluAsnAlaGlyValHisSerGlyAspAlaThrLeuV 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCATATCGAGTACAATGCTTTACATGGAAGCTGATAAAACAGTTAGT 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....GCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAA 897
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C;Accession: A36054
R;Bhargava, A.K.; Woitach, J.T.; Davidson, E.A.; Bhavanandan, V.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 6798-6802, 1990
A;Title: Cloning and cDNA sequence of a bovine submaxillary gland mucin-like protein A;Reference number: A36054; MUID:90370871
A;Accession: A36054
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-563 <BHA>
A;Cross-references: GB:M36192; NID:g163400; PID:g163401
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US-09-323-427-3 x A36054
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C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 IleGlnThrGlyIleThrGlyThrGlySer.......GlyThrThrSe
518 GTCAGCCAGTTTATCATAAATGGACATGC...GATTCTGAAACCGTTGAT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 LysGluAlaSerGluThrThrThrGlyProGlyIleSerThrThrGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 alSerGlyArgValThrGlyValSerGluSerSerSerProGlyThrSer 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 ThrThrVal.......IlePro...GluSerSerAsnThrGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AATAACAATCAATTTTAATACACGT...AATGCATTCGAAGGACATGTTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homolog -
                                                    .....GlyProLeuGlyGluLysLysSerProGlyAspIleT
                                                                                                                                                                      LysThrGlyCysThrThrSerLeuProProProProAlaCysTyr....
                                                                                                                                                                                                                                ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG
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                                                                                                                 AATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTG
                                                                                                                                                                                                                                                                                           {\tt yrProGluThrThrValValAlaThrGlyGluGlnGlu...ThrGluThr}
                                                                                                                                                                                                                                                                                                                                                     ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                   rThrSerLysSerAsnArgIleThrThrSerSerArgIlePro....T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AAAGTTGATCGTGCATATCGAGTACAATGCTTTT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rgThrThrGluThrArgIleLeuSerGlyThrThrArgGlyArgSerGly
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Gaps: 18
Percent Identity: 20.290
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A;Genome: plastid
A;Note: this apparently degenerate plastid is referred to as the apicoplast
C;Keywords: hydrolase; plastid; serine proteinase
                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-95,'N',96-765 <WIW>
A;Cross-references: EMBL:X95276; NID:g1171591; PID:e220210; PID:g1171612
                                                                                                                                                                                                                                                                                                                                R;Wilson, R.J.M. submitted to the EMBL Data Library, January 1996 A:Reference number: S78483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Wh. J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium A;Reference number: S72277; MUID:96346169
A;Accession: S72278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
seq_documentation_block:
ATP-dependent Clp proteinase (EC 3.4.21.-) homolog - Plasmodium falciparum plastid C:Species: plastid Plasmodium falciparum
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C:Accession: S72278; S78483
                                                alignment_scores:
   Quality:
                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: S78483
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-765 <WIL>
                                                                                                                                                                                                            A;Gene: clpC
                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X95276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:S72278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown
    Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 rAspSerThrLysCysCys......TyrThrCysLysProT 470
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90.00
0.720
55.556
Length: 225
Gaps: 20
Percent Identity: 27.111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.; Why
                                                                                                              hypothetical protein YHR102w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change
  A; Description: The sequence A; Reference number: $46691
                        submitted to the EMBL Data Library, May 1994 A; Description: The sequence of S. cerevisiae
                                                                   R; Latreille,
                                                                                           C; Accession:
                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                seq_name: pir2:S48944
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                                                                                                                   24 - Sep - 1999
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C;Superfamily: unassigned Ser/Thr or Tyr-specific pc;Keywords: ATP; serine/threonine-specific protein F;21-276/Domain: protein kinase homology <KIN>F;29-37/Region: protein kinase ATP-binding motif
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A;Molecule type: DNA
A;Residues: 1-1080 <LAT>
A;Cross-references: EMBL:U00059; NID:g529116; PIDN:AAB68860.1; PID:g529127; MIPS:YHR102w
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-323-427-3 x S48944
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A;Cross-references: SGD:S0001144; MIPS:YHR102w
A;Map position: 8R
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CGTCACCGTGCACTTCTGCAACATAAT 1017
                                                                                                                                                                                                                                                      CCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACC
                                        spTyrIleIleGluAsnAsnIleAsnLeuAspAlaLeuAlaGluAspAsn
                                                                                                                                                                      GGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCG 961
                                                                                                                                                                                                            LysSerIleAlaSerAsnAspAsnGluIleLysArgValAsn.....
                                                                                                                                                                                                                                                                                                                                             CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAA 861
                                                                                                                                                                                                                                                                                                                                                                                     y {\tt SerIleProGluAsnGluProSerLysProSerGluAlaProLysProS}
                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTATTACCATTAAAGAACCAAATAGCGAATGTTCGACCACAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGAT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leArgAlaHisLysAlaThrProThrSerIleLeuLysGluLeuIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysGluPheIleAlaLeu.....CysLeuAspGluAspProLys..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGACCA.....ACCGGTCAACCAGTTCAATTTGCTA 511
                                                                                    AT . . . . . . . .
                                                                                                                            .GluGlyAspValGluMetLysTrpAspPheAspSerLeuSerSerSerA
                                                                                                                                                                                                                                                                                                   erGln.....AsnGlyGlyGlyAspGluAlaGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....GluArgLeuSerAlaAspAspLeuLeuLysSerLysPheI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATT
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Ratio:
                                                                                  .....GATAATCAAGCTTTGCCAGTTGATTTA 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: pir2:C71618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                1205
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Ratio:
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seq_name: pir2:C71618

seq_documentation_block:
hypothetical protein pFB0315w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Accession: C71618
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: C71618
A;Residues: 1-1712 <GAR>
A;Residues: 1-1712 <GAR>
A;Genetics:
A;Gene: pFB0315w

alignment_scores:
Ouality: 90.00
Ratio: 0.584
Percent Similarity: 45.161 Percent Identity: 19.941
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alignment_block: US-09-323-427-3 x C71618 Align seg 1/1 to: C71618 1116 rValTyrGluTyrValIleGluLysTyrLysArgValHisValLeuTyrL 173 ATGATCAAGAAGGTTGCCGGA 222 223 ATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAA 272 MetLysLysLysLysThrGlnGluTyrValAspIleGlu.....Th ACGGTGATACTGTGGAAATTCTAAATGCTGATG euLeuLeuLysGluLysSerAlaTyrGlnAsnHisLeuGlyLysAsnTyr 1238 TGATACTTTCTGCGCGGTTGTCCATTCCT...GCTTTGTCGATGATGGTA uSerSerPheIleAsnTyrGlnIleLysThrAsnAspMetLeuTyrAsnL CAGCCAGTTTATC.....ATAAATGGACATGCGATTCTGAAACCGT 560PheAsnHisIleIleAsnSerTyrGl 1205 TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT ysLeuGluPheLeuIleLysLysLysMetGlnHisTyr..... AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 469 tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 1183 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166 CATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTAC euGlyArgLeuLeuGlnIleValGluLysLeuPheLysLysTyrIleLeu 1149 TC...CACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATC ::: = = ::: = = from: ; 0 = 1712GATGTGCTCTT 651 1195 607 1222 519 419 369 319

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posterior-group protein tudor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C;Accession: A41519; S19019
R;Golumbeski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.
Genes Dev. 5, 2060-2070, 1991
A;Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes a novel prote A;Reference number: A41519; MUID:92038995
A;Accession: A41519
                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-2515 <GOL>
alignment_block:
                                                                                                                                      alignment_scores
                                                                                                                                                                                                                       C; Superfamily: posterior-group protein tudor
                                                                                                                                                                                                                                                   A;Cross-references: FlyBase:FBgn0003891
                                                                                                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: X62420; NID: g8753; PIDN: CAA44286.1; PID: g8754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: pir2:A41519
                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1005 TCTGCAACATAATGGACAACCTG 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1255 alleTyrPheArgSerPheValTyrAsnAsnIleLysValSerLysLysL 1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rAspAsnValSerTyrPheCysPheThrMetTyrLysIleTyrLeuArgA 1322
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                                                                                Quality:
Ratio:
                                                      90.00
0.552
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                                                      Percent Identity:
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                                                2125 rAlaSerProProValValArgLeuThrThrLysAspLysArgSerLeuL
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AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC 377
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                                                                                                          TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 721
                                                                                                                                                             .....LysGlyValValAlaValGluPheValAsnLysSe
                                                                                                                                                                                                                       GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAA 671
                                                                                                                                                                                                                                                                    spAlaLeuLeuAspSerCys.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheThrLeuIle...LysProValAlaGlu.....IleCysSerMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
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C;Accession: H69898

C;Accession: H69898

R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

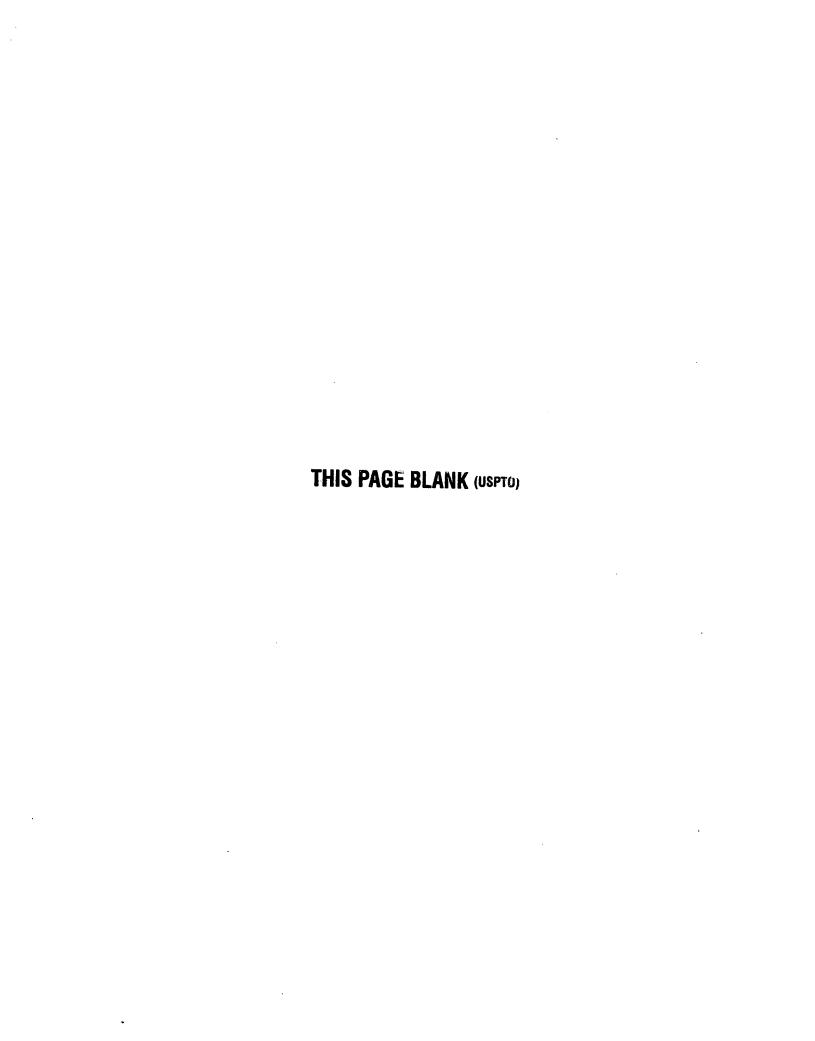
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T. M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Hinters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Togano, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Herence number: A69580; MUID:98044033

A; Reference number: A69580; MUID:98044033

B. Status number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-323-427-3 x H69898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PID:e1185369; PID:g2634290 A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein yobI - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1201 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:H69898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2192 leValLysThrLeuGlnSerLeuLysLysGluLysLeu.....LysLys 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2159 GlnLysArgAsnGluAsnSerGluCysIleIleSerTyrGlyAsnSerPr 2175
                                  112 ATAACAATTATTAATACACGTAATGCATTCGAAGGACATGTTTATGT 161
                                                                                                                                            552 LeuLeuGluLeuGluArgGluLysGlnGluIleArgAlaGlnSerLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       969 T 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            869 CAGCTGCGCAACTTCGTTTACTCAAGAAAGATCTGCAGAACCGGAGAAT 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        819 ACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTG 868
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                                                                                                                                                                                                                        62 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yobI
n.....ValLeuIleThrLysMetAsnSerLysAspValPheSerA 582
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0.511
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Gaps: 17
Percent Identity: 18.367
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84.8		839
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753 838	CTTTTCTATCAA	704 827
N	ysThrLeuSerValIleLeuAsnAspAla	
0	TGCTAAATATTTGGAATATCCAACAGATTTAATGGCTGGC	σ
<u> </u>	uThrIleTyrAspPheValValGlnArgAsnLeuTyrGlu	799
л .	ECALLY SECONDERINALLY SERVICED SOCIEDADO PRES ECALEGRADADO POR LA ECALEGRADA DE LA CALEGRADA DE LA CALEGRADA D	610
609	TTCCTGCTTTGTCG::::::::::::::::::::::::	563 783
562 782	TCATAA	513 771
771	SerLysTyrLeuAsnLeuL	758
512	GGACCAACCGGTCAACCAGTT	463
758	eAlaAspIleIleArgMetAsnLysGluSerV	744
462	CAAACTCAAATTGTCCCGATGCCAGTATGCC	428
743	AsnTyrThrGlnGln	727
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397	GCTGATAAAACAGTTAGTGCA	369
677	AsnTyrIleMetAspHi	664
368	TTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT	319
o ;	uValGlyAlaGluPheLysGlnIleGluValLeuAsnPheHisLeuL	4
		ת
268	TOTTG	249 631
ω	erLeuSerAspIleLysPheValPheSerIleLysAsnHisGlu	\vdash
248	catgcaa	242
614	AsnHisTyrIleThrTyrPheTyrPro	598
241	CGGAATTTCACTTCCA	212
597	LIL	582
211	GAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG	162

	ValLysHisAlaMetIleMetLys 890	883
	948 CCTTGAAATTAGCGATGATAATCAAG 973	948
882	877 uAspLeuAspLysArg 882	877
947	898 AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC 947	898
877	865 GluProGluGluSerPheLeuGluLeuLeuAsnArgGl 877	865
897	CGTTTACTCA	851
864	848 spAsmIleAspIlePheValGluLysValLeuThrGluGluIleGlu 864	848
850	r.	804



SwissProt_38:VP3_BTV10 +
SwissProt_38:PHY4_AVESA +
SwissProt_38:YEW2_YEAST +
SwissProt_38:P11A_HUMAN +

82.50 82.50 82.50 82.00

112.11 109.95 105.70 109.66

12.92 13.62 15.10 14.93

P06594 avena sativa P32634 saccharomyces P42336 homo sapiens P12435 bluetongue virus

saccharomyces

(oat cer

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Swissprot_38:NRK1_YEAST + Swissprot_38:NRK1_YEAST + Swissprot_38:SR5_RAT + Swissprot_38:AMD_HUMAN + 88
Swissprot_38:AMD_HUMAN + 88
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Swissprot_38:AMD_RAT + 83
Swissprot_38:AMD_RAT + 83
Swissprot_38:BPEB_DLODI + Swissprot_38:BPEB_DLODI + Swissprot_38:BPEB_DLODI + Swissprot_38:BPEB_DCOIT + Swissprot_38:BPEB_D
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SwissProt_38:AMD2_XENLA +
SwissProt_38:PXR1_SCHPO +
SwissProt_38:PYR1_SCHPO +
SwissProt_38:MUCS_BOVIN +
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Database:
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SwissProt_38:YQH3_CAEEL +
SwissProt_38:YAY3_SCHPO +
SwissProt_38:APMU_PIG +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database: SwissProt_38:*
Database sequences: 82229
Database length: 29864866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-323-427-3 to: SwissProt_38:*
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1.96 9.44
1.6 10.88
1.49 11.33
1.20 11.16
1.29 12.25
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  1895 | P41295 | Calenorhabditis elegation |
1896 | P41295 | Calenorhabditis elegation |
2244 | 009794 schizosaccharomyces |
563 | P98091 bos taurus (bovine) |
1080 | P38692 saccharomyces cerevi |
2515 | P25823 drosophila melanogast |
363 | P98091 rattus norvegicus (rat) |
974 | P19021 homo sapiens (human) |
407 | P49707 gallus gallus (chicke |
1128 | P06593 avena sativa (oat) |
1126 | Q10093 schizosaccharomyces cerevi |
1117 | Q14126 homo sapiens (human) |
1025 | 042611 fugu rubripes (japani |
1026 | P42337 mus musculus (mouse) |
1361 | P11704 spinacia oleracea (superiore) |
1361 | P11704 spinacia oleracea (superiore) |
1361 | P15154 clostridium difficil |
1485 | 039575 chlamydomonas reinha |
1485 | 039575 chlamydomonas reinha |
1491 | P37622 escherichia coli hy |
1410 | P37622 escherichia coli hy |
1410 | P37622 escherichia coli hy |
1410 | P37622 escherichia |
1624 | P34855 apis mellifera ligust |
1624 | P34855 apis melifera ligust |
1624 | P23351 neurospora crassa mi |
1625 | P3351 neurospora crassa mi |
1626 | P3351 neurospora crassa mi |
1627 | P16731 bos taurus (bovine) |
1628 | P16731 bos taurus (bovine) |
1629 | P16735 bacillus gallus (chicke |
1630 | P35729 synechocystis sp. (str |
1640 | P3351 neurospora crassa mi |
1651 | P355729 synechocystis sp. (str |
1652 | P3351 neurospora crassa mi |
1653 | P355729 synechocystis sp. (str |
1653 | P357729 synechocystis sp. (str |
1653 | P357736 bacillus gallus (chicke |
1653 | P357736 bacillus gallus (chicke |
1654 | P357736 bacillus gallus (chicke |
1655 | P35774 dictyostelium discoide |
1656 | P35774 dictyostelium discoide |
1657 | P35774 dictyostelium discoide |
1677 | P35774 dictyostelium discoide |
1788 | P36417 dictyostelium discoide |
1798 | P36468 herpes simplex virus |
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SEQ_documentation_block:
ID CUTI_CABEL
STANDA
AC Q03755, Q18693;
DT 01-FEB-1994 (Rel. 28,
DT 15-JUL-1998 (Rel. 37,
DE CUTICLIN 1 PRECURSOR.
GN C4762.1.
OS Caenorhabditis elegar
OC EMARYOCA; Metazoa; N
CUT-1 OR C4762.1.
OS CAENORHABDITIA; PAECURSOR.
GN CUT-1 OR C4762.1.
OS CAENORHABDITIA; PAECURSOR.
CUT-1 OR C4762.1.
OR RABDITIA; 91323673.
RA SEBASTIANO M. LASSAN
RT noncollagenous compor
RL Dev. Biol. 146:519-51
RN 520UENCE FROM N.A.
STRAIN-BRISTOL N2;
RA SUBMITTED CONSTITUTION: COMPONI
CC -I-FUNCTION: COMPONI
CC -I-SUBCELLULAR LOCA;
PALMER S.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: COMPONENT OF THE CUTICLES. IT FORMS A RIBBON
-- APPROXIMATELY 2 MICRONS WIDE RUNNING ALONG THE LATERAL LINES
UNDERNEATH THE ALAE. CONTRIBUTES TO THE FORMATION OF EXTRACELLULAR
ENVELOPES PROTECTING THE ORGANISM FROM THE ENVIRONMENT.
-- SUBCELLULAR LOCATION. SECRETED.
-- TISSUE SPECIFICITY: LOCALIZED IN A NARROW BAND NOT EXPOSED
TO THE EXTERIOR, RUNNING UNDERNEATH THE ALAE.
-- IDEVELOPMENTAL STAGE: EXPRESSED DURING DAUER LARVA FORMATION.
-- DOMAIN: THE SMALL REPEATS A-A-P-[AVI] ARE ALSO PRESENT IN MANY
PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUT1_CAEEL STANDARD; PRT; 424 AA. Q03755; Q18693; O1-FEB-1994 (Rel. 28, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) CUTICLIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M55997; AAA27995.1;
EMBL; Z49125; CAA88934.1;
PIR; A49772; A49772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEBASTIANO M., LASSANDRO F., BAZZICALUPO P.; "Cut-1 a Caenorhabditis elegans gene coding for noncollagenous component of the cuticle."; Dev. Biol. 146:519-530(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C47G2.1; CE02165
                                                            Repeat.
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alignment_block:
US-09-323-427-3 x CUT1_CAEEL
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                                                                      AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC
                                                                                                              \verb|nLeuGluTyrProThrAspLeuMetAlaGlyGlnGluAlaHisValTyrL|
                                                                                                                                            TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA
                                                                                                                                                                        GlnIleLeuAsnGluGluGlyCysAlaLeuAspLysPheLeuLeuAsnAs
                                                                                                                                                                                                    GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAA 671
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ysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnIleSerIleThr
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Seq_documentation_block:
ID YOH3_CAREEL STANDA
AC Q09276;
DT 01-NOV-1997 (Rel. 35,
DE HYPOTHETICAL 55.1 KD
C Caenorhabditis elegar
OC EMBARTSTOL N2;
RA SULSTON J;
RA SULSTON J;
RA SULSTON J;
RA SULSTON J;
CC This SWISS-PROT entry
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Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 55.1 KD PROTEIN C43C3.3 IN CHROMOSOME
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                       WORMPEP; C43C3.3; CE01525.

Hypothetical protein; Transmembrane; ATP-binding TRANSMEM 11 31 POTENTIAL.

TRANSMEM 426 446 POTENTIAL.

NP_BIND 171 178 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                             EMBL; 247067; CAA87330.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
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ATP (POTENTIAL).; 09C77468 CRC32;

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alignment_block:
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                                           GCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCA
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PheArgThrPheArgPheGlyAsnGlnSerThrValPheValHisCysGl
                                                                                       ..IleIleAspProLeuAlaAsnValAsnAspGlnIleTyrPheSerLys 306
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alignment_block:
US-09-323-427-3 x YAY3_SCHPO
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHRO
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                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast)
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SEQUENCE
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J. Biol. Chem.
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01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).
                         porcine submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:galnac transferase peptide binding site."; Biol. Chem. 272:9709-9719(1997).

-i- FUNCTION: APONUCIN IS PART OF MUCIN. THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE
                                                                                                                  GERKEN T.A., OWENS C.L., PASUMARTHY M.; "Determination of the site-specific O-glycosylation pattern."
                                                                                                                                                                                                           JOHNSON W.C. JR., HILL R.L.; "Structural properties of porcine submaxillary gland J. Biol. Chem. 262:11339-11344(1987).
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ECKHARDT A.E., TIM
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alignment_scores:
Quality:
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US-09-323-427-3 x GALU_PSEAE
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GALU_PSEAE STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00483; NTP_transferase; 1.
Transferase; Kinase; Nucleotidyltransferase.
SEQUENCE 279 AA; 30939 MW; D967F501 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRALIPMATE TABLE C., PENG H.;
CHANG H., LEE C., PENG H.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases
Submitted (DEC-1993) to The EMBL/GenBank/DDBJ databases
Submitted (DEC-1993) to The EMBL/GenBank/DDBJ databases
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
UTP--GLUCOSE-1-PHOSPHATE URLDYLYLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE
PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE
URIDYLYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE).
                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE PROKARYOTIC UDPGP FAMILY.
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                                          74
                                                                                                                                                                                               uAlaLeuAspAlaGlyLeuAsnGluIleSerIleValThrGlyArgGlyL
TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTG
                                    AsnGlnIleLysGlyThrAspLysGluLysTyrLeuValGlyIleArgLy
                                                                              GGT...TGCCGTAATGAAGGTGGACGTCAAGTTGCCGGAATTTCACT
                                                                                                                  ysArgAlaLeuGluAspHisPheAspIleSer....TyrGluLeuGlu
                                                                                                                                                       GTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAA 183
                                                                                                                                                                                                                                   AGAAATTGAATGTGGACCAACTTCAATAACAATC...AATTTTAATACAC
                                                                                                                                                                                                                                                                                                            LeuProValValAsnLysProLeuIleGlnTyrGlyVal.....GluGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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Seq_documentation_block:
ID AMD2_XENIA
AC P12890;
DT 01-OCT-1989 (Rel. 12,
DT 01-OCT-1989 (Rel. 37,
DE 01-DEC-1998 (Rel. 37,
DE 01-DEC-1998 (AEI.)
DT 15-DEC-1998 (Rel. 37,
DE 02-DEC-1998 (REL. 37,
REL 02-DEC-1998 (REL 02,
REL 02-DEC-1998 (R
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01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE II PRECURSOR
(EC 1.14.17.3) (PEPTIDE C-TERMINAL ALPHA-AMIDATING ENZYME II
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia
Eukaryota; Metazoa; Chordata; Craniata; Pipidae; Xenopod.
                                                                                                                          -i- FUNCTION: C-TERMINAL ALPHA-AMIDATION OF BIOLOGICAL PEPTIDES
-i- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + O(2) =
PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)0.
                                                                                                                                                                                                                                        Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                               "Cloning of cDNA encoding a new peptide C-terminal alpha-amidating enzyme having a putative membrane-spanning domain from Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                     OHSUYE K., KITANO K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                644 GTGCTCTT
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                                               PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O. (THE PRODUCT IS UNSTABLE AND DISMUTATES TO GLYOXYLATE AND THE CORRESPONDING DESGLYCINE PEPTIDE AMIDE).
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               COPPER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WADA Y., FUCHIMURA K., TANAKA S., MIZUNO K.,
                                                                                                                                                                                                                                            Commun. 150:1275-1281(1988).
               ASCORBATE
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Xenopodinae;
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alignment_block:
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PROSITE; PS00085; CU2_MONOOXYGENASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M19032; AAA49667.1; -. PIR; A27715; URXLA2.
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or send an email to license@isb-sib.ch).
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                          AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
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Seq_documentation_block:
ID YLK3_CABEL STANDA
AC 01-NOV-1995 (Rel. 32,
DT 01-NOV-1998 (Rel. 32,
DT 15-DEC-1998 (Rel. 32,
DT 15-DEC-1998 (Rel. 32,
DT 15-DEC-1998 (Rel. 32,
DT 15-DEC-1998 (Rel. 37,
DE PUTATIVE SERINE/THREC
DE (EC 2.7.1.-).
GN 01044.3
OS CAENORABDITION NA
GRADULAY A., WATERSTON NA
RL STRAIN-BRISTOL N2;
RA PAULEY A., WATERSTON
RL SUBMILLARITY: STRON
CC -1- SIMILLARITY: STRON
CC -1- SIMILLARITY: STRON
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                                                                                                                                                                                                               WORMPEP; D1044.3; CE01206.

PROSITE; PS00107; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS01186; EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAULEY A., WATERSTON R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: STRONG, TO ZC84.1.
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC [
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Metazoa, Nematoda,
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01-NOV-1995 (Rel. 32, Created)
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                                                                                                                                                                                                                                                  SerGlnCysValGlySerGlnGlnCysLeuSerAsnSerGlnCysIleSe 1323
                                                                                                                                                                                                                                                                                                                            hrAsnGlnValCysIleSerAsnGlnCysTyrAsnTyrValSerIleGly
                                                                                                                                                                                                                                                                                                                                                                 CGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAA 777
                                                                                                                                                                                                                                                                                                                                                                                                    lCysThrAsnAsnIleCysValSerThrPheCysSerValSerCysSerT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrCysGlnCysThrAsnGlyAlaThrAlaMetTyrGlyTyrCysIleSer
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                                                                                                                                                                                                                 ACCACAATGTTCAGAACCACAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....GlyGlySerCysSerPheSerGlnGlnCysLeuAsnAsnAlaVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leAsnGlyMetCysTyr......AsnThrValGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATT
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                                                                                                                                                                         rSerIleCysGlnCysProGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysGlnGlnThrGlnThrLeuVal.............
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   (Rel. 32, Created)
(Rel. 32, Last sequence)
(Rel. 39, Last annotation)
                                                                                STANDARD;
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0.940
47.847
32, Last sequence update)
39, Last annotation update)
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Gaps:
                                                                              2244 AA
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PFAM; PF00117; GATase; 1.
PFAM; PF00185; OTCace; 1.
PFAM; PF00289; CPSase_L_chain; 2.
PFAM; PF00744; Dihydrooratase; 1.
PFAM; PF00988; CPSase_sm_chain; 1.
                                                                                                                                                                                                                                                                                   PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
PFAM; PF00117; GATase; 1.
                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a obetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                  EMBL; X81841; CAA57433.1; -. EMBL; Z54328; CAA91130.1; -. HSSP; P00968; JJDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "As in Saccharomyces cerevisiae, aspartate transcarbamoylase is assembled on a multifunctional protein including a dihydroorotase-like cryptic domain in Schizosaccharomyces pombe."; curr. Genet. 28:138-149(1995).
                  DOMAIN
                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND ATCASE) (BY SIMILARITY).

1- CATALYTIC ACTIVITY: 2 ATP + GLUTAMINE + CO(2) + H(2)O = ORTHOPHOSPHATE + GLUTAMATE + CARBAMOYL PHOSPHATE.

1- CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE = ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BADCOCK K., CHURCHER Submitted (OCT-1995)
                                                                                  DOMAIN
                                                                                                                   DOMAIN
                                                                                                                                                    DOMAIN
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SOUCIET J.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URA1 PROTEIN [INCLUDES: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5); ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3 URA1 OR SPAC22G7.06C.
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: FIRST AND SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.
MISCELLANBOUS: GATASE (GLUTAMINE AMIDOTRANSFERASE) AND CPSAS
(CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE
GLUTAMINE-DEPENDENT CPSASE (GD-CPSASE) (EC 6.3.5.5).
MISCELLANEOUS: IN EUKARYOTES EC 6.3.5.5 IS SYNTHESIZED BY TW
PATHWAY-SPECIFIC (ARGININE AND PYRIMIDINE) UNDER SEPARATE CO
SIMILARITY: THE CRASES DOMAIN IS SIMILAR TO OTHER CPASES.
SIMILARITY: THIS PROTEIN CONTAINS A DEFECTIVE DHOASE DOMAIN.
SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE
NATIOUTEAUSCEPANCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., mitted (CCT-1995) to the EMBL/GenBank/DDBJ databases. FUNCTION: THIS PROTEIN IS A "FUSION" PROTEIN ENCODING ENZYMATIC ACTIVITIES OF THE PYRIMIDINE PATHWAY (GATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                   PS00097; CARBAMOYLTRANSFERASE; PS00442; GATASE_TYPE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96020160.
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                                                   1525
                                                                                  1515
                                                                                                                                                                                                    biosynthesis;
                  1854
                                                                                                                   478
                                                                                                                                                    438
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                  1935
                                                 1853
                                                                                  1524
                                                                                                                   1514
                                                                                                                                                    477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rmatics Institute. There are no rest institutions as long as its content
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                                                                                                                                                                                  Ligase; Transferase; Multifunctional enzyme GATASE (GLUTAMINE AMIDOTRANSFERASE)
(BY SIMILARITY).
BOUNDARY BETWEEN I
(BY SIMILARITY).
DEFECTIVE DHOASE I
(BY SIMILARITY).
BOUNDARY BETWEEN I
(BY SIMILARITY).
                                                                                                                   CPSASE (CARBAMOYL-PHOSPHATE
                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                  BOUNDARY BETWEEN ENZYMATIC
                                                                                                                                                                   (BY SIMILARITY)
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                  ENZYMATIC DOMAINS
                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
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                                                                                                                                                    DOMAINS
                                                                                  DOMAINS
                                                                                                                   SYNTHASE)
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alignment_block:
US-09-323-427-3 x PYR1_SCHPO
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CONFLICT
SEQUENCE
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ACT_SITE
ACT_SITE
               640 GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA 689
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                                                                                                                                                                                                                                                                                                                                                                                                              394
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                                                                                                           rPheAspGlu...AlaAspLysPheCys...........
                                                                                                                                                                                                                                              hrSerProGluMetIleAspGlyAlaGluAsnArgPheLysPheSerArg
                                                                                                                                                                                                                                                                                                             aAsnAsnIleAlaLeuProLeuHisArgGluAsnValLysIleLeuGlyT
                                                                                                                                                                                                                                                                                                                                                                            GluGlnGluSerSerGlyIleIleIleAlaMetGlyGlyGlnThrAl
                                                                                                                                                                                                                                                                                                                                                                                                            GCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tValAsnTyrAsnProGluThrValSerThrAspTyrAspGluAlaAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATTTCGTTTCATCCATTATTTGTTACC.....AAAGTTGATC
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                                                                              TCGATGATGGTAACGGTGATACTGTG.....GAAATTCTAAATGCTGAT
                                                                                                                                             CGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTG
                                                                                                                                                                                                              CCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATG
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                                             .AspThrValGlyTyrProValLeuValArgPro 1170
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GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GIC -> RYF (IN REF. 1).
CAVRA -> LQFAQ (IN REF. 1).
ELL -> DV (IN REF. 1).
G -> E (IN REF. 1).
G -> E (IN REF. 1).
G -> E (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 365
Gaps: 17
Percent Identity: 20.274
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ATCASE (ASPARTATE TRANSCARBAMYLASE) (BY SIMILARITY).
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seq_name: SwissProt_38:MUCS_BOVIN
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P98091;
                     MUCS_BOVIN
                                                                                                                                                   ...GlyValAspMetIleSerMetAlaThrAspValIleMetGly 1325
                                                                                                                                                                                                                                                        rgAla.....SerArgSerPheProPheValSerLysValIle...
                                                                                                                                                                                                                                                                                                            GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA 1047
                                                                                                                                                                                                                                                                                                                                                                eGlnPheIleAlaLysAspAsnGluIleLysValIleGluCysAsnValA
                                                                                                                                                                                                                                                                                                                                                                                                                   CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACC
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                     STANDARD;
                     PRT;
                     563
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BHARGAVA A.K., WOITACH J.T., DAVIDSON E.A., BHAVANAN "Cloning and cDNA sequence of a bovine submaxillary protein containing two distinct domains."; Proc. Natl. Acad. Sci. U.S.A. 87:6798-6802(1990).-i- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SUBMAXILLARY MUCIN-LIKE PROTEIN.
                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the EMBL outstation in the property of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=SUBMAXILLARY GLAND;
                                                                                                                          modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE
-i- SIMILARITY: TO PORCINE APOMUCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
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SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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alignment_block:
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Quality:
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Repeat; Glycoprotein.
DOMAIN
REPEAT 61 71
REPEAT 148 158
REPEAT 148 158
DOMAIN 338 404
DOMAIN 471 555
SIMILAR 1 282
DISULFID 471 518
DISULFID 485 532
DISULFID 498 550
DISULFID 7 554
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HSSP; P00214; 1FTC.
PROSITE; PS01208; VWFC; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
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ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGA
                                                                                                                                  LysGluAlaSerGluThrThrThrGlyProGlyIleSerThrThrGlySe
                                                                                                                                                                                       alSerGlyArgValThrGlyValSerGluSerSerSerProGlyThrSer 279
                                                                                                                                                                                                           TTTCGTTTCATCCATTATTTGTTACC.............
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                                                                                                                                                                                                                                                                    TACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCA 307
                                                                                                                                                                                                                                                                                                                                                rgThrThrGluThrArgIleLeuSerGlyThrThrArgGlyArgSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTC 110
                        yrProGluThrThrValValAlaThrGlyGluGlnGlu...ThrGluThr
                                                   ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC
                                                                             rThrSerLysSerAsnArgIleThrThrSerSerArgIlePro....T
                                                                                                                                                                                                                                                                                             ThrThrVal.....IlePro...GluSerSerAsnThrGlyTh
                                                                                                                                                                                                                                                                                                                        CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG
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CTCK.
TO PORCINE APOMUCIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
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BB7D4189 CRC32;
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Gaps:
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seq_name: SwissProt_38:NRK1_YEAST
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STRAIN=S288C / AB972;
MEDLINE; 94378003.
MEDLINE; 94378003.
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J., DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J., DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J., DU Z., TAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J., KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y., KUCABA T., HILLIER L., MACRI C., MARDIS E., MENEZES S., MOUSER LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.
                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                  Submitted (MAY-1994) to the
                                                                                                                                                                                                                                          SEQUENCE FROM STRAIN=DC-5;
                                                                                                                                                                                                                                                                                                                                                                            NRK1 OR YHR102W.
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(EC 2.7.1.-)
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SGD; L0001276; NRK1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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762 CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTT
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PROTEIN_KINASE_DOM; 1.
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alignment_scores:
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01-MAY-1992 (Rel. 22, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation updat
                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Tudor, a posterior-group gene of Drosophila melanogaster, novel protein and an mRNA localized during mid-oogenesis."; Genes Dev. 5:2060-2070(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383
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                                                                                                                         Developmental protein. SEQUENCE 2515 AA; 285236
                                                                                                                                                        FLYBASE; FBgn0003891;
PFAM; PF00567; TUDOR;
                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
-I- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea;
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Ol-JUL-1993 (Rel. 26, Created)
Ol-FEB-1995 (Rel. 31, Last sequence update)
Ol-FEB-1996 (Rel. 33, Last annotation updat
                                   EMBL;
                                                                                         modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                PANETTA R., GREENWOOD M.T., WARSZYNSKA A., DEMCHYSHYN L.L., DAY R., MIZNIK H.B., SRIKANT C.B., PATEL Y.C.; "Molecular cloning, functional charterization, and chromosomal localization of a human somatostatin receptor (somatostatin receptor type 5) with preferential affinity for somatostatin-28."; Mol. Pharmacol. 45:417-427(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                   -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-28. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: PROMINENT IN THE PITUITARY AND SMALL INTESTINE. LOW LEVELS IN ISLETS AND SPLEEN. NOT DETECTED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'CARROLL A.-M., LOLAIT S.J., KONIG M., MAHAN L.C.;
"MOLecular cloning and expression of a pituitary somatostatin receptor with preferential affinity for somatostatin-28.";
Mol. Pharmacol. 42:939-946(1992).
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Gaps: 6
Percent Identity: 24.342
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7 (POTENTIAL).
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6 (POTENTIA
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3 (POTENTIAL).
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seq_name: SwissProt_38:AMD_HUMAN
alignment_scores:
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-!- FUNCTION: C-TERMINAL ALPHA-AMIDATION OF PEPTIDES.
-!- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + O(2) PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O. (THE PRODUCT IS UNSTABLE AD DISMUTATES TO GLYOXYLATE A CORRESPONDING DESCLYCINE PEPTIDE AMIDE).
-!- SUBCELLULAR LOCATION: SECRETORY GRANULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P19021;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE
(EC 1.14.17.3) (PAM).
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                  modified and this statement
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SIGNAL
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                                                                                                                                                                                                                                                                    PROSITE; PS00084; CU2_MONOOXYGENASE_1; PROSITE; PS00085; CU2_MONOOXYGENASE_2;
                                                                                                                                                                                                                                                                                              MIM; 170270;
                                                                                                                                                                                                                                                                                                        EMBL; M37721;
PIR; A35477; I
                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb~sib.ch).
                                                                                                                                                                                                                                                                                                                                                          entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLAUDER J.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                 non-profit
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                                         ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
TAAAACAGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                                                                  AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                              hrAsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer
                                                                                                                                                                            CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
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Percent Identity: 18.944
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alignment_block:
US-09-323-427-3
                                                                                                                                alignment_scores:
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Align seg 1/1 to: CGE1_CHICK
                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                             EMBL; U28981; AAA74981.1; -...
EMBL; U28990; AAA81647.1; JOIN
EMBL; U28982; AAA81647.1; JOIN
EMBL; U28983; AAA81647.1; JOIN
EMBL; U28984; AAA81647.1; JOIN
EMBL; U28985; AAA81647.1; JOIN
EMBL; U28986; AAA81647.1; JOIN
EMBL; U28987; AAA81647.1; JOIN
EMBL; U28988; AAA81647.1; JOIN
EMBL; U28988; AAA81647.1; JOIN
                                                                                                                                                                                                 CONFLICT
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
G1/S-SPECIFIC CYCLIN E1.
                                                                                                                                                                                                                             PROSITE; PS00292; CYCLINS; 1.
PFAM; PF00134; cyclin; 1.
Cyclin; Cell cycle; Cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. The statement is a content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LI H., LAHTI J.M., VALENTINE M., HOUSTON J., KIDD V.J.;
Submitted (JUN-1995) to the EMBL/GenBank/DBbJ databases.
-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE
(START) TRANSITION. INTERACTS WITH A MEMBER OF THE CDC2/CDK
PROTEIN KINASES FAMILY TO FORM MPF (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN E SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                  EMBL; U28989; AAA81647.1; HSSP; P30274; 1VIN.
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                                                                              Length: 313
Gaps: 16
Identity: 21.406
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S (IN AAA81647).
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344 LyshisPheArgGlyIleAlaProGluAspLeuHisAsnIleGlnThrHi
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                                  CTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGA
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seq_documentation_block:
ID PHY3_AVESA STANDARD;
AC PO6503;
DT 01-JAN-1988 (Rel. 06, Creator Physology (Rel. 21, Last DT 01-JAN-1992 (Rel. 38, Last DT 01-JAN-1992 (Rel. 38, Last DT 15-JUL-1999 (Rel. 38, Last DT 15-Ju
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PFAM; PF00360; phytochrome; PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2. PFAM; PF01590; GAF; 1.
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Avena sativa (Oat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                   MENDEL; 1305; AVESa; PhyA; 1.
PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commendative data the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRIMM R., KELLERMANN J., SCHAEFER W., RUEDIGER W.; "The amino-terminal structure of oat phytochrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HERSHEY H.P., BARKER R.F., IDLER K.B., MURRAY M.G., "NucLeotlide Sequence and characterization of a gene phytochrome polypeptide from Avena."; Gene 61:339-348(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete amino acid sequences for two gene etiolated Avena.";
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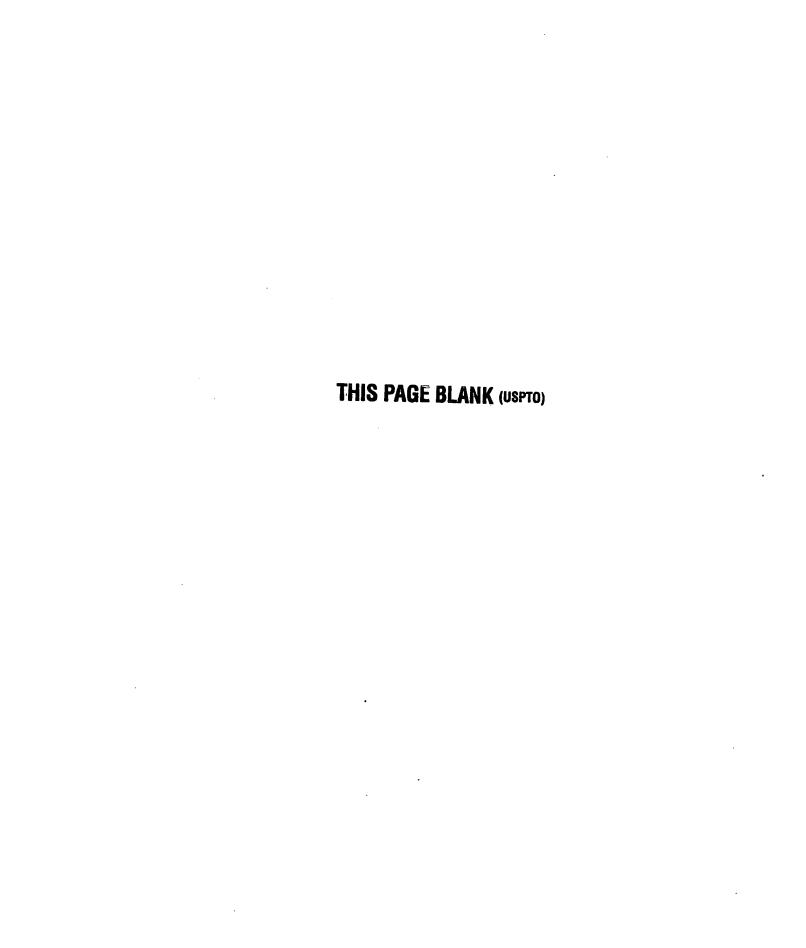
HERSHEY H.P., BARKER R.F., IDLER K.B., LISSEMORE J.L., QUAIL P.

"Analysis of cloned cDNA and genomic sequences for phytochrome:
                                                                                                                                                                                                                                                                                                                                           EMBL; X03242; CAA26999.1; -. EMBL; M18822; AAA76820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR CANCELS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBBNIT OF RIBULOSE-BISCHOSPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sIleAsnSerLeuAspLeuLeuAspLysAlaGlnAla
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21, Last sequence up
38, Last annotation
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	on regulation; Photoreceptor; Phytochrome;	Chromophore;
ET BINI	ily. 0 0 21 321 CHROMOPHORE.	
	278 278 L -> F (I 1128 AA; 124861 MW; 49DAA	
alignmen	t_scores: Quality: 86.50 Length: 28	
Percent	atio: 0.618 rity: 48.95	
alignment_b US-09-323-4	t_block: 23-427-3 x PHY3_AVESA	÷
Align s	eg 1/1 to: PHY3_AVESA from: 1 to: 1128	
471 771	TTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTC	520 778
521 778	CGATTCTGAAACCGTT :::::: gAspGluValLeu	561 793
562 794	GATACTTTCTGCGGGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG	611 806 .
612 806	TGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATT : ::: ::: :::	661 823
662 823	TGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	711 833
712 834	CACGTATACAAATATGCGGATCACAGCTTTTCTATCAATG ::: :: :: :: :: :: :: :: :: :: :: :: :	755 850
756 850	CCAGATCAGTATTACCATTAAAGAACCAAATAGCGAA	792 867
793 867	TGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT	837 882
838 882	AAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGGCAACT {	881 899
882 899	TCGTTTACTCAAGAAAAGATCTGCAGAAACCGGAGAAATATCATTGATGTAC !	931· 915
932 916	GA	947 932
948 932	CCTTGAAATTAGCGATGATAATCAAGCTTTGCCAG 9 :::::::::::::::::::::::::::::::::::	982 948
983 948	TTGATTTACGTCACCGTGCACTTCTGCAACATAATGGA	1020 964
1021 965	CAACCTGTAATACTTGCTGCAGTACAA 1	1047 981

1048



92.50 91.50

133.56 132.73

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Sequence Strd Orig ZScore Es sp_invertebrate:Q19707 + 1382.50 2830.20 2 sp_invertebrate:Q19707 + 1382.50 2830.20 2 sp_invertebrate:Q19808 + 654.50 1132.89 2 sp_invertebrate:Q98709 + 655.00 1132.89 2 sp_invertebrate:Q19808 + 664.50 1112.68 1 sp_invertebrate:Q19503 + 595.00 1005.71 9 sp_invertebrate:Q19503 + 596.00 1005.71 9 sp_invertebrate:Q2164 + 546.50 924.55 sp_invertebrate:Q29808 + 477.50 804.24 1 sp_invertebrate:Q29807 + 477.50 804.24 1 sp_invertebrate:Q23097 + 476.00 802.80 2 sp_invertebrate:Q23097 + 476.00 802.80 2 sp_invertebrate:Q23097 + 476.00 802.80 2 sp_invertebrate:Q25680 + 453.50 760.05 3 sp_invertebrate:Q25680 + 433.50 760.05 3 sp_invertebrate:Q25680 + 433.50 760.05 3 sp_invertebrate:Q25680 + 409.50 682.49 1 sp_invertebrate:Q25677 + 401.50 669.67 3 sp_invertebrate:Q25677 + 365.00 597.70 3 sp_invertebrate:Q25677 + 293.00 484.21 8 sp_invertebrate:Q25677 + 293.00 484.21 8 sp_invertebrate:Q23587 + 141.00 206.53 4 sp_invertebrate:Q23687 + 133.50 20.9.54 sp_invertebrate:Q23687 + 133.50 20.9.54 sp_invertebrate:Q23687 + 133.50 20.9.54 sp_invertebrate:Q23687 + 115.00 177.11 sp_invertebrate:Q23687 + 115.00 177.11 sp_invertebrate:Q23687 + 115.00 177.11 sp_invertebrate:Q23687 + 115.00 177.11 sp_invertebrate:Q23687 + 115.00 181.37 0 sp_invertebrate:Q3688 + 105.00 177.11 sp_invertebrate:Q368
                                                                       sp_vertebrate:091697
sp_human:005707
sp_mammal:018758
sp_mammal:077509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database: SPTREMBL_12:*
Database sequences: 225878
Database length: 69334122
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Query length: 1161
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Sequence
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                            sp_bacteria:051229
                                                sp_bacteria:Q9ZEG6
                                                                                                                                                                         sp_mamma1:062672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MODEL-frame+_n2p.model -DEV=x1p
-Q=/cgn2_1/USPTO_spool/US09323427/runat_14042000_170514_19920/app_query.fasta.
-Q=/cgn2_1/USPTO_spool/US09323427/runat_14042000_170514_19920/app_query.fasta.
-DB=SPTREMBL_12 -QEMT-fastan -SUFFIX=backtrans.rspt
-QAPOP=12.000 -GAPEXT=4.000 -MINNATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM-ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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NO_XLPXY -WAIT -THREADS=1
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Copyright (c) 1993-2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-323-427-3 to:
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3.4e-47
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2.1e-31
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3.3e-20
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3.002
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3.0037
3.0037
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386 (093115 ascaris lumbricoides (
387 (093115 ascaris lumbricoides (
388 (093116 ascaris lumbricoides (
389 (019707 caenorhabditis elegans 
364 (09xvm7 caenorhabditis elegans 
206 (09xvm7 caenorhabditis elegans 
207 (096775 brugia maláyi. cuticii 
290 (021808 caenorhabditis elegans 
315 (093532 caenorhabditis elegans 
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316 (093532 caenorhabditis elegans 
317 (022164 caenorhabditis elegans 
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324 (04298 caenorhabditis elegans 
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i 077509 bos taurus (bovine).
i Q9zeg6 carnobacterium diverge
i 051229 borrelia burgdorferi i
i 097239 plasmodium falcipan
                                                                                                                     1 Q20550 caenorhabditis elégans
1 062672 bos taurus (bovine). bo
091697 xenopus laevis (african
Q05707 homo sapiens (human). un
                                                                                                 018758 sus scrofa
burgdorferi (ly
odium falciparum
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dorferi (ly
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sp_virus:Q66951 +
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SEQUENCE
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seq_name: sp_invertebrate:Q93115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-NOV-1998 (TrEMBLrel. 08, CUT-1-LIKE CUTICLIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ascaris lumbricoides (common roundworm).
Eukaryota, Metazoa, Nematoda, Secernentea, Rhabditia, Ascaridida,
Ascaridoidea, Ascarididae, Ascaris.
                                                                                                                                                                  "cut-1-like genes of Ascaris
Gene 193:81-87(1997).
                                                                                                                                                                                                                                         154 GTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG
                                                                                                                                                                                                                                                                                                           104 CAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACAT
                                                                                                                                                                                                                                                                               33.roThrSerIleThrValAsnPheAsnThrArgAsnProPheGluGlyHis
                                                                                                           alleProValAspAsnGlyValGluGlyGluProGluIleGluCysGlyP
                                                                                                                                                                                                                                                                                                                                                                   GATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGAC
ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTC
                                                                                                                                                                                                                           AlaTyrValLysGlyLeuTyrAspGlnGluGlyCysArgSerAspGluGl
                                                                                                                                                                                                                                                                                                                                                      U73005; AAB66646.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 1653.50
Ratio: 4.593
milarity: 92.784
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CUT-1-LIKE (
BDEB1169 (
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132.73 1.99
141.49 2.12
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1 094829 homo sapiens (human).
44 1 096440 leishmania chagasi.
1 1 066951 feline infectious pe
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Seq.
ID AC
DT DT
                                                                                                                 seq_name:
Q19707 PRELIMINARY;
Q19707;
Q1-NOV-1996 (TremBLrel. 0:
01-NOV-1996 (TremBLrel. 0:
01-JAN-1999 (TremBLrel. 0:
F22B5.3 PROTEIN.
                                                                       _documentation_block:
Q19707 PRELIMINARY;
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|| ::||| :::|||| || |||||||::: ::::::
la.....ArgHisAlaArgGlyGlnGlnValIleLeuSerProAlaAsn 347
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
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EMBL; Z50044; CAA90355.1;
SEQUENCE 389 AA; 42983
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                                                                                                                                     sThrValSerThrGlnIleGluValSerAspLeuThrThrAlaPheGlnT
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Secernentea; Diplogasteria;
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Tylenchida;
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alignment_block:
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Percent Similarity:
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Cuticle.
SEQUENCE
                             183
                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE GIORGI C., DE LUCA F., DI VITO M., LAMBERTI F.;
"Modulation of expression at the level of splicing of cut-1 RNA in infective second-stage juvenile of the plant parasitic nematode Meloidogyne artiellia.";
                                                                                                                                                                                                          133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
[1]
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                          ProPheGluGlyHisValTyrValLysGlyLeuPheAspGlnAlaGlyCy
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                                                                                                      CGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAAT
                                                                                                                                                                                                                                                                                                                                                                                   GCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTG
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TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGA
                                                       GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCC
                                                                                     \tt uGlyGlnProIleGlnPheAlaThrIleAlaGlnGlnValTyrThrSerG
                                                                                                                                              ValValProMetProValCysLysTyrGluIleLeuGluGlyAlaAlaLe
                                                                                                                                                                                                       alSerAlaGlnLeuGluValSerGluIleThrThrGlnPheGlnThrGln
                                                                                                                                                                                                                    TTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAA 438
                                                                                                                                                                                                                                                                lAspArgAlaTyrArgValGlnCysPheTyrMetGluAlaAspLysThrV
                                                                                                                                                                                                                                                                                TGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   luIleGluCysGlyProThrSerIleThrValAsnPheAsnThrArgAsn
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_x96677; CAA65452.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 AA;
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                                                                                                                                                          q_documentation_block:
09XVM7; PRELIMINARY;
09XVM7; QYXVM7;
01-NOV-1999 (TrEMBLrel. 12, La
01
SEQUENCE FROM N.A. MEDLINE; 94150718.
BURTON J.;
"2.2 Mb of contiguo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1078 TCAATGTTTATGGG.TTTAAGCATTGCATTGATTGCTGCCGTCATTATTA 1126
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                                                                                                                                         Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACAGGT......GGTGCCGCAGCAAAACCTGCTGCAGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spLeuThrAlaGlyGlnGluAlaHisValTyrLysTyrAlaAspArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1His 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt rgPheIleTyrGlnGlyGlyGlnGlnValCysMetSerSerPheArgAla}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eArgHisHisHisLeuMetGluAsnLeuSerAlaGluProGlnArgA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGTCACCGTGCACTTCTGCAACATAAT.....GGACAACCTGTAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|aIleProAlaArgValGlnArgLeuArgThrArgGlnLeuArgLeuLeuA|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ......CAACTTCGTTTACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaAlaThrProProAlaAlaAlaProProAlaProIleAlaProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \tt rGluCysAlaArgProLysCysAlaGluProSerGlyPheAsnAlaValL
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of contiguous
                                                                                                                                         Nematoda; Secernentea;
pidea; Rhabditidae; Pelo
  nucleotide
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Last sequence update)
Last annotation update)
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  sequence
                                                                                                                                                                                                                                                                                                                                                                                            364
                                                                                                                                         Peloderinae;
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     from
                                                                                                                                                                     Rhabditia; Rhabditida;
  chromosome
                                                                                                                                         Caenorhabditis
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alignment_block:
US-09-323-427-3 x Q9XVM7
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RY MEDLINE; 94150718.

RA MILSON R., ANINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA GRANDER D., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA LIGHTNING J., LLOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A.; SONNHAMMER E., STADEN R., SULSTON J.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT "2.2 Mb of CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III of C.

RT "2.2 Mb of CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III of C.

RT "2.2 Mb of CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III of C.

RT "2.2 Mb of CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III of C.

RT "2.2 Mb of CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III of C.

RT "2.2 Mb of CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III of C.

RT BLEARY SEQUENCE 364 AA; 40843 MW; 3FEC30BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 uArgGlnArgValLeuAsnProLysGlyLeuAlaValArgThrThrIleT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 TTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lePheValLysAspPheAlaSerGluGluValCysThrSerArgGlyThr
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                                                                            PheGlyLeuIleGlyGlnGlnValTyrHisGlnTrpLysCysAspAsnAs
                                                                                                                                                            TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
                                                                                                                                                                                                                                         hrCysThrTyrGlnIleLeuSerGlyGlyProPheGlyGluProValGlu
                                                                                                                                                                                                                                                                                                                         TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                     rValAspGluIleSerThrIleSerTyrAsnValAsnLeuThrMetProT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuLeuCysLeuTyrArgGluSerGlnValThrValAlaAsnAsnIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrIleSerPheHisProTyrPheIleThrLysValAspArgThrTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyArgLeuSerAlaPheLeuGluIleGluIleGlyLeuCysGlyAlaLe
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3.455
77.491
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. ACCGTTGATACTTTCTGCGCGGTTGTCC
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alignment_block:
US-09-323-427-3 x Q9XYU9
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                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9XYU9 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9XYU9;
O1-NOV-1999 (TrEMBLrel. 12,
O1-NOV-1999 (TrEMBLrel. 12,
O1-NOV-1999 (TrEMBLrel. 12,
CUTICULIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.;

RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.;

"Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF125580; AAD28743.1; -.

NON_TER 1 1

NON_TER 206 AA; 22602 MW; 4DEE20DO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wuchereria bancrofti.
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Wuchereria.
                                                                                                                                                                                                                                                          556
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                                                                                                                                                         606 TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA 655
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                                                                                                                                                                                                                 1 ThrValAspThrPheCysAlaValValHisSerCysPheValAspAspGl
                                                                           ACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTGTCGATGATGG
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                    GAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG
                                                                                                                                   yAsnGlyAspLysValGluLeuLeuAsnAlaAspGlyCysAlaLeuAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isThrCysSerValAspAspGlyArgGlyGluThrSerPheLeuIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aProValValGly 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTAAAACAGGT 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlnGluCysValArgProIleCysGluAspValGluGlyGlyGlyAl
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pLysGlyMetIleIleLeuIleLysGluAspSerPheCysMetValValH
                                                         ysPheLeuLeuAsnAsnLeuGluTyrProThrAspLeuMetAlaGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerAsnGlyCysSerIleAspLysPheLeuLeuSerAsnLeuGluTyrPr
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           695.00
4.064
86.364
                                                                                                                                                                                                                                                                                                                                                                               Length: 198
Gaps: 4
Percent Identity: 69.192
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Last annotation update)
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SQ

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alignment_block:
US-09-323-427-3 x 096775
                                                                                                                                                 alignment_scores:
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                                        Align seg 1/1 to: 096775
                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1047
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                                                                                                                                                                                                                                                     cut-1-11ke genes are present in the filarial nematodes Brugia pahangi and Brugia malayi and, as in other nematodes, code for components of the cuticle.";
                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Secernentea; Filarioidea; Onchocercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                               CUTICLIN (FRAGMENT).
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304 GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                                                                                                                                                Submitted (NOV-1998) to the EMBL; AJ012617; CAA10074.1;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
LEWIS E.K., HUNTER S.J., TETLEY L., PAVIA NUNES
                                                                                                                                                                                                                                                                                                                                                                                 Brugia malayi.
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                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluAlaHisValTyrLysTyrAlaAspArgSerGlnLeuPheTyrGlnCy
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                                                                                                                       Quality:
Ratio:
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127 t
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                                                                                                                                                                                          AA;
                                                                                                         662.00
5.296
98.425
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                                       from:
                                                                                                                                                                                          MW;
                                                                                                           Percent Identity:
                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                        to:
                                        127
                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
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354

17

AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG ValIleSerPheHisProLeuSerValThrLysValAspArgAlaTyrAr 17

403

34

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Seq_documentation_block:
ID Q21808
AC Q21808;
AC Q21808;
AC Q21808;
DT Q1-NOV-1996 (TrEMBLrel. Q1)
DT Q1-NOV-1996 (TrEMBLrel. Q2)
DT Q1-ANN-1999 (TrEMBLrel. Q2)
DE RO7E3.3.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemato
OC Rhabditina; Rhabditoidea;
RN [1]
RP SEQUENCE FROM N.A.
COTTAGE A.;
RA COTTAGE A.;
RA COTTAGE A.;
RA SUBMITTER 94130718.
RA MILSON R., AINSCOUGH R., A
BONFIELD J., BURTON J., CC
RA CRATON M., DEAR S., DU Z.
RA GARDNER A., GREEN P., HAWR
RA JONES M., KERSHAW J., KIRS
RA LIGHTNING J., LLOYD C., MC
RA PARSONS J., PERCY C., ARE
RA PARSONS J., PERCY C., ARE
RA MATSON A., WEINSTOCK L., W
RT "2.2 MD of contiguous nucl
RT elegans.";
RA MATSON A., WEINSTOCK L., W
RT "2.2 MD of contiguous nucl
RT elegans.";
RA MATSON A., WEINSTOCK L., W
RT "2.2 MD of contiguous nucl
RT elegans.";
RA MATSON A., WEINSTOCK L., W
RT "2.2 MD of contiguous nucl
RT elegans.";
RBL; Z49207; CAA889068.1;
SQ SEQUENCE 290 AA; 33215
alignment_block:
                                                                                                           alignment_scores
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                                             Percent
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BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A
CRAXTON M. DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SWALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUGIN M., WATERSTON R.,
WARTSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                           Nature 368:32-38(1994).
EMBL; Z49207; CAA89068.1;
SEQUENCE 290 AA; 33215
                                                                                                                                                                                                                                         WATSON A., WEINSTOCK L., WILKINSO
"2.2 Mb of contiguous nucleotide
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                 GCCAGTTGATTTACGTC.....
                                                                     ....GluLeuCysMetThrAlaIleGlyThrThrLeuLeuValPheLeuA 259
                                                                                                       GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 977
                                                                                                                                          AsnPhe.....AspMetArgIleSer....
                                                                                                                                                                                AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT 927
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021540 PRELIMIN.
021540; Cremblr:
01-NOV-1996 (Tremblr:
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Eukaryota; Metazoa; Nematoda; Secernentea;
Rhabditina; Rhabditoidea; Rhabditidae; Pel
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       367
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                                                                                                                                  ATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT
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                                                                                                                                                                                                          rLeuAsnProLysGlyIlePheValGluValSerIleValPheMetPheH
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                                                                    isSerLeuPheMetThrLysThrAspGlnThrValLysValGlnCysPhe
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Peloderinae; Caenorhabditi
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seq_documentation_block:
ID 019053
AC 019053;
AC 019053;
AC 019053;
AC 019053;
AC 019053;
AC 019053;
AC 019082;
AC 019083;
AC 019082;
AC 01-JAN-1998 (TYEMBLrel. 05
DT 01-JAN-1999 (TYEMBLrel. 09
DE 204D5.3 PROTEIN.

GN E04D5.3 PROTEIN.

OC EMABLYSOTA; Metazoa; Nematoo
OC Rhabditina; Rhabditoidea;
RN [1]
RP SEQUENCE FROM N.A.
RA MCMURRAY A.;
RN [2]
RN SEQUENCE FROM N.A.
RA MCMURRAY A.;
SEQUENCE FROM N.A.
RA MCMURRAY A.;
ANSCOUGH R., A
RA MILSON R., AINSCOUGH R., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: sp_invertebrate:Q19053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523
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                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda;
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8 (TrEMBLrel. 05,
9 (TrEMBLrel. 09,
                                                                                                                                                                                                 Rhabditoidea;
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    ANDERSON K
                                                                                                             the
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                                                                                                               EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                   sequence update)
  K., BAYNES C., BERKS M., COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                     484
                                                                                                                                                                                                 Peloderinae;
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                         BERKS M.,
                                                                                                                                                                                                    Caenorhabditis
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alignment_block:
US-09-323-427-3 x Q19053
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    Quality:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HANKINS T., HILLER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SOUNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
  194
                                           626 TTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG
                                                                                                                                                                                                                                                                           145 luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
EMBL; Z66496; CAA91280.1; -.
SEQUENCE 484 AA; 53325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 TACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATC
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alIleAspAlaAsnGlyCysSerValAspGlyValIleLeuGlnAsnLeu
                                                                                        sValHisSerCysThrValTyrAspGlyGlnGlyGlyProProValThrV
                                                                                                                                   TGTCCATTCCTGCTTTGTCGATGATGGT...AACGGTGATACTGTGGAAA
                                                                                                                                                                                   TyrHisLysTrpThrCysValAlaGluLeuGluAsnValTyrCysMetLy
                                                                                                                                                                                                                                   TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT
                                                                                                                                                                                                                                                                                                                                                                    uLeuGluSerGluThrGlnLeuProValCysArgTyrGluIleLeuAsnG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCT
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74.104
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Percent Identity: 45.020
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ID Q93532 PRELIMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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XA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
ANDERSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
ANDERSON R., DURTON J., COUNELL M., COPSEY T., COOPER J., COULSON A.,
ANDERSON R., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
AND JONES M., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
AND JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
AND LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
AND LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
AND LIGHTNING J., LLOYD C., MICKURAY A., SAUNDERS D., SHOWNKEEN R.,
AND LIGHTNING J., FORMAN B., COOPERA A., SAUNDERS D., SHOWNKEEN R.,
AND LOON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
AND THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
ANTSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
AND THE REST. TO SEASON J., TO SEASON J.,
AND THE REST. TO SEASON J., TO SEASON J.,
AND THE REST. TO SEASON J., TO SEASON J.,
AND THE REST. TO SEASON J., TO SEASON J.,
AND THE REST. TO SEASON J., WOHLDMAN P.;
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Eukaryota; Metazoa; Nematoda; Secernen
Rhabditina; Rhabditoidea; Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                                 110 CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTAT 159
                                                                                             41 nIleAspAsnGlyLeuGlnGlyGluProLeuIleArgCysGlySerGluS
                                                                                                                                                                                                                           30
                                                                                                                                                                                                                                                                                          10 CGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCC
                                                                                                                                                        GGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTT
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278542; CAB01742.1;
NCE 315 AA; 35785
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Ratio:
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bditidae; Peloderinae; Caenorhabditis.
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Gaps:
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RP RN RP
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                                                                                                                                                                                                                                                                     _documentation_block:
Q22164 PRELIMINARY;
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01-NOV-1996
01-JAN-1999
                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                            T04F8
                                                                                                                                                T04F8.4 PROTEIN
SEQUENCE FROM N.A
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191 sLeuAsnAspProSerThrGluGluArgIleSerTyrAsnValProLeuP
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGA 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aProGlyGlnAsnGlnThrSerProPheCysValThrValHisSerCysA
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                                                                                                                                                                                                                                                                                                                                                                                          uThrGlyGlyGlnLeuSerGlnValCysSerTrpThrValArg 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTT 692
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                                                                                                                                                                (TrEMBLrel. 01; Created)
(TrEMBLrel. 01; Last sequence update)
(TrEMBLrel. 09, Last annotation update)
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alignment_block:
US-09-323-427-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VANDERS D., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
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EMBL; Z66565; CAA91480.1;
SEQUENCE 384 AA; 43964
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGGTCTTTATGATCAAGAAGGTTGCCGT .........AATGA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAA 112
AGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG
                                                                                                                                          laIleAspValSerAsnLeuProThrGluSerValGlnSerAspLeuPro
                                                                                                                                                                                        AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
                                                                                                                                                                                                                                                                                                                                ValLeuIleIleSerPheHisProLeuPheLeuThrArgMetAspLysAl
                                                                                                                                                                                                                                                                                                                                                    ACTGTTGTCATTTCGTTTCATCCATCATTTTTTTTTTACCAAAGTTGAICGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysGlySerTyrAsnArgProGluCysArgValAspTyrSerThrLysAs
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                                                                                             ATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACC
                                                                                                                                                                                                                                                                                 ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                           \verb|snMetAspArgGlnArgMetIleAlaProGluGlyMetMetPheSerThr|\\
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                                            MetProThrCysSerTyrThrIleArgArgAspGlnLeuAspGlyProIl
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seq_name: sp_invertebrate:Q9XVN2
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 94150718. WHITE S.; "2.2 Mb of contiguo
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O9XVN2;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,
                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                  F53B6.6 PROTEIN. F53B6.6.
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                                                                                  Rhabditina; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                 TTACCATTTCGTTTAAATTTCGTCCAAATCAG 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAspGlyGlnGlyGluLysGlnMetIleIleAspGluArgGlyCysHi
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                                                                                                                                                                                                                                                                                                                alValValTyrHisArgTyrCysLysAsnGlu
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 nucleotide
                                                                                  Rhabditidae;
                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                     Created)
                                                                                                   Secernentea; Rhabditia; Rhabditida;
                                                                                                                                                                                                                                   PRT;
 sequence
                                                                                                                                                                                                                                   610
                                                                                  Peloderinae;
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   from
   chromosome
                                                                                Caenorhabditis.
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alignment_block:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                  144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
EMBL; Z81086; CABO3116.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 94150718.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                              hrLeuHisProArgGlyIleSerPheSerPheThrMetIleThrSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGATCAAGAAGGTTGC.....CGTAATGATGAAGGTGGACGTCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euAlaProGlnHisValAspGlnGluTyrSerLeuProValCysAlaTyr
                                                                                                                                                                                                                                                                                              HisProPhePheValThrGlyMetAspArgAlaPheSerIleArgCysPh
                                                                                                                                                                                                                                                                                                                                      CATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTT
TGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATA
                                   HisLeuLysAsp...GlyIleGluGlyHisValLeuArgPheAlaGlnVa
                                                                               GAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCAT
                                                                                                                                                                   TCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTAT
                                                                                                                                                                                                          ePheLeuGluSerIleLysGlyLeuAsnAlaGluIleAspValGlyThrL
                                                                                                                                                                                                                                                  TTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAspLysGlnHisCysValGlnHisSerAlaAspAlaHisSerSerPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTACACTTATTGCATTGTCTTATTCG....ATTCCGGTTGACAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
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2.762
68.519
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565
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Section of the contract of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WELNSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q93967 PRELIMINARY; PRT; 440 AA.
Q93967; Q94405;
Q1-FEB-1997 (TrEMBLrel. 02, Created)
Q1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
Q1-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOBSON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                      LENNARD N.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOBSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTATTACCATTAAAGAACCAAATAGCGAATGT......GTTCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alTyrGlyIleLeuIleHisSerCysTyrAlaAspAspGlyHisGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oGlnCysSer 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAATGTTCA 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isValPheLysTyrAlaAspLysValGlnLeuTyrPheThrCysThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uProGlnIleGluTyrGluHisGlyAlaIleSerAlaTyrThrAsnAlaH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATAATTTGGAATATCCAACAGAT...TTAATGGCTGGCCAAGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysPheGluLeuValAspAspArgGlyCysSerThrAspProPheLeuLe
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   Quality:
                                                                                                                                       440 AA;
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                                                                                                    JOINED.
MW: 3F2BBBA2 CRC32;
Length:
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      320
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US-09-323-427-3 x Q93967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477
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7 ATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGAT
                                                                                                                  Ratio:
                                                                                                   2.296
65.000
                                                                                              Gaps: 9
Percent Identity: 33.438
                              ţo:
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CATTAAAGAACCAAATAGCGAATGT..... rgValLeuHisGlnTrpHisCysAsnAspGln......MetTyrGly CTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTT TCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAA CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC lyMetLysSerLeuArgSerValAspProArgGlyMetTyrTyrGlyIle yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG TyrAlaLysGlyArgAlaGluLeuGluAspCysTyrLysAspAspPheGl spGluIleArgIleTrpValLysThrArgLysIlePheAlaGlyArgIle LeuLysIleLeuIleIleAlaTrpThrGlyTrpArgValAlaAsnAlaIl LysPheAlaAspLysProGlyValTrpPhePheCysGlnValGlnMetCy AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC TGGAATATCCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATAC pValIleAspAspLysGlyCysProIleAspProIleLeuIleThrGlyI AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAAAAAATA ValLeuIleAsnAsnCysTyrValThrAspGlyPheGlyLysLysAlaAs GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA TGGTGGA...CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC IleProGlyCysThrTyrSerIleHisArgSerThrIleAspGluLeuAs ATGCCAGTATGCCGTTATGAAATT.....TTGGA 476 luLeuGlyValSerMetIleProThrThrGluLeuGluAlaArgHisGly 153 $a Tyr {\tt HisValLysCysPhePheGluGluAlaAsnLysGlyLeuThrAlaG}$ ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA ACGTCAAGTTGCC......GGAATTTCACTTCCATTTGATTCATGCA TATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG eSerTleAspAsnGluTleTleGlyGluProAspIleGluCysLeuGluA pAlaGlyArgProAlaGlyAsnValIleGlnPheAlaArgValGlyGluA ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC ThrValValValSerPheHisProLeuPheIleThrLysValAspGlnAl .GTTCGACCACAATGT. 447 120 170 137 87 187 397 347 70 53 200

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alignment_scores:
Quality:
Ratio:
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US-09-323-427-3 x Q23097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

RY MEDLINE; 94150718.

AN HILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRELLE P.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRELLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORÇIMORE B., O'CALLAGHAN M.,

RA LAISTON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"1.2 M of Contiguous nucleotide sequence from chromosome III of C.

"1.2 M of Contiguous nucleotide sequence from chromosome III of C.

"1.3 MILSON R., WILKINSON-SPROAT J., WOHLDMAN P.;

"1.4 Marson R., Weinston R., WILKINSON-SPROAT J., WOHLDMAN P.;

"1.5 M of Contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q23097 from: 1
                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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Q23097 PRELIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  023097;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                  Nature 368:32-38(1994).
EMBL; Z71267; CAA95850.1; -.
SEQUENCE 387 AA; 43212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                             185 GTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILKINSON J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W01A8.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          903 TGCAGAACCG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853 GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283
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                                                                                                                                                                                       48
                                                                                        64 rLysProPheArgGlyAsnIlePheValLysGlyArgAlaLysAspLysS
                                                                                                                                                                                                                               85 CCAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACG
erCysArgGlnSerTyrAlaAsnAsnGlyThrAsnSerTyrSerLeuPro
                                                                                                                                                                                {\tt ProLysValIleCysAlaGluAsnAspLeuAlaLeuAspIleValThrSe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rProLysPro 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGluGluLysAlaProSerSerArgArg.....LysThrTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lySerMetSerArgValIleSerValGlyGlyGluAspAsnGlyGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               476.00
2.235
59.167
                                                                                                                                                                                                                                                                                                                                                                                   Length: 360
Gaps: 8
Percent Identity: 31.389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D127FF23 CRC32;
                                                                                                                                                                                                                                                                               to: 387
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351	TCTCAATGTTTATGGGTTTAAGCATTGCA ::::::: alProArqLeuLeuLeuProValLeuPro	336
٠ ر		1 4
0	TGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAA	
100 334	CAGTTGATTTACGTCACCGTGCACT ::: ::: /alLeuAspProAlaAspArgGlyLe	955 324
954 323	GAATATCATTGATGTACGAACTGATATCAACACCCTTGAA :::	307
0	AsnArgThrL	304
904	CTGCGCAACTTCGTTTACTCAAGAAAAGATCTG	855
303	::: uLeuSerGluAlaSerGlyAspGly	295
ū	TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGC	1
810 294	AACCAAATAGCGAATGTGTTCGACCACAATGT	779 278
7	erAsnGlnLeuTyrPheThrCysGlnIleArgLeuCysGlnLysG	o,
778	GATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG	729
728 261	CCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC ::::::	682 245
4	pPheAspGlyCysAlaThrAspProPheLeuLeuSerGluLeuSerTyr	N
ω .	TGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTGGAATAT	w
631	TGATGGTAACGGTGATACTGTGGAAATTCTAA ::: ::: rAspGlyAspGlyGluAspHisAlaValValA	582 211
581 211	CATAAATGGACATGCGATTCTGAAAACCGTTGATACTTTCTGCGCGGGTTGT	532 198
531 197	GACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTAT ::: ::: ::: ::: lyProAsnGlyProThrLeuThrTyrAlaAsnValGlyAspIleValPhe	181
181	::: MetProLysCysGluTyrSerValArgArgAspG	164
481	CTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTG	432
6	IleValThrGlnAsnIleAspValSerMetIleProThrThrGluLe	148
147	LysasnaspargalabheHisValLysCysPheTyrMetGluProAsp aacacmaaGmGcacacmagaGGTaTCTGaaaTCAGAAACTGGTTTTTCA	131
00	TGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGAT	332
w	::: ::::::	\vdash
w	TTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGT	285
284 114	TITGATTCATGCAATGTTGCGCGTACAACGATCTCTGAATCCAACGTGGTAT :::	235 98

1105 TTGATTGCTGCCGTCATTATTACCATTTCG

1134

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EN (2]

REQUENCE FROM N.A.

REDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA WILSON R., BORTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA BONTIELD J., BORTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRATTON M., DEAR S., DU Z., DORBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTUMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIPKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATESTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-323-427-3 x Q22680
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: Q22680 from: 1 to:
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   Q22680 PRELIMINARY;
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
                                                                                                                                                  203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
EMBL; 249071; CAA88879.1; -.
HSSP; P03000; 1TIF.
SEQUENCE 609 AA; 68882 MW;
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                                                                                                                                                                                                                                                                                             153 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            103 CCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 CGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AspAsnSerAsnTyrAsnPhe...TyrTyrThrHis......me
                                                                                                                                              GTGGACGT.....CAAGTTGCCGGAATTTCACTTCCATTT...GAT
                                                                                                                                                                                                                    ysThrArgLeuThrAsnArgProIleValMetAspLeuProPheArgGly
                                                                                                                                                                                                                                                                                                                                                                   SerGluGlyIleArgLeuHisIleAsnProThrGlyThrPheGlyGlyHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tGlu.Pro.....ProLysLeuGluCysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATT 52
TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGT
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2.399
65.854
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Gaps: 11
Percent Identity: 37.282
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBA2EEOC CRC32;
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285 ProIleLys 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGCGTTGTCCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTTCAAACTCA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProCysAsnValArgArgArgAsnValAlaProProSerIleSerTy
                                        GCTGTTAAA 840
                                                                                                                                                                      nValMetValHisPheSerCysGlnIleThrThrCysGlnLysGlnGluA
                                                                                                                                                                                                                                                                                                                                               rgGlyCysValThrAspPheSerLeuPheProGluValSerTyrSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpThrCysAspSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnGlnArgIleAsnValSerAspIleProSerThrAlaLeuGlnSerLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAAACAGTT
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                                                                                   snGlyCysGluGlyIleSerProProIleCysArgProMetAspLeuGly
                                                                                                                            ATAGC...GAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGA
                                                                                                                                                                                                                 ATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAA
                                                                                                                                                                                                                                                          {\tt AspLeuLysSerAlaPheThrAlaValArgAlaPheArgTyrAlaAspGlue}
                                                                                                                                                                                                                                                                                                     GATTTAATGGCTGGCCAAGAAGCT...CACGTATACAAATATGCGGATCG
                                                                                                                                                                                                                                                                                                                                                                                        ATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                 rCysValValArgAspGluSerGlyLysAspPheGlnPheIleAspGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          snGlyProValValArgPheAlaAsnValGlyAspValValValHisLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt spLysAlaTyrArgLeuAsnCysIleTyrArgGlnGlnGluSerThrLeu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAACAACTGTTGTCATTTCGTTTCATCCATTATTTTGTTACCAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspArgPheGlyPheValValHisSe
                                                                                                                                                                                                                   784
                                                                                                                                                                                                                                                                                                                                               234
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Database :
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Maximum DB seq length: 1000000
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Perfect score:
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         821193 seqs, -1518192014 residues
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-323-427-3
1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              April 16, 2000, 04:52:00; Search time 4841.33 Seconds (without alignments) -728.156 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pr1:*
gb_pr2:*
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gb_ba2:*
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em_pl:*
em_ro:*
em_ba2:*
em_hum3:*
em_hum4:*
gb_pr4:*
gb_htg3:*
gb_htg4:*
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                                                                                             gb_in1:*
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em_vi:*
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                                                                                                                                                                                                                                                                                                                 em_hum2:*
em_in:*
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45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_p13:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match

Length

DB

ij

Description

00000 00000 000 a a 339. 323.6 315 261.4 249 217.2 190.6 156.6 107.4 83.8 74.8 54.8 51.8 51.8 4.6 40265 4.5 40600 4.5 164548 4.2 23953 4.2 31731 4.0 45713 4.0 45713 3.7 165302 3.7 165302 3.7 165302 3.5 10200 3.5 10200 3.5 110000 3.5 110000 3.5 12576 3.5 95713 3.6 12976 3.7 12976 3.7 165302 3 358 39478 2 31536 2 32412 3 39736 5 110000 1 36306 1 36069 724 5792 2584 637 U67530 4 CEY53H1B 2 CEY53H1_2 AAF090533 AB017910 AC005739 AF207067 SGU40026 CEF53B7 AF044022 AC004479 EGU21005 AE001500 CEY102F5_(ATAC007020 AF085279 CEF22B5 CEC47G2 CELCUT1 AF125580 ALU73005 MAMTCUT1 BMA012617 BPA012618 PFMAL3P6 AC009451 CET04F8 CELK06A1 CELK03H9 CELB0511 CET22C8 CEW06D12 CEF20D1 CEZK265 CEW01A8 CEY39A1_3 CEM142 CEE04D5 CEF53B6 CER07E3 CEY71H9 CEY70D2 CEM28 CELF10E7 N73005 Ascaris lum X96677 M.artiellia AJ012617 Brugia ma AJ012618 Brugia pa Z81086 Caenorhabdi Z66496 Caenorhabdi Z66496 Caenorhabdi Z64907 Caenorhabdi Z71428 Caenorhabdi Z71267 Caenorhabdi Z7267 Caenorhabdi Z82073 Caenorhabdi Z82073 Caenorhabdi Z82073 Caenorhabdi AL02187 Caenorhabdi Z78542 Caenorhabdi Z78542 Caenorhabdi Z82073 Caenorhabdi Z82073 Caenorhabdi Z82073 Caenorhabdi Z82073 Caenorhabdi AF067608 Caenorhabdi AF07207 Caenorhabdi AL021575 Caenorhabd AL0221575 Caenorhabd AL022276 Caenorhabd AL022276 Caenorhabd AL022276 Caenorhabd Continuation (3 of AF090533 Dictyoste AB017910 Dictyoste AC005739 Homo sapi AF207067 Homo sapi Z50044 Caenorhabdi Z49125 Caenorhabdi M55997 C.elegans c AF125580 Wuchereri AC004479 Homo sapi U21005 Euglena gen AE001500 Helicobac U40026 Streptococc Z72510 Caenorhabdi U67530 Methanococc AF044022 Eurytides AL132851 Caenorhab

RESULT 1
CCEF22B5/c
LOCUS
DEFINITION
ACCESSION
VERSION

CEF22B5 25823 bp DNA INV 02-SEP-1999 Caenorhabditis elegans cosmid F22B5, complete sequence. 250044 250044.1 GI:899234 E250044.1 GI:899234 GTP-binding ADP-ribosylation

ALIGNMENTS

KEYWORDS

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FEATURES
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TITLE
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. ImpORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small current sequence of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smilt, Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F22B5.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Coulson,A., Craxton,M., Dear,S., Bu,Z., Hillier,L., Jier,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,
Johnston,L., Jones,M., Kershaw,J., Kisten,J., Laister,N.,
Tatroille B. Hichting, T. Llayd, C. MAM, Tray, D. Marting, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor; Phenylalanyl-tR
Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence Z66523.

The true left end of clone M05D6 is at 25723 in this sequence. The true right end of clone F14E5 is at 4610 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence Z66522.
The true right end of clone F22B5 is at 16002 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The true left end of clone F22B5 is at 24607 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL-1995) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sims, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighbouring submissions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 25823)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end of this sequence (25723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           graphical representation of this sequence and its analysis
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                                                                                                                                                                                                                    gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z66523
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                                                                                                                                                                                                                                                                     /note="similar to RNA binding protein; cDNA EST yk390d8.5 comes from this gene; cDNA EST yk499d6.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="F22B5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .25823) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insert of
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DKFLLNNLEYPTDLMAGOEAHYYKADRSQLFYQCQISITYKEPNEECARPTCSEPQG
EGAYKQANQTAQFFRYLKKRSAPYMENILDVRAELTTLEYLEGNLPSSLTQAQALVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to cuticulin; cDNA EST EMBL:T01970 comes from this gene; cDNA EST CEESX90RB comes from this gene; cDNA EST CEESX90RB comes from this gene; cDNA EST yk386c7.3 comes from this gene; cDNA EST yk386c7.5 comes from this gene; cDNA EST yk504bl2.3 comes from this gene; cDNA EST yk504bl2.3 comes from this gene; cDNA EST yk504bl2.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk543g2.3 comes from this gene; cDNA EST yk652b8.3 comes from this gene;
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EPTLGFDIKTVHFKDFQLNLMDVGGQKSLRSYMKNYFESTDALIMVVDSSDRERLLQC
SEELKKLLGEERLAGASLLVLANKSDLPGAIDVNSIAQVIQMSSVYTSEKKCFLVLDL
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PDGLNFSKVFVSSNPSNAPC"
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/gene="F22B5.3"
                                 AAQAIFQSIIQDLPMKDLKDVLVRCSDKFEDSATWIRPFLRRSHEMTPFAHIKFNRVI
                                                                                                                                                                                                                                                                                                                     /protein_id="CAA90357.1"
/db_xref="GI:3876229"
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/db_xref="GI:3876225"
/db_xref="SWISS-PROT:Q19705"
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VVTQFKVINKRVPKVVADRKKWVKFGSCKGEPAGPQVATTYVAEEVDMQFTRNRAGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F22B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAEIWLDRSNSKAPWDWERLRDTYWKMPTVAFDLDGRTRKRCELMEQLQDEMLEAAKK
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/db_xref="GI:3876228"
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/db_xref="GI:3876227"
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/gene="F22B5.1"
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      AAACTTCTGTAATTTTTAAGGAATGCTTCTTGAAGGTTTAGGATACCGAAATTATAAAGC 3752
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/tasns1ation="MSNWDYLDEVDILPKLPPNFDELRESKKWOERKEALEALLKVLT/
/trans1ation="MSNWDYLDEVDILPKLPPNFDELRESKKWOERKEALEALLKVLT/
DNERLSTKASYAELIGHLQWYLAKDANINCQALAAKCIGKFATGLRAKFSSFAGPLLP
VIFEKHKEK FWLREPLYDCSNEVGRTWGSLETGQEDILAALAKPNPQIKQOTALFVA
ROLDLVPAKOPKGFIKAVVPVFGKLTGDADQDVREASLQGLGAVQRIIGDKNVKNLL
GDASSDEGKMKKIGEYAEKSTASFACHTANPFVSSTPSASAASGTATA
VVSSGAPVAEADPWDFLDAFDVLSKMPDGFDTNIESKKWQERKEALEGLLDLITANPK
LDPKANYGALVERLOKVLEKDANINVAALAANCITGIANGLRTKFQPFAVSVTPFIIFE
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complement(join(12240. .12394,12467. .12541,12691. .12784,
13262. .13392,13465. .13524,13876. .14032))
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18794. .18946,18996. .19449,19497. .19843,20042. .20554,
20672. __21600,21677. .21812)
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/gene="F22B5.7"
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/db_xref="GI:3876232"
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/db_xref="GI:3876230"
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Wilkinson-Sproat,J.
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3103 AGTTTTGGAAGGAAATGTAAGTTGTCAAAATGGTGTTCAT 3064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggatggtggaccaaccggtcaaccagttcaatttgctatcattggtcagccagtttatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aattagcgatgataatcaagctttgccagttgatttacgt 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaaaagatctgcagaaccggagaatatcattgatgtacgaactgatatcaacacccttga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGGAACCAAATGAGGAGTGTGCTCGCCCAACGTGCTCTGAGCCACAAGGATTTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgtatacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccat
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Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A.,
Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Yaughan,K., Waterston,R., Watson,A., Weinstock,L.,
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Z49125.1
                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
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Caenorhabditis
                                                                                                                                                                                                                                                                                     Rhabditina; Rhabditoidea; Rhabditidae; 1 (bases 1 to 34831)
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bditidae; Peloderinae; C
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and Wohldman, P

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FEATURES
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTION: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone C47G2. It may be shorter because we only sequence overlapping sections once, or longer because arrange for a small overlap between because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2 Mb c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions. The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 249912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-APR-1995) Louis, MO 63110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palmer, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature
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15433. .17108
/gene="C47G2.2"
join(15433. .157
                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT: 003755"
/translation="MTWKPIICLAALVLSSAAIPVDNNVEGEDEVECGPNSITVNFNT
RNPFEGHVYVKGLYDQAGCRSDEGGRQVAGIELPFDSCNTARTRSLNPKGVFVSTTVV
ISFHPQFVTKVDRAYRIQCFYMESDKTVSTQLEVSDLITAFQTQVVPMPVCKKEILDG
GPSGQPIQFATIGQQVYHKWTCDSETTDTFCAVVHSCTVDDGNGDTVQILNEEGCALD
KFLLNNLEYPTDLMAQCEAHVYKYADDSQLFYQCQISITIKDDGSECARPTCSEPQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 From this gene; cDNA EST wk278g8.5 comes from this gene; cDNA EST yk262c12.3 comes from this gene; cDNA EST yk262c12.5 comes from this gene; cDNA EST yk262c12.5 comes from this gene; cDNA EST yk265h3.5 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.3 comes from this gene; cDNA EST yk278g8.5 comes from this gene; cDNA EST yk278g8.5 comes from this gene; cDNA EST yk439e8.5 comes from this gene; cDNA EST yk583c11.3 comes from this gene; cDNA EST yk583c11.3 comes from this gene; cDNA EST yk583c11.5 comes from this gene; cDNA EST yk585c11.5 come
                                                                                                                                                                                                LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGICLTP
                                                                                                                                                                                                                                                        GAVKQAGAGGAHAAAAPQAGVEEVQAAPVAAAAPVAAAVAAAAAPAVPRATLAQLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA88934.1"
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/gene="cut-1"
                                                                                                                                                   IGFASFLGIGTIVATALSATIFYVARPTSHKH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=]
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/chromosome="II"
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     .15770,16205.
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     .16531,16772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 computer analysis,
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/note="similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 Comes from this gene; cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:D36131 comes from this gene; cDNA EST SET CDNA EST SABDIC:D3610 comes from this gene; cDNA EST SABDIC:D3610 comes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /di_xref="Stftembl:Q18695"
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RVYWGAQLLTWLILDLLQSYYTAGRETILGETRAPVINNALYYAIYSLCFLAILIYA
MFKGVSINIENLKVIVVSASNTWGLFLLVVLLGHGLVELPRSLWHHGNRHYRLRKTYF
DIEKLASEKSEAEENVKDIYKKVRVLENSMKNDSNGQRKVRFILGKFSDDVIDNLFP
SRQVIDNAHLDESGFCSEAKLISLHKKTIYAVQTLNNATAQWKVLVDRALFLENLAFS
ESNGYNLELSRNTCVPIGVRREWYTRLQFPCRILGIYTVFMTFFVLFSECTFFVVSY
TLSPAAFVTEYASTRPHYKYTQFVAFGIIVLITSAYFTIFRLQIYKYYHLDRGHTD
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25668. .25907.25967. .26054,26106.
26681. .26785,26846. .26914))
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IAQESASEAVTDGRSSDEDSHFARRSLCYDERSKSMPAKKLSKETSIFQMFWAKEEE
ENSLMRLLKFDNFTLEBVLLNEFVYQESRYGKAELVQXITSRENMKALLESLAPKIN
TDLPMKQQYRLSFIASEILTIRGTDVFQKQIVTTEETRKCLVDFLNDKTPLNHLVAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="cDNA EST CEMSB75F comes from this gene; cDNA EST EMBL:Cl362l comes from this gene; cDNA EST yk227d8.5 come from this gene; cDNA EST yk257e7.5 comes from this gene; cDNA EST yk319c4.5 comes from this gene; cDNA EST yk319c4.5 comes from this gene; cDNA EST yk331d4.5 comes from this gene; cDNA EST yk335b12.5 comes from this gene; cDNA EST yk3486d7.5 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(30076. .30134,30184. .30492,31050. .31274,31321. .31480,31534. .31653,31701. .31835,31889. .32104,32160. .32570,32639. .32935,32998. .33215,33263. .33651,33802. .34049)
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KGINIYLPICIILLCAIHYYRVGAYVLHNIGFDQFVEADEMTNDMINSGRSLVQIERN
SIKRSNDRSQRTQNWTNSFGSSNAGNGSTTSKFKRSNKNDEERPMLEDDDEEVEESST
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kfeyykkekfpamqonsilhlsluddfvkvargpengkenymaldpncedmednesflr
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mpaffipqnidsqkllsmmasrimpmdapvssgqkrtsssssenengssavsdklsa"
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                                                                                                                                                                                                                                                                                                             /protein_id="CAA88937.1"
/db_xref="GI:3875033"
/db_xref="SPTREMBL:Q18696"
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                                                                                                                                                                                                                                                                translation="MWAEGKRRNNRKKSRRDREGTSASSDAYSSDSDAEDDITQDDDD/
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/db_xref="GI:3875032"
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6054,26106. .26227,26277. .26608,
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REFERENCE
AUTHORS
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SOURCE
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Local Similarity /4.2
409; Conservative
                                                                                                                                                                                                                                                                                                     CGCTGCTCCAC
                                                                                                                                                                                                                                                                                                                                        agctgcgcaac 880
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                                                                                                                                                                                                                                                                                                                                                                                                     ttcagaaccacaaggattcggagctgttaaaaccaggtggtgccgcagcaacacctgctgc 869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tatcattggtcagccagtttatcataaatgggacatgcgattctgaaaccgttgatacttt 569
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                                                                                                                                                                                                                                                                                                                                                                                  CTCAGAGCCACAAGGATTCGGAGCCGTCAAACAAGCTGGTGCCGGAGGAGCTCATGCCGC
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                                 cuticle protein; cuticlin 1
C.elegans DNA.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematod
Rhabditina; Rhabditoidea; R
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1 (bases 1 to 2310)
Sebastano, M., Lassan
                                                                                                                                                          CELCUT1 2310 b
C.elegans cuticlin
M55997
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MDETLIAKIADNLIVEEGCPAEELVKKSALISASAKILEAFIKIMFYSNAPAQOLEEI
ERNLIERHYSYGLMRECMDNIPYEHSYOPDERIVEGILAURLPNILOTYLRDIEAN
GSVWQPLLRLIIELCNTNCMSTHEKIAVAFRSLPFINLIKAAKHLPRASUTHCLLYKY
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WADDFSSFFTISFTAANASSSSCADAWPGSDIHLOGEASDWPLNNSHESKASDPVMVG
LAASISHPGDSSEA"
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Lassandro, F. and
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                                   Nematoda; Secernentea; Rhabditia; Rhabditida; oidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                           GGAGGACCATCCGGACAACCAATCCAGTTCGCCACCATCGGACAACAAGTCTATCACAAA
                                                                                                                                                                                                                                                                                             acaactgcttttcaaactcaaattgtcccgatgccagtatgccgttatgaaatttttggat 477
                                                                                                                                                                                                                                                                                                                                    CCATGCTTCTACATGGAGTCCGACAAGACTGTGTCCACACAGATCGAAGTCTCGGATCTC
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gaaccaaatagcgaatgtgttcgaccacaatgttcagaaccacaaggattcggagctgtt
                                       tacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccattaaa
                                                                                         TGGACTTGCGATTCTGAGACCACTGACACCTTCTGCGCCGTCGTTCACTCTTGCACTGTC
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                          TACAAATATGCCGATCGCTCCCAACTCTTCTATCAATGCCAAATCTCCATCACCATCAAG
                                                                           CUT-1 a Caenorhabditis elegans gene coding noncollagenous component of the cuticle Dev. Biol. 146, 519-530 (1991)
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91323673
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join(1186. .1920,1971.
/gene="cut-1"
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/product="cuticlin
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/db_xref="taxon:6239"
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75.1%;
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Pred. No. 2e-64;
0; Mismatches 130;
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les 396; Conserv
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ccgcagcaaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaac
                                                                                                                                                                                            ATAAAGTAGAGCTATTAAATGCTGATGGTTGTGCTTTGGACAAATTTCTACTTAATAATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCAACGACCACTGCACTGCACCGCCAAGGTTTTGGCGCCAATTAAAACGCGCAATGGTG
                                          TAGAATATCCAACAGATTTAATGGCTGGACAAGAAGCACGTATACAAATACGCTGATC 180
                                                                                                                                                    tggaatatccaacagatttaatggctggccaagaagctcacgtatacaaatatgcggatc 733
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Wuchereria
AF125580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-FEB-1999) Research & Training Center on Vectors of Diseases, Ain Shams University, Abassia Square, Cairo, Egypt Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chases 1 to 724)
2 (bases 1 to 724)
Ramzy,R., Helmy,H., Adely,M., Curtis,K. and Weil,G.
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Ramzy, R., Helmy, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wuchereria bancrofti L3
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ASRQAAAFRYLKKRDVRDENIVDYTDLIALDINEEFTSLPNALRHRSSLLAHENGHP
VIVARMTQGICMSITGEFTLAGMLIFVIVSVATIVAITLLRSHSTKV"
112 c 128 g 236 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Wuchereria bancrofti"
/db_xref="taxon:6293"
/dev_stage="L3 larvae"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD28743.1"
/db_xref="GI:4741875"
/translation="TVDTFCAVVHSCFVDDGNGDKVELLNADGCALDKFLLNNLEYPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cuticulin-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Ascaris lumbricoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       country="Egypt:
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                                                                                                                                                                                                                                                                                                                  Score 261.4; DB 35; Pred. No. 8.7e-52;
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A partial sequence
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U73005
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Gene 193 (1), 81-87 (1997)
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Timinouni, M. and Bazzicalupo, P.
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Eukaryota; Metazoa; I
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           /translation="MCRAVSFLALFGLAAAIPVDNGVEGEPEIECGPTSITVNENTRN
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FHPLEITKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQTQIVPMPVCRYEILDGGP
TGQPIQFATIGQQVYHKWTCDSSTVDTFCAVVHSCFVDDGSGDTIQILMEEGCALDKY
LLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQITTIKEPNSECPROTCSEPQGFGA
                                                                                                                                                         join(882. .954,2851. .3239,31/gene="ascut-1"
/note="cuticlin gene; ASCUT-proteins of other nematodes"
                                                                                                                                                                                                                                       882. .929
                                                                                          /product="CUT-1-like cuticlin protein precursor"
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/db_xref="GI:1657625"
VRPGGSIAPKKQRRCQLRLIKKSGGDYDNTLDVRTDFSALDISDRDEALPMDLRHRAF
                                                                                                                                                                                                                                                        /note="site of transplicing by
                                                                                                                                                                                                                                                                      /gene="ascut-1"
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                                                                                                                                                                                                                                                                                                                                    /gene="ascut-1"
/product="CUT-1-like
                                                                                                                                                                                                                                                                                                                                                                                                                                     /variety="suum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Ascaris lumbricoides"
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                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                          /gene="ascut-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:6252"
                                                                                                                                                                                                                                                                                                                                                                                    'gene="ascut-1"
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         AUTHORS
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                                                                    JOURNAL
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Direct Submission
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
Biologia Molecolare, Via Orabona 4, 70126, Bari, ITALY
2 (bases 1 to 2584)
De Giorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
Modulation of expression at the level of splicing of cut-1 RNA in
                                                                                                1 (bases 1 to De Giorgi,C.
                                                                                                              Meloidogyne artiellia
Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria;
Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;
Meloidogyninae; Meloidogyne.
1 (bases 1 to 2584)
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X96677
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5064. .5070
/gene="ascut-1"
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join(930. .954,2851. .3239,3583. .4083,4499. .4690)
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4694. .5081
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Pred. No. 7.7e-49;
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                  aacaacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtgcata
                                                                                                                                                           ttatgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcact
                                                                                                                                                                                                          ARTCACCGTCAATTTCAACACACACGCAACCCTTTCGAGGGGCACGTCTATGTGAAAAGGCCT
                                                                                                                                                                                                                             aataacaatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtct
CTCCACAACGGTGGTCATCTCCTTCCATCCACAGTTTGTCACCAAAGTTGACCGGGCCTA
                                                                                       tccatttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtatttttgt
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                                                                                                                                                                                                                                                                            TGCAATTCCAGTGGACAACGGTGTGGAAGGCGAGCCAGAGATTGAATGTGGCCCCAACCTC
                                                                     TCCGTTCGACTCTTGCAATGTTGCCCGCACTGATGCT - - - GAACCCAAAGGAGTGTTCGT
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97218031
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join(<467, .943,1139, ...
/gene="Mtcut-1"
467, .2052
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2518. .252
a 639 c
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1825. .>2
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CMSSFRANHLLRYGHCNGCSHWWVHSTYCLFIVVFFSNEIK"
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<467. .943
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56.8%;
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                                                                                                                                                                                                                                                                                                                                                                  Score 217.2; DB 3 Pred. No. 2.4e-41;
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Mol. Bio
99339397
                    cut-1-like genes are present in the filarial nematodes, pahangi and Brugia malayi, and, as in other nematodes, components of the cuticle
                                                                                                                                                      BMA012617 637 bp
Brugia malayi cut-1 ge
AJ012617
AJ012617.1 GI:3858954
                                                                   Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 637)
Lewis, E., Hunter, S.J., Tetley, L., N
                                                                                                                      Brugia malayi
                                                           Devaney,E
                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                                 Brugia malayi.
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            Biochem. Parasitol.
                                                                                                                                             gene; cuticlin.
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                                                                      Tetley, L., Nunes, C.P.,
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TITLE
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Best Local Similarity
Matches 334; Conser
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Direct Submission
Submitted (06-NOV-1998) Devaney E., Veterinary Parasitology,
University of Glasgow, Bearsden Road, Glasgow, G61 1QH, UK
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/gene="cut-1"
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/translation="visfhplsvtkvdrayrvqcfymeadktvstqievseittafqt
Qivpmpvcryeildgcptgqpiqfatigqpvyhkwtcdsetvdffcavvhscfyddgn
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/product="cuticlin"
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Pred. No. 4.4e-35;
D; Mismatches 54
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                                               ACCGTTGATACCTTTTGCGCAGTTGTCCACTCCTGCTTTGTGGATGATGGCAACGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-NOV-1998) Devaney E., V. University of Glasgow, Bearsden Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cut-1-like genes are present in the filarial nematodes,
pahangi and Brugia malayi, and, as in other nematodes,
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1 (bases 1 to 358)
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                                                                                                                                                                                                                                                                                                          /number=1
350. .356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brugia pahangi"
/db_xref="taxon:6280"
join(<1. .191,350. .>356)
/gene="cut-1"
                                                                                                                                                                                                                                                                                          /gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:096776"
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                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA10075.1"
/db_xref="GI:3970656"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(<1. .191,350. .>356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="cut-1"
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                                                                                                                                                                    Score 156.6; DB 34;
Pred. No. 4.6e-27;
0; Mismatches 24;
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d, Glasgow,
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G61 1QH, UK
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REFERENCE
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                                                                                              CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATATCCAACAGGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, usir predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                 overlap between neighbouring submissions.
This sequence is the entire linsert of clone F53F1. The true right end of clone M04G12 is at 21759 in this sequence. The start of this sequence (1...101) overlaps with the end of sequence z81103. The end of this sequence (39379. .39478) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Boulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
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Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                         sequence
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Current sequence finishing criteria for the C. eleg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              available information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEF53F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 39478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                  AL021448
                                                                                                                    complement(14923.
/gene="F53F1.1"
                              16033. .16271,1
/gene="F53F1.1"
                                                             complement(join(14923. .15347,15663. .15774,15835. .15984, 16033. .16271,16318. .16486))
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                                                                                                                                                                                 /clone="F53F1"
                                                                                                                                                                                                            /chromosome="V"
                                                                                                                                                                                                                                           /db_xref="taxon:6239"
/note="predicted using Genefinder; similar to
                                                                                                                                                                                                                                                                      ∕organism="Caenorhabditis elegans
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   cuticlin"
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/note="predicted using Genefinder; similar to cuticlin; cDNA EST EMBL:D72018 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C1251 comes from this gene; cDNA EST EMBL:C10682 comes from this gene; cDNA EST EMBL:C10682 comes from this gene; cDNA EST EMBL:C10682 comes from this gene; cDNA EST yk3163.3 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h10.5 comes from this gene; cDNA EST yk31092.3 comes from this gene; cDNA EST yk31092.3 comes from this gene; cDNA EST yk31092.5 comes from this gene; cDNA EST yk19109.3 comes from this gene; cDNA EST yk19109.5 comes from this gene; 
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AVNPVDIQNSLYGDVQVECDSRTISVQLKTEKDFVGVIFVKDFXYNLLCLXRESQVY
ARLETEIGLGALRQRYLUPKGLAVRTTITISESHPYFTTKVDRTYNLLCLXRESQVY
ANNISVDEISTISYNVNLTMPTCTYQILSGGPFGEPVEFGLIGQQVYHQWKCDNDKGM
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18714. .20251
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NYEIVHLEELKTYAKVPPCANQLEYHPHFARIPLQKYCKEKNIFFQAFSSLARHEPKL
IEDPVVVELAKKHNTSVPLVLLAWALRQNVGIVPKSVTPSRIVENFKVIDIALTPEDI
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                                                                                            25572. .26408
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join(21582. .21670,21781. .22009)
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19919. .200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKNSFLTFFKSPYMYVVGITNYHNKAIQKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IILIKEDSFCMVVHTCSVDDGRGETSFLIDSNGCSIDKFLLSNLEYPGNLLAGQEAHV YKFADRDALFFQCQISITVKEPDQECVRPICEDVEGGGAPVVGPPPYGMISKNLVNIW
join(25572. .25660,25850. .26408)
/gene="r53F1.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB03128.1"
/db_xref="GI:3877460"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F53F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18339. .18524)
/gene="F53F1.2"
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18339. .185
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/db_xref="GI:3877456"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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.20008,20072. .20251)
753F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .17599,17683. .17926,17977. .18146,18197. .18286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .19056,19113.
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gene

/note=*predicted using Genefinder; similar to cuticilin; cDNA EST SPREL:07107 comes from this gene; cDNA EST EMBL:07180 comes from this gene; cDNA EST EMBL:071810 c

Query Match 9.3%; Score 107.4; DB 34; Length 39478; Best Local Similarity 61.7%; Pred. No. 2.1e-15; Matches 171; Conservative 0; Mismatches 106; Indels 0; Gaps

0;

617 ctgtggaaattctaaatgctgatggatgtgctcttgataaatatttgctaaataatttgg 676

QΥ

gene

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15110 TGAGACCAATATGTGAAGATGTAGAAGGCGGTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTATCCGGGAAACTTACTCGCTGGGCAAGAAGCTCATGTGTATAAGTTTGCTGATCGAG 15171
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right enc 248585.

Sequence 248585.

The true left end of clone 78673 is
                                                                                                                                                                                                                                                                                            bin/display?db-wormace&class*Sequence &object=E04D5
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a smal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rikken, L., Roopra, A., Sanders, D., Showhkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Watkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                       overlapping sections overlapping sections.

Overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone E04D5.

It may be shorter because we only sequence overlapping sections

It may be shorter because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, usi
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                          neighbouring submissions.
The true left end of clone E04D5 is right end of clone E04D5 is at 2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 31536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-OCT-1995) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McMurray,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368 (6466), 32-38 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; Cuticlin-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2 Mb of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 31536)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of this sequence and its analysis
                              is
                              at 31437
11412 in
                                                                                                               at 1 in this sequence. The true in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       833
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                                                       in this sequence. The
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FEATURES
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The end of this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from this gene; cDNA EST yk495615. Comes from this gene; cDNA EST yk4505.15 comes from this gene; yk454d9.3 comes from this gene; cDNA EST yk450b11.3 comes from this gene; cDNA EST yk450b11.3 comes from this gene; cDNA EST yk450b11.5 comes from this gene; cDNA EST yk40b11.5 comes from this gene; cDNA EST yk413f5.3 comes from this gene; cDNA EST yk402d12.3 comes from this gene; cDNA EST yk402d12.5 comes from this gene; cDNA EST yk402d12.5 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk375c1.5 comes from this gene; cDNA EST yk375c1.5 comes from this gene; cDNA EST yk365e8.3 comes from this gene; cDNA EST yk365e8.5 comes from this gene; cDNA EST yk365e8.5 comes from this gene; cDNA EST yk365e8.5 comes from this gene; cDNA EST EMBL:C12803 comes from this gene; cDNA EST EMBL:C13136 comes from this gene; cDNA EST EMBL:C13136 comes from this gene; cDNA EST yk596c5.5 comes from this gene; cDNA EST yk596c5.3 comes from this gene; cDNA EST yk596c5.3 comes from this gene; cDNA EST yk596c6.3 comes from this gene; cDNA EST yk596c5.3 comes from this gene; cDNA EST yk596c5.5 comes from this gene; cDNA EST yk596c5.3 comes from this gene; cDNA EST yk596c5.5 comes from this gene; cDNA EST yk596c5.5 comes from this gene; cDNA EST yk596c5.5 comes from this gene; cDNA EST yk596c5.3 comes from this gene; cDNA EST yk596c6.3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Mote="cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA EST EMBL:D6310 comes from this gene; cDNA EST EMBL:D65192 comes from this gene; cDNA EST EMBL:D68540 comes from this gene; cDNA EST EMBL:D1941 comes from this gene; cDNA EST EMBL:C11194 comes from this gene; cDNA EST EMBL:C11881 comes from this gene; cDNA EST yk412d7.3 comes from this gene; cDNA EST yk459b6.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNOVTRVEEIATNKEILCVELKRTRKILESPKDNFLLTFEPWAVYGPKTAENOKPEP
NVRVSLADGKHVSTESAPKEASWEPOESDASLAARWYGSEVEFYTNNSFERVDHKL
VEKGAYNFALSGPAPANHVAVYVPAVGSTPARFVRHKVESESPPVGNRTFKSDKAVM
TWNORGOSLLILASVEVDKTNOSYYGEOSLYLINIQSGESVVVPLEKKGPIYAAKWNP
NGREEAVCYGYMPAKVTFYNPRGVPIFDTIEGRNDVFYNAFGUIVLICGFGNIAKGK
MEFNDVETKKEIISIEVPHTTHEDWAPDGGHFYCTTTAPKTRIDNSYRHHYTGRNLA
ETHFESPKELWEVRWRPMTGYNKFAIKELTKTDKMAAGLPIRKKDASHPLNNVPAGAV
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join(6082...6250,6307...6379,6432...6509,6564.../
6750...6930,7003...7283,7337...8179,8228...8326)
                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(8619. .8761,8813. .8988,9895. .10028,
10089. .10283,10330. .10614,10730. .10935,11582. .11629,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8619. .11718)
/gene="E04D5.2"
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EQERKAFQLKKKYEEIKVLKQRVANGDQLQPNQMEKIQRENEYLSELSKLTI"
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YIVPVFFIAKVVQFAIPFILILITFERYLWTCTERKRFGITFQVLTLSLSFRKAFSAI

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DEFINITION ACCESSION
                                                                                  RESULT 11
CEF53B6/c
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Best Local Similarity 56.1%;
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                                                                                                                                                                                                                                               agaaccaaatagcgaatgt 795
                                                                                                                                                                                                                                                                                                         CTTCAAATTTGCTGACAAAGCTGGGCTTTATTTCAATTGTCAAATTCAATTAACAATCAA 28082
                                                                                                                                                                                                                                                                                                                                                      atacaaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccattaa 776
                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGATCCTTCAGAATCTTGAGTACACCTCTGACTTGACAGCTGGAAAACTCGCACCAGT 28022
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgatggtaacggtgatactgtggaaattctaa---atgctgatggatgtgctcttgatáa 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACTTGCGTTGCTGAACTTGAGAATGTGTACTGTATGAAAGTTCACTCATGTACGGTTTA 27902
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Caenorhabditis elegans cosmid F53B6, complete sequence 281086
                                                         CEF53B6
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VACVDTSTQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mpsrlamkelkgggepevvcetasisllfktrnsfngkvfvkgy
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gklapvekfadkaglyfncqiqltikdvnygcsntopocptsgyvvebagkttetaep
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YIAETPENAYDGIVGFNDTEQPFTTSAAYTEDGVYSRLIKRNVVESTEQINASNKKRP
VTVGDIDLPERGILVEGLEEMEDGETTNAGDHGATRALREARNSQEKTCFSTSRMYFT
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NLPENYVLLQVAADVIKESLIHRSSRSKRSQLRNAIYTMLAIVTSYLVCNGVHLFLTI
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/db_xref="GI:3875453"
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"E04D5.3"
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Pred. No. 7.8e-10;
                                                           DNA
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AUTHORS
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ORGANISM
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                      source
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Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IT may be shorter because we only sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F53B6. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neighbouring submissions.
The true left end of clone F53B6 is at 1 in right end of clone F53B6 is at 5116 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence Z81523.

The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            start of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditina, Rhabditoidea; Rhabditidae, Peloderinae; 1 (bases 1 to 32412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; Cuticulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z81086.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bin/display?db=wormace&class=Sequence &object=F53B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; Cuticulin; Human platelet tetraspan antigen like; Initiation factor associated protein; Thrombospondin like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 32412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end of this sequence (32306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z81523
                                                                               platelet-endothelial tetraspan
/protein_id="CAB03120.1"
/db_xref="GI:3877452"
                                                                                                                                      /gene="F53B6.
                                                                                                                                                                                                                      1480. .3649
/gene="F53B6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:1627952
                                                                                                                                                                  join(1480. .1638,1707.
3205. .3308,3430. .364
                                                                                                                                                                                                                                                                                                   'chromosome="I"
                                                      codon_start=
                                                                                                                                                                                                                                                                            'clone="F53B6"
                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                            organism="Caenorhabditis elegans"
                                                                                                            note="predicted using Genefinder; Similarity to Human
                                                                                                                                                                     .3649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secernentea; Rhabditia; Rhabditida;
                                                                                                                                                                                            .1946,2437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .32412) overlaps with the start
                                                                                  antigen (SWLPET3_HUMAN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this sequence. The true
                                                                                                                                                                                            .2628,2969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jier, M.,
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В δÃ В δÃ 밁 δÃ 밁 δÃ Вþ Qy В δÃ

CUS

.26926,26974. .27107,

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note="predicted using Genefinder; similar to thrombospondin like; cDNA EST EMBL:214404 comes from this gene; cDNA EST EMBL:21571 comes from this gene; cDNA EST EMBL:612571 comes from this gene; cDNA EST yk195c9.3 comes from this gene; cDNA EST yk195c9.5 comes from this gene; cDNA EST yk28697.3 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk353h1.3 comes from this gene; cDNA EST yk353h1.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4270. .15311)
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complement(50in(4270. .4339,4493. .4547,5071. .5295,
5368. .5662,5891. .6148,6204. .6752,6818. .7287,7546. .7676,
8104. .8184,12576. .12775,13246. .13384,13931. .14132,
14183. .14294,14341. .14457,14994. .15155,15198. .15311))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKCSYTVVFLLFYLLIASFHVDALSWAAWSPWSSCTKTCGGGVS RQLrRCLTSKCSGESVRFKVCAQKTCESKSRLARDTICGGEEIVSRGQCEVCBSRLT GANFLMRVDDGTPCQAATSRAVCSKGSCOIVGCDGLISSSFRFDACGVCGGRGDTDG GKFIWKYSEEYTACASKCDDIVDWSGAGRSIASTSQPIVVCVNALTGRVVPEKLCADK GKFIWKYSEEYTACASKCDDIVDWSGAGRSIASTSQPIVVCVNALTGRVVPEKLCADK CLRFKVSEDFTACASKCDDIVDWSGAGRSIASTSQPIVVCVNALTGRVVPEKLCADK CLRFKVSEDFTACASKCDDIVDWSGAGRSIASTSQPIVVCVQTAHNVTVHVPDTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OWRYGOWTOCSASCLGGKOKAALKCIQVSTĞKSVQWSQCDARRRPPĒKSRPČNQHPCP

PFWLTSKY SDCSMSCGGGTARRSVKCAQTVSKTDGADAHIVLKDDRCHFKK PQETETC

NVVACPATWYSSLINKRHKI KI.KIKKTAQWTESCSRSCDSGERRRQVWGEIRDSRKKTD

RRPDVECDANTK PQTVEVCSFGSCSRPELLSNRVFEQNAEQKKLTLGIGGVATLYQGT

SIK IKCPAKKFDKK I IWKKNCKK I KNDAHIK KVSANG MLRVFHARMEDAGVYECCTDR

LOGNVTLNFK KRDFPASRVDLAPKDQIPSTKNAQRVUVSKEDVLREQASVLHKANVSL

LEALLTAPNDEKAREQLRKYGNELVARWDIGHWSECROKTCHVAGYQARGISCKVTEH
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VPLTAIVTTSLPMVAAIAFCAKNRKTVHAKNKNKNKNKSSKSAKSSKSTRGASKSGKSRR
                                                                                                                                                                                                                                                                                                    gene; cDNA EST yk411f5.3 comes yk411f5.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                           comes from this gene; cDNA EST yk193h3.5 comes from gene; cDNA EST yk411f5.3 comes from this gene; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(20516. .20602,20648. .20953,20999.
21609. .21818))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(20516. .21818)
/gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(19892. .20022,20241. .20283))
/gene="F53B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEIRNVDNSICESLASVRPPETRPCHREDCPRWEASQWSECSSQRCVSSMLAQKRRNV
TCRFTNGTSVDIQHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRLL
SCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTRPAAEENCVSTSCGRWEAGKWSKCTASCGQGVRRRHVACVGGSDCDEGGRPRQE
TTCYAGIPCSIATNSLDWNDRAYLDGNTFGSWDNHNDWQAPRLVAGEWSTCSSTCGTG
VMSRTVECVAVNPISSAPIKLEMSECQDQEQPKLFESCEVRSCPLQEDSKLSEDEAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKWYMHQRAPKLLIPESCCIPSEIERCRSNPFDQDAPPPYYTSTCYEPLQNDLLHVMN
VASWLCITNAIVQVIFVSLKTIKLLNFILLKT"
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LYVDVGRILVIISILSILNYLICFYAIFKEMRCFVTSCAVASIVIAVMLIIGGCIGLN
FRDQLTHYTPLNLKMLTSLRELYGTHDMKGITESWDALQSNFKCCGVNGTDNAQIWKT
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                                                                   SSKAKHSKRSSKSSKKGTSGKSGKGSSKRGGKSSKSKSKKVKTATTSGSQVSTVSAA
TGVSDKQSNSSKSSRKSSKSSKSRKNRRLDSDAQKKMEKSGKSGKVALIPKTQQTTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGYYQSNYWGKRK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(19892. .20283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIKLFHSCDSLEVROKCCSTCTFVERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAB03121.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKSAIGEEGRKKNQLLKRDFSKLANPLSEFSLYREQPDTQFLKNRKIKNVDQQDSRLFSLLEKYIFHSLSINLTIYLKALHFQTRVFPFKSFPHFNTLKFTF
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                                                                                                                                                                                                                                                                                                                                                                                                /gene="F53B6.4"
/genefinder; cDNA EST yk193h3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F53B6.8"
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                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F53B6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .21424
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Best Local Similarity
Matches 127; Conserv
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                                       29651
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                                                                                                       407
                                                                                                                                                                                                                                                                                                                                                  ttgtaacaacagttgtcatttcgttcatccattatttgttaccaaagttgatcgtg 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cacttccatttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtattt 286
                                   TTGGGTATGTTAACTCTGAAGTATTAAATCAATT 29618
                                                                                                                                                                                                                                                                                                           CATTTTCCTTCACAATGATCACCTCGTTTCATCCATTCTTTGTGACGGGAATGGATCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATTCCAATTGGAGCATGCAATATGCGGAGGCAACGAACACTGCATCCACGTGGAATAT 29772
                                                                                                tatctgaaatcacaactgcttttcaaactcaaat 440
                                                                                                                                                                       CATTCAGTATTCGATGTTTCCTCGAGTCAATTAAAGGATTGAACGCGGAAATTGATG
                                                                                                                                                                                                                                    catatogagtacaatgcttttacatggaagctgataaaacagttagtgcacagattgagg 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="Cab03116.1"
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HPFFVTGMDRAFSIRCFFLESIGLNAEIDVGTLAPQHVDQBYSLPVCAYHLKDGIEG
HVLRFAQVGQKVTHVNFCDQDASHVYGILIHSGTLAPQHVDQBYSLPVCAYHLKDGIEG
HVLRFAQVGQKVTHVNFCDQDASHVYGILIHSGTLAPQHVDQBYSLPVCAYHLKDGIEG
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HVLRFAQVGQKVTHVNFCXADKVQLYFTCTVQLCYKHDGGCEGITPPQCSGHSHGI
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complement(27666, .30589)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MILSDQNFLQTQWKEPQTAQSKNTESKCEFHGNSNEVKPIGSLN
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ELADEKIPLRLQKSKGLLNLIDKNFATLAFCRCWIDRLGETKYLMALKGKCSYSTASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Similarity to Rat initiation factor 2 associated
glycoprotein (SW:I2A6_RAT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(27666. .27862,27919. .27959,28076. .2877
28905. .29001,29330. .29417,29467. .29606,29648. .29915,
30107. .30301,30478. .30589))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCYRRGPMEYHPYDMNMPPKLVPRPPLHYKFDPPLTERGQIVSETYGRGLLNAGIRPF
EVFCSPDMKSVQTAAFLIKGLGLSYTTINIDPALLSYROMLPTNFQEMLLSPKAFFNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVPNHPELNQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVETVDDILQCIKKPTCQMNFISLKKGEAQIMDSPILPLTKSLYLVKPFYWTDVPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYPINIQYLPSQGFIRAENIEDYNLRIQAFFKKNIAKIEQKQVVVISDNVMVDLTRNE
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/db_xref="GI:3877450"
/translation="MSRESPVSLAQLVERETFNLKVRGSSPLVSHAESMGLIFPNWVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="TTT Lys K-tRNA; predicted preliminary prediction; similar (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F53B6.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(26258. .26342,26501. .2
27153. .27288,27334. .27459)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMLILTLFTDRWMAMVGACILQSFAGKIIGKRANLLLNLII"
26258. .27459
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/db_xref="GI:3877451"
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/gene="F53B6.5"
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23555. .24160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="F53B6.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.48;
59.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74.8;
Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bin/display705-wormoec&class=Sequence &object=R07E3
bin/display705-wormoec&class=Sequence for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
This sequence is the entire insert of clone R07E3. The true right
end of clone F41E7 is at 36774 in this sequence. The start of this
sequence (1. .115) overlaps with the end of sequence Z68106.
The end of this sequence (39633. .39736) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vauddin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J., and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jes@sanger.ac.uk or rw@nematode.wustl.edu
on Nov 21, 1995 this sequence version replaced gi:798823.
Coding sequences below are predicted from computer analysis, usin
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-MAY-1995) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans
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Caenorhabditis elegans
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Z49207.1 GI:1067021
HTG; ADP, ATP carrier protein; Cuticulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans cosmid R07E3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cottage, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea;
Rhabditina; Rhabditoidea; Rhabditidae; Pelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2 Mb of contiguous nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 39736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 39736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL032624.
/note="Serine and threonine rich protein, Carboxyl terminus is glycine rich; cDNA EST EMBL: COB296 comes from this gene; cDNA EST yk259b4.5 comes from this gene; cDNA EST yk574h3.3 comes from this gene; cDNA EST yk59c11.3 comes from this gene; cDNA EST yk597h8.3 comes from this
                                                                                                                                                                                                  /clone="R07E3"
5080. 8873
/gene="R07E3.6"
join(5080. 5246,5409. 5769,5826. 5942,6381. 6905,
6955. 7075,7125. 7448,7495. 7787,7831. 7980,8037. 8174,
8222. 8405,8470. 8873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Caenorhabditis elegans"
                                                                                                                                                                   /gene="R07E3.6"
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:6239"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-1999
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KVIQISMPPPTMHSKQLNMPVCKYEVLDGSPTGPPVYFATVGQMVYHKWTCDTEHENT FCMLVHSCFVDDGNGQRVQLLNDKGCALDKYLLTNLEYPTDLMAGREAHVYKYADRDN

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EEITTTTKAPTTTTQSTTTTTQLPTTTTTTEPTTTTTTVDPLAENEELEKQAIEVM KSLDDEERIJAEKNYEVQKKOENAARKRINNELKMMOKAREMKNKPHKETTTSLAT EQPKTTTIVASSTETSTVTTDATEATTTTAFTTTVATTTKKRSNIPEAEEDEIET EQPKTTTKKRSNIPEAEEDEIET PACKTTTTKKRSNIPEAEEDEIET AEKTTTKVTEDGPITTBEFPEYIKKRNATVGIKTLTPAQLEAAINAKPIPESASASAAP SSNVETAEVAASAAAAVALPEEIAPPQIALPQLTPDQISQFMRPVASIVEDMRPILG SILQGSSASRARAASVRTYEKTKTPNIRDIMADGYSENSLVGFGSQLAREILNPGILK
                                                                                                                                                                                                                                                                                                                   complement(join(21213. 22011. .22170, 22220. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="Sptrembl:Q21812"
/translation="MIFLVFWFDILLLIFLAVTGKTLGLREYYVNTLVYIFEWGATLN
/translation="MIFLVFWFDILLLIFLAVTGKTLGLREYYVNTLVYIFEWGATLN
EQYEBEEGSYBEEDMFBEDGHKKPRFSSASDLGIINREKSDIIDAKLHETNVPEAKQT
TVSVLVDDTLDFITAGMEAVIEDQVTNRFSAAQLPSWNLLSRTKYSFHFFNWGLTLLW
TAGFWFRYYVLVPGRIALFGIAIVLMIVSTSIIGLVPAAKVRKEVLNRRGMLWGMRIXT
RAFSSYIFHBHKENRANKGGICVANHTSPIDVPVLSCONCYANIGOKQAGFLGFLQTT
LSRSEHHIWFERGEAGDRAKVMDRMREHVNDENKLPIIIFPEGTCINNTSVMMFKKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="cDNA EST yk278a10.3 comes from this gene; cDNA EST yk278a10.5 comes from this gene; cDNA EST yk486f8.5 comes from this gene; cDNA EST yk603d8.3 comes from this gene" /codon_start=1 /protein_id="CAA89072.1" /db_xref="GI:3878960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(11510. .14654)
/gene="R07E3.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(21213. .23259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref."Sptrembl: 021809"
/tagnslation="mastsatldvletskkclagsaaaaisktttapedrvklvlolo/translation="mastsatldvletskkclagsaaaaisktttapedrvklvlolo/rosefamaevkgiroliokiielegaamalwrongagvarclphhtlnpaerdivrntlkordfemaetaktrongarvarclephttaldvkkdgsrkykgmvlknvdrnesfekelagtfvsgglggattlemlypfdfartrlaldvkkdgsrkykgmv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(17917. .18025,18074. .18331,18378. .1855,
18604. .18751,18800. .18877,18947. .19072))
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EDSISFAKRVKRAIAKKGGLIDLEWDGALKRERVSSKLVTLQQKLYFERLARTTTLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(11510. .11773,12101. .12476,12528. .12827, 13402. .13542,13587. .13696,13745. .13863,13912. .14026,
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EGYEQGRDGVKTTFHGDSGVMTGGGHSAPTFDYLNMPSESFGLAPVAPPAPPPPPATQ
ATAAPVTAPKEVAPAPSPFGGGGFGGGGGGGGGGRGNGFGGGSGPSVPFDEVEKNSK
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                                                                           /protein_id="CAA89068.1"
/db_xref="GI:3878956"
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="R07E3.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSLRSTGGALIITFYYEFSKYM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQISITTSGMVCYPLDTVRRSMMMQSGKQIKQYTSTKDCWKTLYKKDGINGFYRGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCLKKIKASEGVASWYKGLSSALQFVIASRAIFFGIFDSIRTSVEDPKSLNFAACWAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA89069.1"
/db_xref="GI:3878957"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene≃"R07E3.4"
/note="similar to ADP,ATP carrier protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="R07E3.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(17917. .19072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQLAGRLVQPDMDSGEPESAEDGIDKKKTAEKVDFTTDDNNVSQEADAKPDSTHENGG
EHVSTTPEESITENTTAEVPASTASTKDTKLSVKIRSEDEKREEDKLSDDEKPNYMKK
LEEIYKKEEELVERELAEMSVAEIFEKEVVIKTTKVTPTSTTTEIPTTTTTEEATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q21811"
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LKKIAMRNNPKYNAPSRSSFTIPPPTFKAEDLDMNKLKRGKGDSIINEKMLTLLLPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA89071.1"
/db_xref="GI:3878959"
                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                        /gene="R07E3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                          'note="similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .14654)
                                                                                                                                                                                                                                                                                                                                    3. .21359,21654. .21739,21787. .2188
.22335,22428. .22542,22637. .22779,
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gene CDS

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Query Match
Best Local
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                                                761
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                                                                                                                                                                                                                                 gatgtgctcttgataaatatttgctaaataatttggaatatccaacagatttaatggctg 700
                                                                                                                        gccaagaagctcacgtatacaaatatgcggatcgatcacagcttttctatcaatgccaga 760
                                                                                                                                                                                                   GATGCGCTCTCGACAAATACCTCCTCACAAATCTTGAGTATCCCCACAGACCTGATGGCGG
TTTCGATCACAGTCAAAGAGCCTGGTCTTGACTAT 22017
                                                                                                GAAGGGAAGCCCACGTATACAAATATGCCGATAGAGATAACATGTATTTTGATTGTCAAA
                                        tcagtattaccattaaagaaccaaatagcgaatgt 795
                                                                                                                                                                                                                                                                                                         100;
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to cysteine proteinase; cDNA EST EMBL:M99104 comes from this gene; cDNA EST EMBL:D69358 comes from this gene; cDNA EST EMBL:D59792 comes from this gene; cDNA EST EMBL:D69368 comes from this gene; cDNA EST EMBL:D69368 comes from this gene; cDNA EST EMBL:D69368 comes from this gene; cDNA EST EMBL:D693692 comes from this gene; cDNA EST EMBL:D693692 comes from this gene; cDNA EST EMBL:C08090 comes from this gene; cDNA EST EMBL:C09692 comes from this gene; cDNA EST EMBL:C09692 comes from this gene; cDNA EST EMBL:C10541 comes from this gene; cDNA EST EMBL:C10305 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="Sptrembl:Q21810"
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LHKEAEFIEPIPESLTAKKGESSSPFPDFFDWRDKNVITPVKAQGQCGSCWAFASTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(29470. .29618 30963. .31067,31117. .31252))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEAAWAIAHGEKRNLSEQTLLDCDLYDNACDGGDEDKAFRYIHRNGLANAVDLPYVAH
RQNGCAVNDHWNTTRIKAAYFLHHDEDSIINWLVNFGPVNIGMAVIQPMRAYKGGVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(26570. .26749,26841. .26917,27073. .27330. .27815,27863. .27958,28006. .28071,28119. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(26570. .28295)
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SDYIIPNDDIISLNWLQRNFDMRISELCMTAIGTTLLVFLNAFLFIISLVSIVHVCCF
                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="caa89073.1"
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/db_xref="SPTREMBL:Q21813"
/trans1ation="MLAVIAGILAVLLILILFFCIRSKDKKQPPSPAEPNRRLPTRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(29470. .31252)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSEYACKNEVIGLHALLITGYGTSKTGEKYWIVKNSWGNTWGVEHGYIYFARGINACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA89070.1"
/db_xref="GI:3878958"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="R07E3.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="R07E3
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/translation="MLINNSGSLPLTLSLYILPDRLLNNVRFFMIDRPAKTVREPALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA89074.1"
/db_xref="GI:3878962"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="R07E3.7"
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                                                                                                                                                                                                                                                                                                                            5.8%;
64.5%;
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                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                               Score 67; DB 34;
Pred. No. 7.2e-06;
                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 comes from this is gene; cDNA EST yk591e7.3 comes
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                    Gaps
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RESULT
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VERSION
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                                                                                                                                                                                                                                                                                                    KEYWORDS
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Fragment Name
CEY39A1_0
CEY39A1_1
CEY39A1_2
CEY39A1_3
CEY39A1_4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGCTATGTGGATAACGGCTACGGTGATAGAGTGGATATTCTTGATTCGAATGGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCTAGACGCGGTGCTTCTCTCAACTCCGGACTACGATACTTCTCTGCGTCTCGCCACG 82172
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACTATGTCTGAAATA 82249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caagaagctcacgtatacaaatatgcggatcgatcacagcttttctatcaatgccagatc 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gctcttgataaatatttgctaaataatttggaatatccaacagattt---aatggctggc 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
197; Conserv
                                                                   Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
2.2 Mb of contiguous nucleotide sequence from chro
                                                                                                                                                                                                                     Rhabditina: Rhabditoidea: Rhabditidae: Peloderinae: 1 (bases 1 to 36306)
                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                  CEM142
 Nature
                elegans
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                HTG; Cuticulin; Homeobox protein EVX1 like
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(6466),
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300001
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52.3%;
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32-38 (1994)
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310000
410000
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                                                                                                                                                                                                                                                                                                                                                cosmid M142, complete
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                                                                                                                                                                                                                                                      Secernentea; Rhabditia; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300001 (299293 Caenorhabditis elegans
                           sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----actttctgcgcggttgtccat 585
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                                                                                                                                                                                                                                     Caenorhabditis
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MEDLINE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overlap between neighbouring submissions.
This sequence is the entire insert of clone M142.
The true right end of clone C44B9 is at 5059 in thi
Start of this sequence (1. .104) overlaps with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both at dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-MAY-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Nov 4, 1996 this sequence version replaced gi:1370039. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bin/display?db=wormace&class=Sequence &object=M142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMurray,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end of this sequence (36203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission
GVGTIDVFTDSVTVLEQEPACQQVTTYSFRFSISTNQKIENS"
                                                                                                                           VSEPSOLLRDADVMYYAIGVTNLVNVHQLHQMTGNPVRVFTVESFEQLDRALADSLTW
SMCKTEFRPGTPEIICGPDRIGVKASTKQPFEGNVFVMDHYHDEECRAGPEKFPDSRS
IGLTVPFSACNVHRYRSLNPKGIFVEVSIVFMFHSLFMTKTDQTVKVQCFYMEADKHV
                                                                                                                                                                                                                                     /db_xref="SPTREMBL:Q21540"
/translation="MRPIPYDISLSITSFLSLILICSANPIDNGLVDSELTHECVTHK/translation="MRPIPYDISLSITSFLSLILICSANPIDNGLVDSELTHECVTHKAVETLLLEXGLQGARPGIPKVAIVITDGQSQDDQFNHPTQLEMAIQRIEYQSGATNTGQALRLTLEKGLQGARPGIPKVAIVITDGQSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:010658"
/translation="mkaeQQQOSIAPGGATFPSQMPRPPPVTEQAITTEAELLAKNQI
TPNDVLALPQITQGFLCSPSANVYNLEFTKFQIRDLDTEHVLFEIAKPENETEENLQA
QAESARYVRYRFAPNFLKLKTVGATVEFKVGDVPITHFRMIERHFFKDRLLKCFDFEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z99276
                            DKDTFGMLVHSCYVDNGYGDRVDILDSNGCGLDAVLLSTPDYDTSLRLATKPYHVFKY
ADRPVLQFQCQITLCLKYDGGCEGITPPQNCKKLPGEDGHHHHHHPEKRRKLVRRLAD
                                                                                                  TVPLSVSMITTVFREQIYQMPQCAYTLRKGAPDGPIVRFATLGESVYHRWECIEVEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(8540 ...8572,9335 ...9416,9468 ...9679,10373 ...10721,
10772 ...10974,11033 ...11175,11871 ...12501)
/gene="M142.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFCMPNSRNNCEHIYEFPQLSQQLMDDMINNPNETRSDSFYFVENKLVMHNKADYSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cDNA EST yk258al.3 comes from this gene; cDNA EST
yk258al.5 comes from this gene; cDNA EST yk532all.3 comes
from this gene"
                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA97806.1"
/db_xref="GI:3878735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA97807.1"
/db_xref="GI:3878736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(3511. .3570,4639. .4750,4821. .5201,5689.
/gene="unc-119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8540. .12501
/gene="M142.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="unc-119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="M142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .36306) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       this sequence. The the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5795)
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MIEILISIOSNIHVSQLWSAVRARGGOFLGPAMQDDVLRLILMTETGECIARKNLV
MYVVQTLASDYPQVSKTCVGHVVQLLYRASGENVLKRDGSSSLMQLKEEFRTYESLRR
EHDSQIVQIAFESGLRIGPDWSALLYADQSHRSHMQSIIDKLQSKNSYQOGVEELRA
LAGSQTSMLVPAYRKFLTQVLPCLEFFAGIEHEDTSMRNIGDALHOIRILLKLHCSQD
DLRKMPKEERRGVILQAEVPGGMGGGPGGSGAEAGRIGGLHPLYSQIDETGRSISRT
NPKONSHNSPQTPPKQPRQKRYQMGIPNRMGYSSDAPPFIPSHQQQPPPQFFNSGHL
PQRERGGRGAPPPPPPQPMPMLIGYDMPGAPMMQATEVLTADGQMVNGTPQRVVIM
QSPHLPGGFVVMIPQQQMVPPPQSMTPVGGPMGMGPMTPSIIVQVPPRTMMTATSP
TGSVIYPAASPPGPPPTIWIOSIGVFKRKSNELKIVRKISFFLNFYDFFLILRKLKK
EKKGADIEFFEKIKSTDFKKYPSSFSRTDGNMEPMFDRGSGMVWGPPGTMLRESGADA
EQLLAKRYEILKRLQPSEDDDDPEDGGIGHVSYTVASSVLDDRMDHPLTMTPVFTID
LPALFISFAMMFTEETMTMIGEMVQNRPRAPSLTAPSSNQPMNVNASASATVQAECEN
RKILDFPLKYRKMTLMFEKYSTCFHYTLLKDYMVFYVLNTUREASRWPBRRRAATIPQ
RKTLMGGOVORTURDASENWINDDEDGGGIGHVSYTVASAGAICH
RKILDFPLKYRKMTLMFEKYSTCFHYTLLKDYMVFYVLNTUREASRWPBRRRAATIPQ
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299276.1:105. .698,299276.1:1364. .1566,299276.1:1666. .1772,

299276.1:4045. .2795,299276.1:3714. .3928,

299276.1:4056. .4104,299276.1:5846. .5958,

299276.1:6478. .6729,299276.1:7169. .7338)
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join(34039. 34101,34448. 34750,35530. 36306,
299276.1:105. 698,299276.1:1364. 1.566,299276.1:1666.
299276.1:2495. 2795,Z99276.1:3714. 3928,
299276.1:4495. 2795,Z99276.1:5846. .5958,
299276.1:6478. .6729,Z99276.1:7169. .7338)
/gene="M142.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mAPTGQGGQWQEVLCCSICNRHFNETFLFVSLICGHVICRKCAE
KPENQTKPCPHDDWKTTHSPSEYPNNVALLSVIFPRKQCMTLSGAVSEAEKRVDQLSI
QIAKFFREADSERGGTVSSREISRTLQRKVLALLCYQWREVDGRLKTLKMCRGISERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D67323 comes from this gene"
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VHYDYKHPTDLPAELLAKFDVIIADPPFLAAECLIKTAHSIRLLGKSDVKVLLCTGAI
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DKTLGELTPNLMKSPALSIRGQQAYLOLKRTIEDTCWCGEDIRVLGLVLVHKPYEVSD
VTKDAKATGFDESRRESSAVLQVYKLISKPMTEYTARAPLDFTIGAIVANYSSSEMSDT
DDIPOLSADTLAALSMFQAEQQEKIEQLOSGIIEKIDEDWQLSQFWYDDETSRKLVAE
VVSNSLDKIVDVKERISEAQGNASEAENAHLRMELRMAESQMAHLDPYTKNNCLLRAL
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/db_xref="SPTREMBL:Q21541"
                                             PVIPMVQVPVQVPIVPAENFNPNVPPPPPPPPQGQPMLVDSAIGLLTPIRPILVAHPQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA97810.1"
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AELNLPEGTIKVWFQNRRMKDKRQRVGGLAWPFPPQMAAYMLNPFAYEMWMKTAAASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:045962"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="M142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MASCNLTASNVAIGACVEIETTNGLSARGVVISFDTTRKVLVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="M142.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTSSDDDESKPVNFSNSPSSSSPSPYSTD"
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                                                                                                                                                                                                                                                                                                                                                                                                               Bonfield, J., Burton J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Dutbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopera, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                          Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@Sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
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                                          available information.
                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                           Dobson, R
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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small contract of the specifications once, or longer because we arrange for a small contract of the specifications once, or longer because we arrange for a small contract of the specific or small contract of the specific or small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we arrange for a small contract or longer because we are longer becau
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IMPORTANT: This sequence is not the entire insert of clone ZK265.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bin/display?db=wormace&class=Sequence &object=ZK265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of this sequence (1. .110) overlaps with the end of sequence
                                                                                                                                                                          complement(join(6676. .7754,7804. .7870))
/gene="ZK265.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYFYPGIKQCRAQRAASSTSQDMRSRLYPLHKAAEDGNAEEIRRFLKIGMDSNLRDDD
SWFPLHAACFHGHLEVVHELLMSPQMTAINAQNKGGATALQXYVYINGNBYLVEILTSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLHDDLHQPSSSTKPFVGHVPGLSLVCVPVFNKESVEVANSRYENLQKMVNLCHNQPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(492.
/gene="ZK265.1"
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                                                                    complement(6676. .7870)
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                                                                                                                                                            SSGWTTVHIGNSAPCILKDDKGLEVLGNLDLTIEKASAGYGGKEKIMTGAAVAKLKVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="predicted using
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18275. .19128
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PHPPPPPAPVAPPKLHDYESPAPVADAHDAAPAAQPYKRRKVARAHMV"
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join(18275. .183
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Best Local
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                                                                                                                                                                         s. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; othicis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis; darcryocystitis; epiddymitis; intrarenal abscess; perinephric abscess; toxic shock syndrome; impetigo; folliculitis; cutaneous abscess; cellulitis; wound infection; bacterial myositis; septic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a Staphylococcus aureus protein, that, based on homology with an Escherichia coli protein, is believed to be a N-acetylglucosamine-6-phosphate deacetylase. The present sequence was obtained from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxits shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                            X33788 standard; DNA; 348
14-SEP-1998; U18987.
12-SEP-1997; US-058710.
(SMIK ) SMITHKLINE BEECHAM CORP BURDHAM MKR, Lonetto MA, Warren WPI; 99-229138/19.
                                                                                                         Staphylococcus
W09912557-A1.
                                                                                                                                                               osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to isolate antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 -
                                                                                          18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W27907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 CAAGCACGTCTTGCAAATGGT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                           aureus coding sequence SEQ ID NO. 45. aureus infection; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           attgctftctgtactacacttattgcattgtcttattcgattccggttgacaatggtgtc 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aatgcattcgaaggacatgtt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCTTACCGTATGAAAGGTAATGAACGTNTTTATTTAATTACCGATGCAATGCGTGCA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Pages 719-720; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                          aureus
                                                                                                                                                               Helicobacter
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/*tag= a
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                  Warren PV;
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                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                           pylori infection; stomach cancer; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.6; D
Pred. No. 0.83
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related to their expression. The polypeptides and vectors containing them CC can also be used in immunisation methods. The products can be used for treating infection, e.g. infections of the upper respiratory tract, CC (e.g. official, bacterial tracheitis, acute epiglottitis, CC thyroiditis), respiratory (e.g. empyema, lung abscess), cardiac (e.g. infective endocarditis), gastrointestinal (e.g. secretory CC diarrhoea, splenic abscess, retroperitoneal abscess), central nervous system (CNS) (e.g. cerebral abscess), eye (e.g. blepharitis, complunctivitis, keratitis, endophthalmitis, preseptal and orbital CC cellulitis, darcryocystitis), kidney and urinary tract (e.g. epididymitis, intrarenal and perinephric abscess, toxic shock cellulitis, wound infection, bacterial myositis), bone and joint infections, (e.g. causing stomach cancer, ulcers and gastritis). The products can also be used for treating in-dwelling devices and wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. aureus coding sequence SEQ ID NO. 8.

S. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; otitis media; bacterial tracheitis; upper respiratory tract infection; otitis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis;
                          New isolated Staphylococcus aureus polynucleotides Claim 20; Page 65-67; 102pp; English.
                                                                                                                                                                                                                                                                                                                Staphylococcus WO9912557-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         darcryocystitis; epididymitis; intrarenal abscess; perinephric abscess; toxic shock syndrome; impetigo; folliculitis; cutaneous abscess; cellulitis; wound infection; bacterial myositis; septic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Staphylococcus aureus polynucleotides Claim 21; page 90-91; 102pp; English. This sequence represents a S. aureus polynucleotide The invention also relates to the polypeptides encoder the invention also relates to the polypeptides encoder the sequence of the polypeptides of the polypeptides encoder the polypeptides of the polypeptid
                                                                                           WPI; 99-229138,
P-PSDB; Y05308
                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP
Burnham MKR, Lonetto MA, Warren
                                                                                                                                                                                                                    14-SEP-1998;
12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                               osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X33781 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The polypeptides can be used for the treatment or prevention of The polypeptide or polynucleotide can also be used to diagnose or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. aureus polynucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 aatgcattcgaaggacatgtt
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                                                                                                                                                                                                                    U18987.
US-058710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                    aureus
                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori infection; stomach
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53.2%;
102pp;
ents a S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.4; DB Pred. No. 0.77;
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polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 348;
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   of the
                                                                                                                                                                                                                                                                                                                                                                                                           cancer; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention by the
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treating infection, e.g. infections of the upper respiratory tract,

(e.g. otitis media, bacterial tracheitis, acute epiglottitis,

thyroiditis), respiratory (e.g. empyema, lung abscess), cardiac

(e.g. infective endocarditis), gastrointestinal (e.g. secretory

diarrheea, splenic abscess, retroperitoneal abscess), central nervous

system (CNS) (e.g. cerebral abscess), epe (e.g. blepharitis,

conjunctivitis, keratitis, endophthalmitis, preseptal and orbital

cellulitis, darcryocystitis), kidney and urinary tract

(e.g. epididymitis, intrarenal and perinephric abscess, toxic shock

syndrome), skin (e.g. impetigo, folliculitis, cutaneous abscesses,

cellulitis, wound infection, bacterial myositis), bone and joint

(e.g. septic arthritis, osteomyelitis), or Helicobacter pylori

infections, (e.g. causing stomach cancer, ulcers and gastritis). The

products can also be used for treating in-dwelling devices and wounds.

Sequence 1182 BP; 416 A; 174 C; 257 G; 335 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The polypeptides can be used for the treatment or prevention of disease The polypeptide or polynucleotide can also be used to diagnose diseases related to their expression. The polypeptides and vectors containing the can also be used in immunisation methods. The products can be used for
                                                   misc_feature
                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V74344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           attgctttctgtactacacttattgcattgtcttattcgattccggttgacaatggtgtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCTTACCGTATGAAAGGTAATGAACGTTTTTATTTAATTACCGATGCAATGCGTGCA 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shock syndrome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aureus contig SEQ ID #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 481. .540
                                                 5881.
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                                                                                                                                                                                                                                                                                                                                 a "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                           .4140
                                              "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" .5940
                                                                                                                                                                                                                                                                   these bases represent a line of missing
"these
                                                                                                                                                                                                             the sequence listing in tare included to maintain given in the specification
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Pred. No. 1.4;
  bases represent a line
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                                                                                                                                                                                                        the specification. They
n the nucleotide numbering
ion for this DNA sequence"
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Best Local S
Matches 75
                                                                  W09814583-A2.
09-APR-1998.
02-OCT-1997;
02-OCT-1996;
                                                                                                                                                                                                                                                                                                      23-SEP-1998 (first entry)
P. falciparum gp190 DNA.
gp190; malaria; MSP-1; merozoite
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(BUJA/) BUJARD H.
Bujard H, Pan W, S
WPI; 98-240088/21
                                                                                                                                                                                                                                                                                                                                                                                                         V35363 standard;
                                                                                                                                                                                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                     V35363;
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밁 Q В δÃ ₽ Ş

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PS Claim 1; Page 321-325; 3271pp; English.

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or Industrial importance can be obtained. Specifically, sequences which are cc likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC s.aureus in a sample. S.aureus is implicated in numerous human diseases, including callulitis, eyelid infections, food poisoning, osteomyelitis, cc skin and surgical wound infections, scalded skin syndrome, toxic shock cs syndrome, etc. Organisms transformed with the DNA sequences can be used to the composition of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-1997;
07-JAN-1997;
05-JAN-1996;
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(HUMA-) HUMAN GENOME SCI INC
Barash SC, Choi GH, Dillon P.
for recombinant production of the polypeptides. The new DNA sequenced their fragments) are useful as primers or probes for isolation bomologues of any of the S.aureus DNA sequences contained on the computer readable medium.

Sequence 7563 BP; 2584 A; 1028 C; 1476 G; 2229 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-S.aureus vaccines
Claim 1; Page 321-325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) and proteins derived stored on computer readable medium and
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ATTGCTTACCGTATGAAAGGTAATGAACGTTTTTATTTAATTACCGATGCAATGCGTGCA CAAGCACGTCTTGCAAATGGT aatgcattcgaaggacatgtt 156 AAAGGTATGCCTGAAGGAGAATATGATTTGGGTGGACAAAAAGTAACTGTTCAATCGCAA 5595 attgctttctgtactacacttattgcattgtcttattcgattccggttgacaatggtgtc 75 l Similarity
75; Conser Conservative 3.0%; 53.2%; 0, Score 35.4; D Pred. No. 3.2; Mismatches DB μ, , Length 7563; 0; Gaps 5535 0

antibody; passive

immunisation;

surface protein; st
unisation; parasite;

stability; vaccine;

DNA; 4940

ВP

10. .4929 /*tag= a

ocation/Qualifiers

/product=

DE-040817. E05441

Tolle

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RESULT
N50530/c
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                                                                                                                                                                         Holder A,
WPI; 85-22
Claim 2; Fig 1; 51pp; English.

The sequence encoding the P195 protein of Plasmodium falciparum (N50530) and a peptide comprising at least one of its epitopes (see P5077) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new DNA sequence, together with a carrier.

Sequence 5760 BP; 2565 A; 630 C; 725 G; 1840 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes the Plasmodium falciparum gp190/MSP-1 (merozoite surface protein). This gene is used in a method for stabilising the gene sequences by reducing the AT content. Such products are useful in vaccines against malaria or for producing monoclonal antibodies (for passive immunisation). The complete gp190 protein can now be produced outside the parasite and has, at least over extended regions, the native pattern of folding. Larger amounts of the protein can be produced recombinantly than would be possible using the parasites as source. Sequence 4940 BP; 2196 A; 597 C; 687 G; 1460 T;
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                                                                                                   malaria
Claim 2; Fig
                                                                                                                                             Cloned DNA sequence encoding
                                                                                                                                                                      (WELL ) WELLCOME FOUNDATION LTD. Holder A, Sandhu J, Odink K, Loc WPI; 85-224845/37.
                                                                                                                                                                                                               22-FEB-1984; GB-004692.
26-SEP-1984; GB-024340.
21-FEB-1985; GB-004429.
                                                                                                                                                                                                                                             21-FEB-1985;
22-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                 Plasmodium
                                                                                                                                                                                                                                                                                                                                                           Malaria vaccine; epitope; antigen;
                                                                                                                                                                                                                                                                                                                                                                          Sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                         N50530;
                                                                                                                                                                                                                                                                                                                                                                                                                     N50530 standard;
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                                                                                                                               useful for expressing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTCTTAAATAGTATTCTAATTCAAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgcgcgtacacgatctctgaatccacgtgg
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                                                                                                                                                                                                                                                                                                                                                 falciparum
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oding the P195 protein
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45.6%;
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Pred. No. 3
                                                                                                                                             plasmodium
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                                                                                                                                                                                                                                                                                                                                                                           of Plasmodium
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Query Match Best Local S Matches 72

l Similarity 72; Conserv

Conservative

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Score 34.8; DI Pred. No. 4.9; O; Mismatches

4.9;

Length 8395;

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Gaps

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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1998.
04-MAY-1998;
14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                         A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1358
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                                                                                                                                                                                                                                           Claim 1;

    used to develop products for the detection of Enterococcus
    use in vaccines for prevention or attenuation of Enterococcus

                                                                                                                                                                                                                                                                                                      WPI; 99-045171/04.
New isolated Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis; contig; detection; Enterococcul infection;
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X13154;
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Sequence
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                                                                                                                                                                                                                                        Page 1103-1107; 2084pp;
8395
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US-046655.
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B₽;
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45.6%;
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2616 A;
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Pred. No. 4.
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                                                                                                                                                                                                                                          English.
1692 C;
                                                                                                                                                                                                                                                                                         polynucleotides and polypeptides detection of Enterococcus and for
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1478
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis genome contig SEQ ID NO:405.

Enterococcus faecalis; contig; detection; Enterococca
vaccine; attenuation; computer readable medium; ds.
Enterococcus faecalis.
WO985055-A2.
12-NOV-1998.
13-NOV-1998.
14-NOV-1998.
16-MAY-1997; US-066009.
16-MAY-1997; US-044031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4187
                                                    1241
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                                                                                                                                                                                                                       171
                                                                                                                                                                                                                                                                                                                                                                                                                         infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721
                     351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated Enterococcus faecalis polynucleotides and polypeptides sed to develop products for the detection of Enterococcus and fo in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                            be used
tcgagtacaatgcttttacatggaagctgataaaacagttagtgcacagattgaggtatc 410
                                                                                                                                                                                                         ttatgatcaagaaggttgccgtaatgatgaaggtggacgtcaagttgccggaatttcact
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                                                 ATCACGTGTTGAAAACAATTCAAAAGGCCCACAAGTTTTTGTAAGCCGTAGTCATCCAGA
                                                                                aacaacaactgttgtcatttcgtttcatccattatttgttaccaaagttgatcgtgcata
                                                                                                                     AAAACAAGATCAAATGCCAAATGAATTTTACCAACCGCATGRTCGGRTTAAAGTTTACGT
                                                                                                                                                   tccatttgattcatgcaatgttgcgcgtacacgatctctgaatccacgtggtatttttgt
                                                                                                                                                                                      TGAACGTCAAGATCGTCGTTATATTTATGTAAACTTAGGTAAAATCGAAGCAGTCTTATC
                                                                                                                                                                                                                                                      AAGAACAATTATTATAATGAATTTAGCGAATATGAAAATGACATCATGCAAGGAATTGT 1120
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                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         521
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                                                                                                                                                                                                                                                                                                                                                                                                                                         prevent or attenuate an
                                                                                                                                                                                                                                                                                                                                       Score 34.6;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                       170;
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RESULT
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Best Local
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used for therapeutic modulation of IL-1 activity
Claim 2; Fig 1; 95pp; English.
This cDNA clone codes for human interleukin-1 receptor accessory
molecule (IL1-R AcM) (see W53897), a new member of the
immunoglobulin superfamily that forms a complex with type 1 IL1-R
and which has higher affinity for IL-1 than the receptor itself,
suggesting that the known high and low affinity forms of IL1-R are
in fact the receptor with or without IL1-R AcM, respectively.
The 2155 bp sequence is present in clone HMEEJ52 (deposited as
ATCC 97666) derived from microvascular epithelium (no details of
                                                                                                                                                                                                                                                                                                                                                                                                                                 and recombinant vectors are claimed. Also claimed are isolated nucleic acid molecules encoding epitope-bearing portions (see w53898-915) of IL1-R AcM. Recombinant IL1-R AcM can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-1998.
26-AUG-1996; U13954.
26-AUG-1996; WO-U13954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal transduction; infection;
rheumatoid arthritis; therapy; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1361 CGTAAGC 1367
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1918 AATGTTTATTTTCCAAAAATGCATAATTATAATATTATTTTAAACACTATGTATCAA 1974
                                                                                                                                                                                                                                                                                           might be linked to disease. Sequence 2155 BP; 709
                                                                                                                                                                                                                                                                                                                          Nucleic acid fragments are useful as diagnostic probes and primers, for isolation of IL1-R AcM-encoding genomic sequences, for in situ hybridisation to determine chromosomal localisation of the gene, for chromosome identification and for identifying mutations that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
Bednarik DP, Olsen HS, Rosen
WPI; 98-230267/20.
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                                                                                                                                                                                                                                                                                                                                                                                                identify \operatorname{IL-IR} agonists and antagonists useful for therapeutic modulation of \operatorname{IL-I} activity, and to raise specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding interleukin-1 receptor accessory protein
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Interleukin-1 receptor accessory molecule; IL-1R ACM; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammalian and insect cells is described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolation given).
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                                                                                                                                                                                                                       Local
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                            atcacagcttttctatcaatgccagatcagtattaccattaaagaaccaaatagcga
                                                                  GTAGTTGTAAACATTATTAATAGCAGCCATCCAATTGTATGCAAACTAATTAAGGTATTG
                                                                                      ggaatatccaacagatttaatggctggccaagaagctcacgtatacaaatatgcggatcg
                                                                                                                                     TCCTGAACAAATAACAGAAAGGGAATTATATATACCTTTTTAATATTATTAGAAGCATTATCT 1857
                                                                                                                                                                    tactgtggaaattctaaatgctgatggatgtgctcttgataaatatttgctaaataattt 674
                                                                                                                                                                                                        88; Conservative
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354..1370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant expression in Escherichia coli, ct cells is described. Recombinant host cells
                                                                                                                                                                                                                       3.0%;
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                                                                                                                                                                                                                                                                                             433
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                                                                                                                                                                                                        Indels
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11

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RESULT 11
V74396/c
ID V74396
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC likely to encode antigens have been identified and these polypeptides can be used in a kit for the immunodatection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus contig SEQ ID #85. Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                  Claim 1; Page 544-549; 3271pp; English.
                                                                                                                                                                                                                                                                                     anti-S.aureus
                                                                                                                                                                                                                                                                                                  stored on computer readable
                                                                                                                                                                                                                                                                                                                                                                Barash SC, Choi GH, Dillon
                                                                                                                                                                                                                                                                                                                                                                                           EP-786519-A2.
30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861
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                 their
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                fragments) are useful as primers or probes for
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the sequence listing in the specification. They
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Query Match Best Local Matches

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04-MAY-1998;
14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                        A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                           Barash SC, Dillon PJ, Kunsch CA; WPI; 99-045171/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis genome contig SEQ ID NO:94. Enterococcus faecalis; contig; detection; Enterococvaccine; attenuation; computer readable medium; ds
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9062 BP; 2756 A;
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21252
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US-044031.
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                                                                                                                                       vaccine; attenuation; computer readable medium; Enterococcus faecalis.

Mo9850555-A2.

12-NOV-1998.

04-MAY-1998; U08985.

14-NOV-1997; US-066009.

06-MAY-1997; US-046031.

16-MAY-1997; US-046555.
                                                                                 (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
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                      New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fouse in vaccines for prevention or attenuation of Enterococcus
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                  of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110000;
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                                                                                                                                                                                                                                                                                                                           infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2022-2024; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the
                                                                                                                                                                                                                                        08-AUG-1996;
31-JAN-1996;
31-JAN-1995;
                                                                                                                        P-PSDB; W02098.

Nucleic acid encoding polypeptide for prevention or treatment of dental caries - which stimulates T or B cell response, and/or adheres to tooth in competition with Streptococcus mutans antiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1996 (first entry)
S. mutans anticon time
                                                                                                                                                                                                                                                                                                                                                                                                                  Caries; antigen I/II; genetic immunisation; Streptococcus mutans.
                                                                                                                                                                                              (UNME-) UNITED MEDICAL Kelly C, Lehner T; WPI; 96-371434/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T36122 standard;
T36122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection
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                                                                                                                                                                                                                                                                                               sequence (vqvsrkglvryfyrskmvkrflklstsiqwtl) that differs from amino acids 618-650 given on page 46 of the specification"
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/note= "bases 2001-2049 code for an amino
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A Streptococcus mutans gene (T36122) codes for I/II antigen (W02098), a 185 kDa cell surface protein at least partly responsifier S. mutans adhesion to teeth. The I/II antigen includes a series of overlapping T-cell, B-cell and adhesion epitopes. Fragments (see also T36111-21) of the gene can be used to produce recombinant polypeptides (W02087-97) carrying such epitopes for use in vaccines for immunisation against dental caries. The DNA

responsible

antigen

can also themselves

immunisation a

nucleic

acid

Disclosure; Page 46-49; 63pp;

English.

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Search completed: April 16, 2000, 04:45:32 Job time: 10031 sec
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                                                                                                                                                                     Query Match 2.9%; Score 34.2; DB 1; Length 4865; Best Local Similarity 49.2%; Pred. No. 5.7; Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps
                                                                                                                                     vaccines.
Sequence 4865 BP;
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                                                   781 cca 783
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US-08-184-009-119	US-08-257-073-2	US-08-526-840B-2	US-08-743-637B-2	US-08-690-095-2	US-08-882-704A-4	US-08-817-926-19	US-08-817-926-1	US-08-920-828-9	US-08-362-577C-9	US-08-921-177-9	US-08-920-827-9	US-08-920-812-9	US-08-470-179-41	US-08-487-826B-13	US-08-647-655-2	US-08-647-655-1	US-08-336-345-2
Sequence 119, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 19, Appl	Sequence 1, Appli	Sequence 9, Appli	Sequence 41, Appl	Sequence 13, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli				

ALIGNMENTS

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RESULT 1
US-07-772-087-1
                                                                                                                                                                                                        FILING DATE: 19911008

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1675
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)83-4300
TELEPAX: (703)83-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 base pairs
TYPE: NUCLEIC ACID
STEAMLDENMES: 404516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/07772087 Patent No. 5275945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/772,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: HSIAO, Humg-Yu
APPLICANT: FODGE, Douglas W.
APPLICANT: LALONDE, James J.
TITLE OF INVENTION: ALKALINE
TITLE OF INVENTION: DETERGENT
                                                                                   MOLECULE TYPE: D
ORIGINAL SOURCE:
STRAIN: 164A-1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
NAME/KEY: CDS
LOCATION: 716..1849
OTHER INFORMATION: /product- "mature protein of
OTHER INFORMATION: 164A-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 Diac
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                        TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1800 Diagonal Road, Suite 500
                                                                                                         164A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                    linear
                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                            double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALKALINE PROTEASES STABLE IN HEAVY-DUTY DETERGENT LIQUIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/07/772,087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Patent No. 5182210

APPLICANT: BINNS, MATTHEW M.;BOURSNELL, MICHAEL ;CAMPBELL, JOAN I.A.;TOMLEY, FIONA M.

TITLE OF INVENTION: FOWLPOX VIRUS PROMOTERS; NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
5182210-9/c
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; LOCATION:
US-07-772-087-1
                                                                                                                                                          5352450-1; Patent No.
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                                                                                    APPLICANT: KOGA, TOSHIHIKO;OKAHASHI, NOBUO;TAKAHASHI, ICHIRG;SHIBUYA, KOJI,OHTA, HIROTAKA
;SHIBUYA, KOJI,OHTA, HIROTAKA
;TITLE OF INVENTION: METHOD FOR PREPARING VACCINE FOR DENTAL
;CARIES AND VACCINAL COMPOSITIONS FOR DENTAL CARIES USED AS NASA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5182210-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
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Best Local Similarity 52.9
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
FEATURE:
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/529,602
FILING DATE: 29-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    410
                                                                                                                                                                                                                                                                                                                                                          350
                                                                                                                                                                                                                                                                                                                                                                                                            290 taacaactgttgtcatttcgtttcatccattatttgtttaccaaagttgatcgtgcat 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 21-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 2.8%;
Local Similarity 55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 11225
                                                                                                                                                                                                                                                  ATGAAATGATAGCTGCTATAGAAGCTGAAATTG 9023
                                                                                                                                                                                                                                                                                                                                          atcgagtacaatgcttttacatggaagctgataaaacagttagtgcacagattgaggtat 409
                                                                                                                                                                                                                                                                                 ctgaaatcacaactgcttttcaaactcaaattg 442
                                                                                                                                                                                                                                                                                                                       ---TAGAAAAAAGACTATTCTATGGAACAGGATATAGATAATAACGAAGATATCCGTACAG 9056
                                                                                                                                                                                                                                                                                                                                                                                         TAGAAACATCTTATTACAGTAAATTGAGTACTTATTTACTAACAAAAGCTGAAAGAGTAT 9113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaatatgcggatcgatcacagcttttctatcaatgccagatcagtattaccattaaagaa 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGCAAGTGGGAAAAATGCTGAAATTAAGAAAGATTACTTAGTTGGTTTTAAAAACGAAT 853
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1022..1846
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716..1021
                                                                                                                                         TOSHIHIKO; OKAHASHI, NOBUO; TAKAHASHI, ICHIRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 2.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB : Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 11225;
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PCT-US96-05320A-705/c
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Best Local S
Matches 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 705, Application PC/TUS9605320A GENERAL INFORMATION:
                                FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Eric K. Steffe
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                  ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 480
OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1586 caaaaagatttagcagactatccagttaagttaaaggcatacgaagatgaacaaacttct 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1526 gatgctaaagctgattacgaagcaaaacttgctaagtatcaagcagatcttgccaaatat 1585
                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1646 attaaagctgcactggcagaacttgaaaaacataaaaatgaagacggaaacttaacagaa 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/476,102 FILING DATE: June 7, 1995
                                                                                                                                                                                                                               APPLICATION NUMBER: PFILING DATE: April22,
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 2.8%; l Similarity 48.6%; 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9410 Key West Avenue
Rockville, MD 20850
United States of America
Johns Hopkins University
720 Rutland Avenue
                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                  HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Craig Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamilton O. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baltimore, MD 21205
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Genome Sciences
     (202)
371-2600
                                                                                                                                                                                                                                                                                                  MSDOS version
                                                                                                                                                                                                                                 PCT/US96/05320A
2, 1996
                                                                                                                                                                                                                                                                                                                                  3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.6; DE Pred. No. 6.4; 0; Mismatches
                                       014PC01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5177;
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US-08-781-802-5/c

; Sequence 5, Application US/08781802

; Patent No. 5969121
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION UMBER: US 60/019,580
PILING DARE: 12-JUN-1996
PRIOR APPLICATION UMBER: 10.0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1038 tgcagtacaaaatggaatctgcatgtcaccatttggcttctcaatgtttatgggtttaag 1097
                                                REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                     FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,995
FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1098 cattgcattgattgctgccgtcattattaccatttcgtttaaattt 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/694,078
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 TGCCGTATAAAATGCAAATTTCACCGCACTTTTTGGCTTTGACATAGACATTGGGATCAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                       APPLICATION NUMBER: US 6 FILING DATE: 11-JAN-1996
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 300 S. CITY: Chicago
                                 TELEPHONE:
                                                                                   NAME: Chao, Mark REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEMIRJIAN, David
CASADABAN, Malcolm
VENTION: Stable Biocatalysts for Ester Hydrolysis
                312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VONSTEIN, Veronika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FONSTEIN, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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AIKENS, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/781,802
10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8%;
56.6%;
                                                                                                                                                                                                         us 60/009,704
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                                                                 95,963-E
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application Patent No. 5728810
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Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-APR-19
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDITIFIC OF INVENTION: PROTEIN, A REPLICABLE VECTOR TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2895 ACATGTTTTGAATAACGTCCATATGGTGAAGAAAATAGCAGCAGATTGATATCTCATTA 2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2655 AGAAGGAAACCCGCGGCTGTTTCGCGCCCACAAATATTCTTGTTAATCAGA 2606
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                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 tcaagttgccggaatttcacttccatttgattcatgcaatgttgcgcgtacacgatctct 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 acatgtttatgtgaaaggtctttatgatcaagaaggttgccgtaatgatgaaggtggacg 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 taccaaagttgatcgtgcatatcgagtacaatgcttttacatggaagctgataaaacagt 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 tagtgcacagattgaggtatctgaaatcacaactgcttttcaaactcaaa 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 gaatccacgtggtatttttgtaacaacaactgttgtcatttcgtttcatccattatttgt 329
                                                     CLASSIFICATION:
                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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OTHER INFORMATION: open reading frame; other possible start codons ATG/met4;
OTHER INFORMATION: TTG/leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
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LOCATION:
                                                                                                                                                                                                                             COUNTRY: U
ZIP: 22046
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NAME: Murphy Jr., GREGISTRATION NUMBER:
                                                                                                                              SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                  Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4090 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                Xu, Ming
Hinman, Michael B.
                                                                                                                                                                                                                                              U.S.A.
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197..1699
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197..1699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Randolph V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%;
Gerald M
ER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                ISOLATED DNA CODING FOR SPIDER SILK PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
                                                                                          US/08/425,069
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Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 161;
                                                                                                                                Version
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                                                                                                                                #1.25
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                                                                                                                                                                                                                                                                                                                                                                                 AND PRODUCTS THEREOF
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INFORMATION FOR SEQ ID NO: 1:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050

REFERENCE/DOCKET NUMBER:

1447-106P

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RESULT 7
US-08-317-844B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; PAGES: 7120-7124
; DATE: Sept.-1990
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-425-069-1
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1615
                                CURRENT APPLICATION DATA:
                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                  APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1555 GGAGGACTTGGAAGCCAAGGTTCTGGTCGAGGAGGATTAGGTGGACAAGGTGCAGGTGCA 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
AUTHORS: Xu, Ming
AUTHORS: Lewis, Rando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CE
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pair
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                               STREET: 301 No. 5989894th Washington CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       850 gccgcagcaaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaa 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     790 gaatgtgttcgaccacaatgttcagaaccacaaggattcggagctgttaaaaacaggtggt 849
                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
APPLICATION NUMBER: US/0 FILING DATE: 04-OCT-1994
                                                                                                                                     ZIP:
                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: Structure of a protein superfiber: TITLE: drafline silk
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LOCATION: 1...2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGCAGCAGCTGGAGGTGCTGGACAAGGAGGATTAGGTGGACAAGGTGCTGGACAA 1674
                                                                                                                                                                                                                                                                                                                                                                                     1, Application US/08317844B
5. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
65; Conserv
                                                                                                                                   22046
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                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                 Xu, Ming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                    Lewis, Randolph V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nephilia clavipes
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                                                                                                                                                                                                   Stewart, Kolasch & Birch
989894th Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dragline silk protein"
                 US/08/317,844B
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                                                     Version
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5.4;
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                                                     #1.25
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US-08-559-303B-72
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                                                                                                                                                                                                                                                           Sequence 72, Application US/08559303B
Patent No. 5824501
GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                    ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
THE PC COMPATIBLE
THE PC COMPATIBLE
                                                                                                                                                                                                              APPLICANT: GRODEN
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                     1615 GCAGCAGCAGCTGGAGGTGCTGGACAAGGAGGATTAGGTGGACAAGGTGCTGGACAA 1674
                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CH
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                       850 gccgcagcaaaacctgctgcagctgcgcaacttcgtttactcaagaaaagatctgcagaa 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  790 gaatgtgttcgaccacaatgttcagaaccacaaggattcggagctgttaaaaccaggtggt 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
              COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: ASCII
                                                                                          COUNTRY: U
ZIP: 10016
                                                                                                                       STATE:
                                                                                                                                       CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 7120-7124
DATE: Sept.-1990
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                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE: Structure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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TELEFAX: (703) 241-2848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Murphy Jr., Gerald REGISTRATION NUMBER: 28,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                   ADDRESSEE:
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es 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOLUME:
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                                                                                                                       NEW YORK
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                                                                                                                                                     90 PARK AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu, Ming
                                                                                                        U.S.A.
                                                                                                                                                                                                                                                            NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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M'S SYNDROME
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                                                                                                                                                                                                                                                                                                           US-07-781-034-4 ; Sequence 4, Application US/07781034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-559-303B-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                 APPLICANT: Fishman, Jay A.

TITLE OF INVENTION: Molecular Cloning of Antigens Shared By
TITLE OF INVENTION: Rat- and Human-Derived Pneumocystis Carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3787
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REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TOTELEPHONE: (212) 697-5995
                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        3847 AGGTTTTGCTTCAAATTGATGGTGTTACTGAAGACAAACTGGAAAA 3892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3727 GTCTTGGAGAACTTACAGAAGTCTGCAAATCTCTGGGGAAAGTTTTTGGTGTCCATTACT 3786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3607 AAACTGTACTAAATGGCAATTTAAAGGTAGACTTTATGGAAACAGAAAATTCCAGCAGTG 3666
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NAME: ELIZABETH A. BOGOSIAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         305 tcatttcgtttcatccattatttgttaccaaagttgatcgtgcata 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              STATE:
                                                                                                                          STREET: Two Mil
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nes 127; Conserv
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                                                                                       COUNTRY:
                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAATATTTTAATACCGTCACTCTCAAGAAGCTTGCAGAATCTTTATCTTCTGATCCTG 3846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcaatgttgcgcgtacacgatctctgaatccacgtggtatttttgtaacaacaactgttg 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gttgccgtaatgatgaaggtggacgtcaagttgccggaatttcacttccatttgattcat 244
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                                                                                                                                               Two Militia Drive
                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 286-0854 or 286-0082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINEAR
                                                                                                                                                              Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOVEMBER 15, 1995
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                                                                                                                                                              Smith & Reynolds, P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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US-07-781-034-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9208328
GENERAL INFORMATION:
APPLICANT: Fishman, Jay A.
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Best Local Similarity
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                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/781,034
FILING DATE: 18-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,166
FILING DATE: 30-SEP-1991
                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19920930
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           636 ACATGGACACGATCATGATCATGAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 aggitgccgtaatgatgaaggtgga 207
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                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                     STREET: Two Mil CITY: Lexington
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                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                        STATE:
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Granahan,
                                                                                                                                                                                                                                                                                                                     Massachusetts
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O
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                                                                                                                                                                                                                 TE: Floppy disk
TBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                    Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617) 861-6240
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                                                                                                                                                                PCT/US92/08328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7%;
Best Local Similarity 51.0%;
Matches 74; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1189 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: van Grimst... APPLICANT: De Haan, Petrus T.
APPLICANT: De Haan, Petrus T.
APPLICANT: Gielen L., Johannes J.
APPLICANT: Peters, Dirk
APPLICANT: Peters, Dirk
APPLICANT: Goldbach, Robert W.
APPLICANT: MYENTION: Improvements in or Relating to Organic
                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
TELEX: 951794
APPLICATION NUMBER: US 08/032,235 FILING DATE: 17-MAR-1993 APPLICATION NUMBER: GB 9206016.9 FILING DATE: 19-MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: No. 5773700ris, Allen E.
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                             STREET: 975 Cal
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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RESULT 12
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                                                       APPLICATION NUMBER: US 08/
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 92C
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO 57737007:5 A116
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                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: De Haan, Petrus
APPLICANT: Gielen L., Johar
                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Improveme
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Sandoz Agro, Inc
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REFERENCE/DOCKET NUMBER: 137-1061
                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                               NAME: NO. 5773700ri: REGISTRATION NUMBER:
                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                   975 California Avenue
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                                           5773700ris, Allen E.
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50.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert W.
                                                                                                 GB 9206016.9
                                                                                                                                   US 08/032,235
                                                                                                                                                                    US/08/214,064
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Pred. No. 12;
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                                                                                                                                                                                                                                                                      Version #1
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(415) 857-1125

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Query Match
Best Local Similarity
~~+~hes 77; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 857-11; INFORMATION FOR SEQ ID NO:
            TELEFAX: (415) 857-1125 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3414 base pairs
                                             REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 354-3592
                                                                                          APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFOORMATION:
NAME: No. 5773700115, Allen E.
REGISTRATION NUMBER: 34.490
REGISTRATION NUMBER: 34.490
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                       FILING DATE: 06-DEC-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Improvement of INVENTION: Compounds
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                  APPLICATION NUMBER: US 0
FILING DATE: 17-MAR-1993
                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
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Peters, Dirk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robert W.
                                                                                                                                                                                                     US_08/032,235
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                                                                                 137-1061
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US-08-764-100-20
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                    TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO:
                                                                                                                                                       APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19 MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700ris, Allen E.
REGISTRATION NUMBER: 34,490
BETTERENE ADOCUMENT NUMBER: 137-106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4970 base pair
                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4318 TCCTATAGATAATTTCCTTTTGTTATCGATTTT 4350
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                            APPLICATION NUMBER: US 0'
APPLICATION NUMBER: US 0'
APPLICATION NUMBER: 17-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 975 Call
                       STRANDEDNESS:
                                          TYPE:
                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                      FILING DATE: 17-MAI APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/764,100 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sandoz Agro, IIC
STREET: 975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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77; Conserv
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                    nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gielen L.,
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De Haan, Petrus T.
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                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible SYSTEM: PC-DOS/MS-DOS
              linear
                                                                                                                  (415) 354-3592
                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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Pred. No. 14;
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Thes 77; Conserve
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US-08-989-478-1/c
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                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,478

FILING DATE:

CLASSIFICATION:
            APPLICATION NUMBER: US 60/035,022

FILING DATE: 10-CAN-1997
ATTORNEY_AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649 cttgataaatatttgctaaataatttggaatat 681
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                                                                                                                                                                                           APPLICATION NUMBER: US 60/035,021 FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/034,382 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: No. 5986082artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAATTGTACATGATTGGATAATTGTAATTCTCCAAACTTTCAATTATAGAATTTAGT
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Ryals, John
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(919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uknes, Scott
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Pred. No. 14;
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Search completed: April 16, 2000, 04:36:46
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US-08-989-478-1
                                                                                                                                                     Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                   1486 ATTTTATGAAATAGTTTTCTTTTAATTAATTTTTTAAAATGATATATTATAAAATTTAAT 1427
1366 GATAAACTTTAGATAAACACCCAATTGCCAAAT 1334
                                                                                                                                                                                                                                                              FEATURE:
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LENGTH: 5655 base pairs
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                           343
                                                                                                                  283 atttttgtaacaacactgttgtcatttcgtttcatccattatttgttaccaaagttgat 342
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
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                                                                                                                                                                                                                                                NAME/KEY:
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                     gaggtatctgaaatcacaactgcttttcaaact 435
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4271..4474
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3427..4162
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2787..3347
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Pred. No. 15;
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Perfect score:
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US-09-323-427-3
1161
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Listing first 45
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Gapop 10.0 , Gapext 1.0
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em_est5: *
em_est6: *
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em_est2:*
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gb_est1: *
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em_est19:*
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em_est17:*
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1359.028 Million cell updates/sec
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465 qb cett20: *
466 qb cett20: *
467 qb cett20: *
488 qb cett20: *
489 qb cett30: *
501 qb cett31: *
502 cem_cett20: *
503 cem_cett20: *
504 cem_cett20: *
505 cem_cett20: *
606 qb cett30: *
607 qb cett30: *
608 cem_cett20: *
609 qb cett30: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No
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665 628	Length
42 37	DB
665 42 AII11196 628 37 AA701731	ID
AI111196 SWOV3MCA1 AA701731 SWOV3MCA1	9 Query Match Length DB ID Description

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Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                   Genes expressed in molting L3
Unpublished (1997)
On Sep 12, 1996 this sequence
Contact: Steven A. Williams
                                                                                                                                                                                                        Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                                                                                                                                                                      Williams, S.A., Lizotte-Waniewski, M.,
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Seq primer: pBluescript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cameroon (forest strain) The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmenybo.org)."
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/Strain="Kumba, Cameroons"
/db_xref="Faxon:6288"
/clone="SWOv3MCA1232"
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SOURCE ORGANISM

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volvulus.

REFERENCE

(bases 1 to 665)

AUTHORS TITLE JOURNAL

Molecular Parasitology

ACCESSION VERSION

mRNA sequence. AI111196 AI1111196.1 GI:3510080

KEYWORDS

RESULT AI111196

DEFINITION

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BASE COUNT
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On Sep 19, 1997 + 14. -
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
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AA701731.1 GI:2704931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 4135853786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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/lab_host="XL1-Blue MRF'"
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(SL96MLW-OvmL3)"
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On Sep 12, 1996 this sequence version replaced gi:1405188.
Contact: Steven A. Williams
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SWOV3WCA1879SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO1879 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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                /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZaP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately down onliting larvae (m.3),2000 larvae from day 1, 2 or 3
                                                                                                                                                                                                                                                                                                            /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
in culture, and converted to double-stranded cDNA using
                                                                                                                                                                                                                                                                /clone="SWmL3CO1879"
/clone_lib="Onchocerca volvulus
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            Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 639)
Williams, S. A., Lizotte-Waniewski, M., Laney, S. and I.
Genes expressed in molting L3 larvae of Onchocerca
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1
Contact: Steven A. Williams
                                                                                                                    Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                                                                                                                                                                          AI322117 639 bp mRNA EST ZZ-L
SWOV3MCAM12G08SK Onchocerca volvulus molting L3 larva
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/db_xref="taxon:6282"
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ggtatttttgtaacaacagttgtcatttcgtttcatccattatttgttaccaaagtt 339
                                              GGAATTGAAGTTCAGATGGATTCATGTAATGTTGAACGATCACGGTCCTTAAATCCTCGA 121
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On Oct 30, 1997 this sequence version replaced gi:2160807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWOV3MCAM02C01SK Onchocerca volvulus molting L3 larva cDNA (SV66MLW-OVmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02C01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Steven A. Williams
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Filarioidea; Onchocercidae; Onchocerca.
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primer: pBluescript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in culture, and converted to double-stranded CDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The
                                                                                                                                                                                                                                                                                                                                                                       slustigm@nybc.org)."
106 c 138 g
                                                                                                                                                                                                                                                                                                                                                                                                                library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams
The library is available from Dr. Sara Lustigman (email:
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/clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
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SW3D9CA349SK Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9) Brugia malayi cDNA clone SW3D9CA349 5', mRNA
                                                                                                                                                                                           College, Northampton, Tel: 4135853826
                                                                                                                                                                                                                                  Molecular Parasitology
Smith College Department of Biological Sciences
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On May 5, 1995 this sequence version replaced gi:797827
                                                                                                                                                                                                                                                                                                                         Brugia malayi
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                                                                                                                                                                                                                                                                                                                                                         Williams, S.A.
                                                                                                                                                                                                                                                                                                                                                                       Filarioidea; Onchocercidae; Brugia. 1 (bases 1 to 776)
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                                                                                                                                            Seq primer: pBluescript
                                                                                                                                                                                                          Department of Biological Sciences, C. College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                          Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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                                                                                                                                                            genome@smith.edu
                              /clone_lib="Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9)"
                                                                /clone="SW3D9CA349"
                                                                           /organism="Brugia malayi"
/db_xref="taxon:6279"
'dev_stage="third stage larvae, nine days after infection"
'lab_host="E. coli XL1-Blue MRF'"
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1 day 9 post-infection,
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1 (bases 1 to 537)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:80
                                                                                                                        Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                    AA668051 537 bp mRNA EST 20-NOV-1997 SWOV3MCAM02A04SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02A04 5',
                                                                                                                                                                                                                               EST
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13 others
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                    ctgaaatcacaactgcttttcaaaactcaaattgtcccgatgccagtatgccgttatga 467
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
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/db_xref="taxon:6282"
/clone="SWOV3MCAM02A04"
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TATACGATCAGGCAGGATGCCGAAATGATGAAGGTGGACGTCAGGTAGCCGGAATTGAAC
                                                                                                 CAATTACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCT 224
                                                                                                                               caataacaatcaattttaatacacgtaatgcattcgaaggacatgtttatgtgaaaggtc 169
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
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On Jan 14, 1998 this sequence version replaced gi:1797124.
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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/clone_lib="Onchocerca volvulus molting L3 larva
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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Contact: Steven A. Williams
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primer: pBluescript SK.
         /note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day I, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
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Sara Lustigman (email:
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SWOV3MCAM03B05 Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVML3) Onchocerca volvulus cDNA clone onch17 5' similar TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR.;, mrNA
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                  Underwood, K. and Marra, M.
Molecular Parasitology OvmL3
Unpublished (1998)
On Jan 19, 1998 this sequence version
Contact: Steven A. Williams
                                                                                                                                                                     Williams, S.A., Lizotte-Waniewski, M., Laney, S., Lustigman, S., Hilliams, F., Allen, M., Bowles, L., Geisel, S., Osci, S., Kucaba, T., Hillier, L., Allen, M., Bowles, L., Geisel, S., Osci, S., Kucaba, T., Martin, J., Steptoe, M., Theising, B., White, Y., Wylie, T., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S.,
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a 124 c 123 g
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The library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S.A.Williams. Th
Library is available from Dr. Sara Lustigman email
slustigm@nybc.org When requesting this clone from Dr. Lustignenstigm@nybc.org When requesting this clone from Dr. Lustignensterence the Williams lab clone id - SWOv3MCAM03BO;
please reference the Williams from Americham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman and (email: slustigménybc.org)."

a 100 c 100 g 166 +
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/db_xref="taxon:6282"
/clone="onch17"
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(SL96MLW-OvmL3)"
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Tel: 4135
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Contact: Steven A. Williams
Molecular Parasitology
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately do nolting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture.
                                                                                                                                                                                                                                                                                                                                                                                                              in culture, and converted to double-stranded CDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams
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/dev_stage="molting L3"
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/db_xref="taxon:6282"
/clone="SWmL3C0691"
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Pred. No. 1.1e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/3D6/MB3D6AA4G10T3.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +44 131 650 6760 Fax: +44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Blaxter ML Institute of Cell, Animal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blaxter, M.L., Waterfall, M., Daub, J.,
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Brugia malayi
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MB3D6AA4G10T3 Brugia malayi day 6 post-infection third stage
SAW96MLW-BmL3d6 Brugia malayi cDNA clone 3D6AA4G10 5', mRNA
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The library was constructed by Michelle Lizotte-Waniewski. The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email genome@smith.edu."
                                                                                                                 using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 2 x 10E5 independent recombinants and average insert size was 900 base pairs.
                                                                                                                                                                                           /note="Vector: lambdaZapII (UniZap XR); Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. mRNA was prepared from third stage larvae of Brugia malayi isolated from the peritoneal cavity of jirds six days after infection. The mRNA was converted to double stranded cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="3D6AA4G10"
/clone_lib="Brugia malayi day 6 post-infection third stage
larvae SAW96MLW-BmL3d6"
                                                                                                                                                                                                                                                                                                                                                /dev_stage="third stage larvae, six days after infection"
/lab_host="E. coli XL1-Blue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Brugia malayi"
/strain="TRS Labs"
                                                                                                                                                                                                                                                                                                                                                                                                 /sex="mixed"
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                               Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:802407.
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 466)
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                                                                                                                                                                                                                                      Tel: 4135853826
Fax: 4135853786
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                                                                                                                                                                                                                      genome@smith.edu
              /dev_stage="moiting L3"
/lab_host="xL1-Blue MRf',
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
                                                                                          /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SwmL3CO758"
/clone_lib="Onchocerca volvulus
                                                                                                                                                                                         Location/Qualifiers
                                                                              (SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         volvulus
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   L3,
were isolated
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Pred. No. 4.2e-62;
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   infected black flies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGAAATGACAACTGCAT 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCGNTTGATTCCTGTAATGTAGCACGTACACGTTCGTTANNTCCACGTGGTATTGTTG
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                                      Unpublished (1997)
on Sep 12, 1996 this sequence version replaced gi:1405277.
Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                      SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO2020 5', mRNA
Smith College Department of Biological Sciences Department of Biological Sciences, Clark Scienc
                                                                                                                   Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernent Filarioidea; Onchocercidae; Onchocerca
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    Clark Science Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296;
                 AA625010
                                                          SWOv3MCA318SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO318 5', mRNA
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Email: genome@sr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       College, Northampton, MA, 01063, USA Tel: 4135853826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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/lab_host="XL1-Blue MRF'"
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/db_xref="taxon:6282"
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83.9%;
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Pred. No. 2.1e-60;
0; Mismatches 57;
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                    tttctatcaatgccagatcagtattaccattaaagaaccaaatagcgaatgtgttcgacc
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                                                                                  ATTATTAAATGCTGATGGTTGTGCTTTGGACAAATATTTGCTCAACAACTTGGAATATCC
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:802391
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 4135853826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 395)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il: genome@smith.edu
primer: pBluescript SK.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //dev_stage="mol/ing L3"
//dev_stage="mol/ing L3"
//lab_host="XL1-Blue MRF/"
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
//note="Vector: Lambda Uni-ZAP XR; Site_1 Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2 or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is -1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        slustigm@nybc.org)."
1 76 c 88 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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A_Geneseq_36:W94027
A_Geneseq_36:R43341
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A_Geneseq_36: W68387
A_Geneseq_36: W59323
A_Geneseq_36: W50144
A_Geneseq_36: R06426
A_Geneseq_36: R11110
A_Geneseq_36: R10322
A_Geneseq_36: R80530
A_Geneseq_36: R43342
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A_Geneseq_36:R06399
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-Q=/cgn2_1/USPTO_Spool/US09323427/runat_14042000_170513_19878/app_query.fasta.1
-Q=/cgn2_1/USPTO_Spool/US09323427/runat_14042000_170513_19878/app_query.fasta.1
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-GAPD=12.000 -GAPEXT=4.000 -MINNATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -MINNATCH=0.100 -LOOPCL=0.000
-XGAPEXT=0.000 -GAPEXT=4.000 -QGAPEXT=7.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS-human40.cd1 -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -ALIGN=15 -MODE=-LOCAL -OUTFMT=pfs -NORM=ext
-MINLEN=0 -MAXLEN=1000000 -USER=US09323427 -NCPU=6 -ICPU=3
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  Documentation
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                                                                                                                                                                                                                                              Mouse protease-activated reception pll0. Recombinant polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type B alpha-amidating enzyme. Segment of desmosomal cadherin, C-terminal amidation enzyme. cE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE-III (peptidylhydroxyglycine Expression plasmid pUCP1CI799 of C-terminal prepro-C-terminal a
                                     Mouse SRY-related protein.
                                                                                          Alpha-Trichosanthin encoded by
                                                                                                          Alpha-facto profibrolase from H. pylori transporter protein, Hydra head activator binding
                                                                                                                                                                                                                                                                                                                                                                                                                            Type A alpha-amidating enzyme.
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                       BAR1 gene product.
                                                                   Ribosome inactivating protein
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Asparaginyl-tRNA synthetase fr
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E. coli colitose or glucose tra
                                                                                                                                                                                                                                                                                                                                      B. sphaericus SLP. Host cell e
Human p110. Recombinant polyp
PtdIns 3-kinase 110 kp cataly!
Human PTP-OB. Protein tyrosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. difficile toxin A. Fusion | Clostridium difficile toxin A
                                                                                                                                                                                  aureus asparaginyl tRNA syn
    zona
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ed C-termin
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  prote
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A_Geneseq_36:R99462
A_Geneseq_36:R97208
A_Geneseq_36:R97210
                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-323-427-5/rev x R20112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: R20112 from: 1
                                                                                                                                                                                                                                                                                                                                                                1065
                                                                                                                                                                                                                                                                   1015 AGGACATGTTTATGTGAAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-465404-A.
08-JAN-1992.
27-MAY-1991;
01-JUN-1990;
10-AUG-1990;
30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                  526 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q20269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R20112;
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                                                                                                                                                                                  ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                                                              TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                            Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                     AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                  lAlaAspGlyTyr.....
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to: 935

.....Cys

547

916

966

871

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seq_name: A_Geneseq_36:R20112
 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _documentation_block:
                                                                                                                           prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyoH -> R-NH2. It can be used to produce peptides win amidated C-termini, e.g. calcitonin, growth hormone, LH-RH.
                                                                                                                                                                                     The sequence was deduced from a cDNA insert from pAE-III-202-4 (FERM BP-3172). The vector serves as a source for a DNA fragment encoding pHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to
                                                                                                                                                                                                                                                           Novel DNA encoding peptidyl hydroxy:glycine N-C lyase (PHL) used to prepare PHL which can be used in the amidation of peptide(s) e.g. human calcitonin.
Claim 4: Page 18: 28pp: English.
                                                                                                                                                                                                                                                                                                                                                  (CIBA ) CIBA GEIGY AG. Iwasaki Y, Shimoi H, S Kawahara T, Kangawa K; WPI 92-010570/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amidation; PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-1992 (first entry)
AE-III (peptidylhydroxyglycine N-C lyase precursor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R20112 standard;
                                    Quality:
                     Ratio:
                                                                                                                935 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP-141678.
JP-210535.
                                                                                                                                                                                                                                                                                                                                                                                                                              JP-329911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- AE-III
/note- "including PAM
383 935
100.00
0.541
47.315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= PHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
79
79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 19
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102.98
96.88
96.88
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10.64
13.76
13.76
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2756
4655
4655
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! Human calcium sensor protei
! Human kidney calcium sensor
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612

778

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681 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628 laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 leProHisSerLeuThrMetValProAspGlnGlyGlnLeuCysValAla
  85 CTCAATGTTTATGGGTTTAAGCATTGCATTGATT...GCTGCCGTCATTA
                                                             ValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGlyVa
                                                                                                     GTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTT
                                                                                                                                                                                   TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCT
                                                                                                                                                                                                                           aGlyValProThrGlnGluLysGlnAsnValValGlnGluSerSerAlaG
                                                                                                                                                                                                                                                               TGATATCAACACCCTTGAA.....ATTAGCGATGATAATCAAGCTT
                                                                                                                                                                                                                                                                                                            GCA.....GAACCGGAGAATATCATT...GATGTACGAAC
                                                                                                                                                                                                                                                                                                                                                                                            alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisArgSerValLysLysAlaGlyIleGluValGluGluIleThrGluTh 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAAT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alGlnGlyPheMetLeuAsnPheSerAsnGlyAsp.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 628
                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyAspAlaHisAlaAsnAlaValTrpLysPheSerProSerLysAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGCTGATGGATGTCTTGATAAATATTTG.....CTAAATAATTT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gly......ValLeuTyrAlaValAsnGlyLysProTyrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nTrpGlyGluGluThrSerSerAsnValProArgProGlyGlnPheArgI 580
                                                                                                                                           lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eAspMetProHisAspIleAlaAlaAlaAspAspGlyThrValTyrValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspArgGluAsnGly...ArgIleGlnCysPheHisAlaGluThrGlyAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......GlyTyrSerAlaProV
                       39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
    US-09-323-427-5/rev x P94856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: A_Geneseq_36:P94856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: P94856 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                    1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1065
828 AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
                                                                                                                                                                                                                                                                                                                                                                                          507 lAlaAspGlyTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-1987; JP-177184
05-DEC-1987; JP-306867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840 leAlaIleAlaIlePheIleArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-1989.
15-JUL-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P94856 standard; protein;
                                                           leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                 AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                                                                     AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                   ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
                                                                                                                                           nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI
                                                                                                                                                                                 Asn ... SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                                                                                                                                                                ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
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JP-177184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĀĀ;
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43.103
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Gaps: 12
Percent Identity: 21.552
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871 512 916

871

561

742

308 725 358 709

807

185 773 226 757 258 692 437 675

664 531 646 631 635

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and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp; English.
The sequence encodes a derivative of the mature C-terminal alphamidating enzyme from plasmid pXA799.
The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.
Although pXA799 is similar to pXA457 at the N-terminus, it has an are hydrophobic elements suggesting a membrane function.
See also N93060.
                                                                                                                                                                                                                                                                                                                                                    (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka S, Matsuo H, Mizuno WPI; 89-017279/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-1990 (first entry)
Expression plasmid pUCP1CI799
alpha-amidating; pAX799; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        823 | SerPheValLeuIleIleThrLeuLeuIleIleProIleAlaValLeuI
                                                                                                                                                                                                                                                  Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences.
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                                                              has an area
                                                                    of.
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alignment_block:
US-09-323-427-5/rev x P94854
                                                                                                                                                                                                                        alignment_scores:
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                                                                         Align seg 1/1
                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   documentation_block:
                                  1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                 Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences. Disclosure; 7pp, English. English plasmid pXA799 contains a sequence derived from Xenopus laevis. The plasmid was screened from an E.coli library using plasmid pX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1990 (first entry)
C-terminal prepro-C-terminal alpha-amidating enzyme alpha-amidating; pax799; alpha amide; ds.
                                                                                                                                                                                                                                                                            See also N93060.
Sequence 875 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUNR) Suntory Ltd.
Ohsuye K, Kitano K, Tanaka
WPI; 89-017279/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-1989.
15-JUL-1988; 306508.
17-JUL-1987; JP-177184.
05-DEC-1987; JP-306867.
                                                                                                                                                                                                                                                                                                                 to screen a larger library.
Although the gene product is similar to that of pXA457 at the N-terminus, it has an area of hydrophobic elements suggesting a membrane function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; N90791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P94854 standard; protein;
CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 732
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seq_documentation_block:
ID R73053 standard; Prot AC R73053 standard; Cfirst e Peptidyl C-terminal a KW trichostatin; CHO.
OS Not specified. Locat FH Key 1...3 FT peptide 1...3 FT peptide 1...3 FT Peptide 7.labe PN 26-APR-1995.
PR EP-649900-A.
PR 08-SEP-1994; 306587.
PR 08-SEP-1994; 30587.
PR (SUNR) SUNTORY LTD.
PI FURUKAWA K. Ohsuye K
                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: A_Geneseq_36:R73053
                        26-APR-1995.
07-SEP-1994; 306587.
08-SEP-1993; JP-257881.
(FURU/) FURUKAWA K.
(SUNR) SUNTORY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             731 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \verb"eGluMetProHisAspIleAlaAlaGlyAspAspGlyThrValTyr"
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  Ohsuye K,
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/label=
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  Sugimura
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enzyme;
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DR PT DR CCC CCC CCC
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US-09-323-427-5/rev x R73053
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing protein prodn. from cultured animal cells - by adding a trichostatin to the medium, effective at low concn. and not injurious to host cells
Disclosure; Page 10-15; 19pp; English.
Disclosure; Page 10-15; 19pp; English.
Jmu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alphamu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alphamuniase enzyme (AE)) were suspended in F-12 medium to which aliquots of trichostatin were added. Cells were cultured for 3 days at 37 deg and then assayed for AE. Without trichostatin, AE productivity was 708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities were respectively 866, 1897, 1894 and 3359 U/ml.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  530 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                         632 laValSerTyrAlaPro.....
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N-PSDB; Q87970.
                                                                                                                                                                                                                                                          GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA
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                                                  TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA
                                                                                                                                                   TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                                                                     Gly.....ValLeuTyrAlaValAsnGlyLysProTyrTy
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                                                                                                                                                                                                                                                                                                                                                                                                           uPheValLys...GlnIleLysHisGlnGluPheGlyArgGluValPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA 779
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.MetLeuAsnPheSerAsnGlyAsp.....
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Percent Identity:
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seq_documentation_block:
ID R88469; standard; Prot AC R88469; of irst e DT 14-AUG-1996 (first e DT 14-DEC-1995).
PF D 19-DEC-1995; prevention; os Feline infectious per PN J07327683-A.
PD 19-DEC-1995; prevention; of infection infection infection infection infection. The spike CC cell with the spike proteing collimate infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding feline infectious peritonitis I virus spike protein used in a vaccine for prevention and treatment of FIPV-I infection claim 1; Page 14-17; 23pp; Japanese.

This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host cell with the spike protein DNA and expressing the sequence such sequence 1464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1994; 129300.
10-JUN-1994; JP-129300.
(KITA) KITASATO KENKYUSHO
WPI; 96-072341/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feline infectious peritonitis 1 virus spike protein.
Feline infectious peritonitis 1 virus; FIPV-I; spike protein;
vaccine; prevention; treatment.
Feline infectious peritonitis 1 virus.
                                                                                                                                                                                                                                                          789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 LysAsnSerThrThrGlyGluIlePheThrValValProCysAspLeuTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            755 rAlaGlnValAlaValIleAsnAspGluIleValGlyAlaIleThrAlaV 772
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                                                                                                                                                                                                                                                                                                                                                         alAsnGlnThrAspLeuPheGluPheValAsnAsnThrGlnAlaArgArg
                                                                                                                                                                                                                                                                                                                                                                                                         TTTCACTTCCA.....TTTGATTCATGCAAT.....GTTGCGCGT
TCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATG 704
                                                                                                                                                                                                    TTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTAC
                                                                                                                                                                                                                                                                                                    ACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCAT 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAA 939
                                          snCys.....ThrSerAlaIleThrTyr 825
                                                                                                  AATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTA
                                                                                                                                                  oGlnPheTyr.....TyrIleThrLysTrpAsnAsnAspThrSerSerA
                                                                                                                                                                                                                                                    SerArgSerSerThrProAsn.....PheValThrSerTyrThrMetPr
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Ratio:
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SerSerPheAlaIleCysAsnThrGlyGluIleLysTyrValAsnValTh 842

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Dr Ac Dr
                                                                                                                                                       seq_name: A_Geneseq_36:W88310
                                                                                                          _documentation_block:
                                                                                                                                                                                                                                                                                                           1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1006
26-APR-1999 (first entry) E. coli colitose or glucose transferase.
                                                      W88310 standard; Protein; W88310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372
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                                                                                                                                                                                                                                                                                                                                                          78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||::: |||::::: :::||||||||::::::
||GlyAlaArgLeuGluSerLeuMetLeuAsnAspMet.......
                                                                                                                                                                                                                                                                                                         IleGlyGlyMetAlaLeuGlySerIleThrSerAlaValAlaVal.ProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rAspValAlaAspLeuValCysAlaGlnTyrTyrAsnGlyIleMetValL 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serGlyLeuGlyThrValAspAspAspTyrLysLysCysSerSerGlyTh 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TA.....AATGCT.....GAT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hrGlyAsnIleSerIleProLysAsnPheThrValAlaValGlnAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rHisValGluIleValAspAspSerIleGlyValIleLysProValSerT
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                                                                                                                                                                                                        heAlaMetGlnValGlnAlaArgLeuAsnTyrValAlaLeuGln 1070
                                                                                                                                                                                                                                                     TT......CGTTTAAATTTCGTCCAAATCAGA 6
                                                                                                                                                                                                                                                                                                                                                     TTTATGGGTTTAAGCATT...GCATTGATTGCTGCCGTCATTATTACCAT 32
                                                                                                                                                                                                                                                                                                                                                                                                       euProGlyValValAspGlyAsnLysMetSerMetTyrThrAlaSerLeu 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leGlyLysArgSerAlaValGluAspLeuLeuPheAsnLysValValThr 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAAGAAAGATCTGCAGAACCGGAGAATATCATTGAT.....GTACGA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sLeuGlyGlyLeuTyrPheAspGlyLeuSerSerLeuLeuProProLysI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euThrGlnTyrThrSerAlaCysGlnThrIleGluAsnAlaLeuAsnLeu 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrIleGlnIleGlnValLysProValValValAsp.....CysAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACCTGTAATAC 129
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Principles acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food, principles or patient samples

Principles or patient samples

Principles or patient samples

Principles or patient samples

Principles or patient samples

Principles or patient samples

Principles or patient sequence of the protein encoded by the wbdM gene of a gene cluster (see x06748) involved in the biosynthesis of the Escherichia coli Olli O antigen. The protein shows high the mology with TrsE of Versinia enterocholitica, and is predicted to be a colitose or glucose transferase. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wax (flippase) and wzy (polymerase) particularly wbd (transferase), wax (flippase) and wzy (polymerase) genes, within o antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in testing food- or faecal-derived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: W88310 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-323-427-5/rev x W88310
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22-JUL-1997; AU-008162
01-MAY-1997; AU-006545
(UNSY) UNIV SYDNEY.
Reeves PR, Wang L;
WPI; 99-059669/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1100 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1009 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 960
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W09850531-A1.
12-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; X06748.
                                                                                                                                                                                                                                                                                                                                          GCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erPhePheArgAlaLeuPheGlnValLysLysIleIleValAlaLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAACAATCAATTTTAATACACGTAATGCATTCGAAGGAC.....A 1010
gLeu.....SerAspPheLeuAlaSerIleThrThrAsnValS
                                             ATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGAT
                                                                                                                                                                                                                                                                                                                                                                                        ProAspIle.....IleHisSerHisMetPheHisAlaAsn..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuThrGlyIleSerGluValLysProThrGlnAsnIleAsn.....
                                                                                           ThralaHisAsnLysAsnGluGlyGlyAsnAlaArgMetPheCysTyrAr
                                                                                                                                              ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAG
                                                                                                                                                                                         lePheSerArgPheIleArgMetLeuIleProAlaValProLeuIleCys 108
                                                                                                                                                                                                                                       TGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTG...ATCGTGCAT 813
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Ratio:
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AU-006545
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0.533
46.281
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18
21.763
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Seq ID AC AC DT DE KW KW KW OS PN PPR PR PR PR PR
                                                                                                                                                                                                                                                                                                                                                seq_name: A_Geneseq_36:W13825
                    28-AUG-1996; U14192.
31-AUG-1995; US-521872.
11-OCT-1995; US-540804.
26-JAN-1996; US-590399.
                                                                                                                                                                                                                                                                                                         _documentation_block:
                                                                                                       04-JUN-1997 (first entry)
Yeast transcription regulatory factor SRB8.
Transcription regulatory factor; suppressor of RNA polymerase SRB8; RNA polymerase II; holoenzyme; SWI/SNF.
Saccharomyces cerevisiae.
W09708301-Al.
06-MAR-1997.
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(WHED)
                                                                                                                                                                                                                                                                                   W13825 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAAT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laGluLysIleAlaGluThrLeuLysIle...AspAspAsnAlaArgLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....AACACCCTTGAAATTAGCGATGATAATCAAGCTTTG
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WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                   Protein; 1226 AA
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alignment_block:
US-09-323-427-5/rev x W13825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II
pri and one or more regulatory proteins, pref. suppressor of RNA
pri polymerase B proteins or SWI/SNF proteins
Pri polymerase B proteins or SWI/SNF proteins
Pri Claim 11; Fig 10a-b; 154pp; English.

Rovel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5,
SRB6, SRB7, SRB8, SRB10 and SRB11 (W13821-28) are transcription
Cregulatory factors that act as positive and negative regulators of
CRNA polymerase II activity, and are components of the RNA polymerase
CI I holoenzyme. They were identified using methods designed to
Clientify transcription factors involved in RNA polymerase II
C-terminal domain (CTD) function. SRB8 and SRB9 appear to repress
CTD activity. Genomic clones (T59904-11) for the SRBs have been obtd.
SRBs can be used to treat diseases resulting from alteration or
Cende that modify gene, pref. by gene transfer technology. They
can also be used in in vitro transcription of DNA and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: W13825 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1148 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1048 AACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA
                                                                                                                                                                                                                                                                461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 eIleLysValProThrTyrIleArgLysLeuIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chao DM, Koleske AJ, WPI; 97-179258/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cpds. that modify gene transcription.
Sequence 1226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 659
                                                                                                    CTGAAATCACAACTGCTTTTC....AAACTCAAATTGTCCCGATGCCA
                                                                                                                                                                                                                                                                                                              GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC
                                                                                                                                                                                                                                                          \verb|nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yrAspValLysPheTyrGluIlePheAsnPheAspGlnValValGluIle
                                                                                                                                                        euSerHisLeuCysSerGlyTleLeuSerSerValAsnArgThrValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGATCTCTGAATCCACGTGGTATTT............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValGlnLeuLeuIleAsnLeuLysIleSerProLeuMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAAT
                                                 LeuLysTlePheLysTlePheCysTleAspLeuGluValPheHisHisPh
                                                                                                                                                                                                       TG.....ATAAAACAGTTAGTGCACAGATTGAGGTAT
                                                                                                                                                                                                                                                                                                                                                                  ThrGluGlnIleLysMetArgIleLeuSerAsnAspIleThrAsnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                      .....TTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....SerGlnTyrAsnMetValLeuArgAsnValMetGluT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGTCTTTATGATCAAG...AAGGTTGCCGTAATGATGAAGGTGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..SerSerGlyLeuLeuTyrLeuGlnAspSerAsnAspLysPheValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetMetProSerLeuTyrArgLeuLeuAsnIleLeuIleThrTyrGlyIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.50
0.468
48.338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
Percent Identity:
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С
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16
20.716
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alignment_block:
US-09-323-427-5/rev x R06400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1015 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1065 TGTGGACCAACTTCAATAACAATCTAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 CysGlnProThrAspValAlaValAspProGlyThr......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA in libraries were prepared from human thyroid gland poly(A) RNA in lambda gtll and gtll. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtll library, including gtllOchT2.

Restriction analysis indicated that gtlOchT2 encoded a different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The enzyme is useful for prodn. of physiologically active alphamidated peptides from their C-glycyl precursors. See also Q05630 and Q05632.

Sequence 776 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type of enzyme to one of the other two clones. The DNA can be inserted into vectors for expression in E.coli or (more efficiently)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding sequences
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CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nTrpGlyGluGluSerSerGlySerSerProLeuProGlyGlnPheThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alProHisSerLeuAlaLeuValProLeuLeuGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC
                                                                                                                                                                                                                                                                                                                                                                                eValArgGluIleLysHisSerSerPheGlyArgAsnValPheAlaIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspArgGluAsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.....ACTG 861
                                                                                                     ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT 576
                                                                                                                                                                                                                  ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
                                                                                                                                                                                                                                                                        erTyrIlePro.....
                                                                                                                                                                                                                                                                                                                          AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA 676
                                                  .....AspGlnGluProValGlnGlyPhe......
                                                                                                                                                          ....GlyLeuLeuPheAlaValAsnGlyLysProHisPheGly..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TT.....GTCATTTCGTTTCATCCATTATTT.....GTTACCAAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .SerArgIleValGlnPheSerProSerGlyLysPheIleThrGl 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.00
0.592
45.652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                504
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seq_name: A_Geneseq_36:R06379
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                                                                                          Disclosure; pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA in lambda gt11 and gt10. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gt10 library, including gt10ch9101.

Restriction analysis indicated that gt10ch9101 encodes a different type of enzyme to one of the other two clones. The DNA can be inserted into vectors for expression in E.coli or (more efficiently)
in animal cells.

The enzymes are useful for prodn. of physiologically active alpha-amidated peptides from their C-glycyl precursors.

See also Q05630 and Q05631.

Sequence 866 AA;
                                                                                                                                                                                                                                                                                                                                  17-JAN-1990; J00042.
17-JAN-1989; JP-005878.
(SUNR ) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka
WPI; 90-254034/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1990 (first entry)
Lambda gtlOchlOl encoded C-terminal alpha amidating enzyme.
C-terminal alpha amidating enzyme; human thyroid gland;
Lambda gtlOchlOl.
                                                                                                                                                                                                                                                     C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new coding sequences.
                                                                                                                                                                                                                                                                                                                    N-PSDB; Q05632
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
WO9008190-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R06379 standard; protein; 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 lValGluThrLysMetGluAsnLysProThrSerSerGluLeuGlnLysM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTGATTTACGTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....ValMetAsnPheSerAsnGlyGluIleIleAspIlePhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leAlaIlePheIle 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ValLeuIleThrThrLeuLeuValIleProValValValLeuLeuAlaI 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .................LysProValArgLysHisPheAspMetProHi 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA
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                                                                                                                                                                                                                                                                           DNA
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alignment_scores:
 Quality:

87.00

Length:

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325 TAAAACAGGTGGTGCCGCAGCAAA	375 AGCGAATGTGTTCGACCACAATGT ::: 710 ValLysLysAlaGlyIleGluVal	425 CACAGCTTTTCTATCAATGCCAGA ::::: 693 hrAsnThrValTrpLysPheThrL	475 AGATTTAATGGCTGGCCAAGAAGC ::::: ::::: 676 SASpIleValAlaSerGluAspGl	525 GATGGATGTGCTCTTGATAAATAT	575 CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAAT ::::::::::::::::::::::::::::	625 ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGCGTTGTC :: :: 645AspGlnGluProValGlnGlyPhe	675 ACCGGTCAACCAGTTCAATTTGCT ::: 632GlyLeuLeuPheAla	725 AAATTGTCCCGATGCCAGTATGCC :: ::! 628 erTyrIlePro	775 AGTTAGTGCACAGATTGAGGTATC 611 eValargGluIleLysHisSerSe	822 GATCGTGCATATCGAGTACAA 595 AspārgGluāsnGlyārgIleGln	860 TTGTCATTTCGTTTCATC	865 A	915 AATGTTGCGCGTACACGATCTCTG	965 ATGAAGGTGGACGTCAAGTTGCCG		1065 TGTGGACCAACTTCAATAACAATC ::::::::::::: 524 CysGlnProThrAspValAlaVal	Align seg 1/1 to: R06379 from:	alignment_block: US-09-323-427-5/rev x R06379 .	Ratio: 0.592 Percent Similarity: 45.652 Pe
AAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT	AGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT	CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT ::::: hrasnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer	AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT ::::: ::::::::::::::::::::::::::	GATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC	GCT	CATT	ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA ::: ::: :::	AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA :: :: erTyrIlePro	AGTTAGTGCACAGATTGAAGTATCTGAAATCACAACTGCTTTTCAAACTC 	GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAAC	TTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT :::::::: ::: alproHisSerLeuAlaLeuValProLeuLeuGlyGlnLeuCysValAla	ACTG GlnPheThrV	AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC ::	ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC		TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA	1 to: 866		Gaps: 13 Percent Identity: 18.944
276	326 726	376 709	426 693	476 676	526 665	576 652	626 644	676 631	726 628	776 611	823 594	861 578	866 561	916 545	966 544	1016 535			

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alignment_scores:
Quality:
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                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                US-09-323-427-5/rev x R06399
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                                                                                                                                                                       1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; pp; English.

Disclosure; pp; English.

CDNA libraries were prepared from human thyroid gland poly(A) RNA in lambda gtl1 and gtl0. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtl0 library, including gtl0chT201.

Restriction analysis indicated that gtl0chT201 encodes a different type of enzyme to the other two clones. The DNA can be inserted type of enzyme to the other two clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lambda gtl0ch201 encoded C-terminal alpha amidating enzyme. C-terminal alpha amidating enzyme; human thyroid gland; lambda gtl0ch201.
                                                                                                                                    631 CysGlnProThrAspValAlaValAspProGlyThr.....
                                                                                                                                                                                                                                                                                                                                                                                                          This enzyme is useful for prodn. of physiologically active alphamidated peptides from their C-glycyl precursors. See also Q05631 and Q05632.

Sequence 974 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-terminal alpha amidating enzymes from human thyroid gland converting C-terminal glycyl peptide(s) or protein, and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUNR ) SUNTORY LTD.
Ohsuye K, Kitano K, Tanaka
WPI; 90-254034/33.
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17-JAN-1989; JP-005878.
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leAlaIlePheIle 887
                                                                                                     .ValLeuIleThrThrLeuLeuValIleProValValValLeuLeuAlaI
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seq_documentation_block:
ID R74171 standard; Protein;
AC R74171;

3038 AA.

seq_name: A_Geneseq_36:R74171

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-09-323-427-5/rev x R74171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT Novel DNA encoding triol poly-ketide synthase - used to isolate and PT identify homologues of triol poly-ketide synthase, and in the treatment of hyper-cholesterolaemia
PS Claim 12: Figure 2: 107pp; English.
CC The full-length TPKS-encoding DNA in plasmid pLoA was CC designated pTPKS100. Splicing of the introns from the DNA CC sequence and translation of the 9114 nt ORF results in a CC protein of 3038 AAs (R74]71) with a mol. wt. of 269,090 CC protein of 3038 AAs (R74]71) with a mol. wt. of 269,090 CC daltons. Inspection of the TPKS AA sequence for active called sites residues and motifs known to be associated with CC polyketide synthases and fatty acid synthase (FAS) activities cresulted in the identification of candidates for expected CC sites (see FT). Except for the presence of a methyl transferase, CC cont present in FAS, the succession of activities on the control of the presence of the p
                                                                                                                                                                                                                                                                                         Align seg 1/1 to: R74171 from: 1
                                                                   1096 CAATGGTGTCGAAGGTGAGCCAGAATTGAATGT.....GGACCAACTT 1053
                                                                                                                                                                                                                     1146 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA 1097
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/label= misc feature
misc_difference 1450. .1460
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N-PSDB; Q92323.
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Conder MJ, Davis CR,
Reeves CD, Vinci VA;
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11-MAY-1995.
28-OCT-1994; U12423.
02-NOV-1993; US-148132.
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Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-1996 (first entry)
Aspergillus terreus triol polyketide synthase.
Triol polyketide synthase; TPKS; HMG-COA reductase inhibitor;
hypercholesterolaemia; LDL- cholesterol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                              ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro....
.....GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3038 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= misc :
e 1603. .1612
/label= misc :
e 2521. .2535
/label= misc :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= keto reductase
2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- dehydratase motif
1446. 1450
/label- methyl transferase motif
1932. 1937
/label- enoyl reductase motif
2164. .2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.00
0.481
38.347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label acyl carrier protein motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label | keto-acyl synthase motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hendrickson LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetyl/malonyl transferase motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 472
Gaps: 24
Percent Identity: 19.703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcada PC,
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1448		1446
330	AAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG	379
1445	IleLeuGluIle	1442
380	GCT	429
430 1441	CAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT::: ::: :::	479 1426
480 1426	TGATAAATATTTGCTAAATAATTTGGAATATC	511 1409
512 1409	GGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	558 1394
w	OHisValArgLeuValGlnArgValGlyGlnHisLeuLeuProThrVal	7
59		559
559 1377	TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT	601 1360
1360	ß	1351
602	ATAAATG	651
1350		1341
<u>بر</u>	AlaPheHisLeuGinLysGinIleGiuTrpLeuGiu	9 2
02	TTTCAAACTCAAATTGTCCCGATGCCAGTA	742
1326	ATGGAAGCTGATAAAACAGTTAGTGAGGACAGATTGAGGTATCTGAAATCAC ::: ::::::::::::::::::::::::::::	1313
1312		1296
793		827
828 1296	GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCA :::: yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA	873 1279
1279	roProAspAlaSerThrAspHisAlaMetPheAlaArgTrpSerTrpGl	0
874		921
922 1262	ATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT :::	968 1247
1246	yAspTyrLeuSerGlyAspIleValValPheAspAlaGlu	1233
ט נ	E-C-C-C-E-C-C-C-C-C-C-C-C-C-C-C-C-C-C-C	1000
1010	ACAATCAATTTTAATACACGTAATGCATTCGAAGGACIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1047
1216	euCysLeu	1200
1048	CAATA	1052

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alignment_block:
                                                                                              alignment_scores:
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                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1479 nAlaArgGluGlnPheAlaProPheGluAspArgMetValPheGluProL 1496
                                                                                                                                                     Prodn. of alpha amidating enzyme - using prokaryotic or eukaryotic expression vectors having transcriptional promoter Claim 3; page 19; 24pp; English.
The corrsp. DNA sequence hybridises, under stringent conditions, with a DNA sequence (I) which encodes an alpha amidating enzyme (AEE) and is foreign to the host cell into which it is transformed. (I) is connected to a promoter and is contained in an expression vector. The AEE encoded is used as a catalyst in the conversion of a peptidyl substrate to a corresp. peptidyl amide. This can be used for making a protein biologically active, e.g. calcitonin or growth hormone releasing factor. See also Q05637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1463 GlyPheAsnSerTyrThrTyrThrAspIleSerThrGlyPhePheGluGl 1479
                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1990; 301034.
06-FEB-1989; US-307366.
(UNIG-) UNIGENE LAB INC.
Betelsen AH, Mehta NM, Beaudry GA;
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 90-248308/33.
N-PSDB; Q05636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP-382403-A.
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Protein encoded by sequence which hybridises alpha amidating enzyme; peptidyl amide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R06427 standard; protein; 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gCysThrGluProPhe 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCATGTCACCATTT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheIlePheGlyLeuPheAlaAspTrpTrpAlaGlyValAspAspGlyAr 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyGlnMetValIleLeuGluIleThrHisLysGluHisThrArgLeuGly 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....LeuGluLysThrMetAlaHisAlaArgSerLeuLeuLysProGlyG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euAspIleArgArgSerProAlaGluGlnGlyPheGluPro...HisAla 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....GCTGCAGTACAAAATGGAAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTTTGCCAGTTGATTTACGTCAC...CGTGCACTTCTGCAACATAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......CGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATC 241
                                                         Quality:
Ratio:
                                  86.50
0.588
43.363
                              Length: 339
Gaps: 14
Percent Identity: 17.994
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Align seg 1/1
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                                                836 lGluProLysValGluAsnLysProThrSerSerGluLeuGln.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     634 CysGlnProThrAspValAlaValGluProSerThr.......
332 GAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAA 283
                                                                                                                                                                                                                                                                                                                                                                              {\tt sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alProHisSerLeuAlaLeuValProHisLeuAspGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nTrpGlyGluGluSerSerGlySerSerProArgProGlyGlnPheSerV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValLysLysAlaGlyIleGluValGlnGluIleLysAlaGluAlaValVa
                                                                                                                                                                                                                      ....CAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTT..
                                                                                                                                                                                                                                                                             hrAsnThrValTrpLysPheThrLeuThrGluLysMetGluHisArgSer
                                                                                                                                                                                                                                                                                                                                ......AAATATGCGGATCGATCACAGCTTTTCTATCAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATTTAATGGCTGGCCAAGAAGCTCACGTATAC........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGGATGTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....ValMetAsnPheSerSerGlyGluIleIleAspValPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AspGlnGluProValGlnGlyPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....GlyPheLeuPheAlaValAsnGlyLysProTyrPheGly..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erTyrIlePro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eValArgGluIleLysHisAlaSerPheGlyArgAsnValPheAlaIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspArgGluAsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATCGTGCATAT...CGAGTACAATGCTTTTACATGGAAGCTGATAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asn...SerArgIleValGlnPheSerProSerGlyLysPheValThrGl 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTTGTAACAAC 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....Суs
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                                                                                                          ... CGACCACAATGTTCAGAACCACAAGGATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysProValArgLysHisPheAspMetProHi 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       966
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	CAGTTGATTTACGTC 168	182
884	.ValLeuIleThrThrLeuLeuValIleProValLeuValLeuLeuAl	868
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851	Lys	851
283	AAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCC	332
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836	alLysLysAlaGlyIleGluValGlnGluIleLysAlaGluAlaVal	820
364	ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGT	405
819	ırAsnThrVal	803
406	AAATATGCGGATCGATCACAGCTTTTCTATCA	441
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442	TTAATGGCTGGCCAAGAAGCTCACGT	475
786	ysHisPheAspMetPr	776
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526	CTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAA	575
762	:	755
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754	::: heAlaValAsnGlyLysProTyr	742
626	TTCAATTTGCTATCATTGGTCAGCCAGTTTATC	675
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676	AATTGTCC	725
738	eValArgGluIleLysHisAlaSerPheGlyArgAsnValPheAlaIleS	721
726	TGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACT	775
721		705
776	TCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA	822
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823	.ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAC	864
889	1 ly 1 lu 2 lu 2 luSer 2 er 2 luGluSer 2 luPhe	671
865		865
671	AsnSerArgIleValGlnPheSerProSerGlyLysPheValThrGl	656
866	ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAAC	915
655	Cys	655
916	ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC	965

IleValMetPheIle 889

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alignment_block:
US-09-323-427-5/rev x W13009
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       micrometastases, not bound to desmosomes, to separate, enrich of detect living or fixed carcinoma cells by cell sorting methods as a therapeutic to deliver agents, e.g. other Ab or toxins, to target cells. The Ab provides rapid and reliable detection of metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) directed against epitopes of the present sequence can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, useful for diagnosis and treatment of carcinoma micrometastases Claim 7; Page 5: 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; psg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Franke WW, Schaef
WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnose, i.e. to detect carcinoma cells, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE19531033-A1.
27-FEB-1997.
                 TTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT.......
                                                                                                                                                                                AAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCA 950
                                                                                                                                                                                                                         snValLysGluGlyIleHisPheLysSerSerValIleSerIleTyrVal 348
                                                                                                                                                                                                                                                                                                                                                                                         LeuAspPheSerValIleValAlaAsnLysAlaAlaPheHisAspSerIl
                                                                                                  AGTTGCCGGAATTTCACTTCCATTTGATTCATGCAAT.....
                                                                                                                                                                                                                                                               ATGCATTCGAAGGA......CATGTTTATGTG
                                                                                                                                                                                                                                                                                                        eArgSerLysTyrLysProThrProIleProIleLysValLysValLysA 332
                                                                                                                                                                                                                                                                                                                                                T.....GAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                               TTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAAT 1070
                                                       nIleIleGlyAsnPheGlnAlaPheAspGluAspThrGlyLeuProAlaH
                                                                                                                                      SerGluSerMetAsp......ArgSerSerLysGly....
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0.822
51.232
Percent Identity:
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alignment_block: US-09-323-427-5/rev x R20026

Percent Similarity:

Quality: Ratio:

85.00 0.582 43.976

Percent Identity:

14 18.072

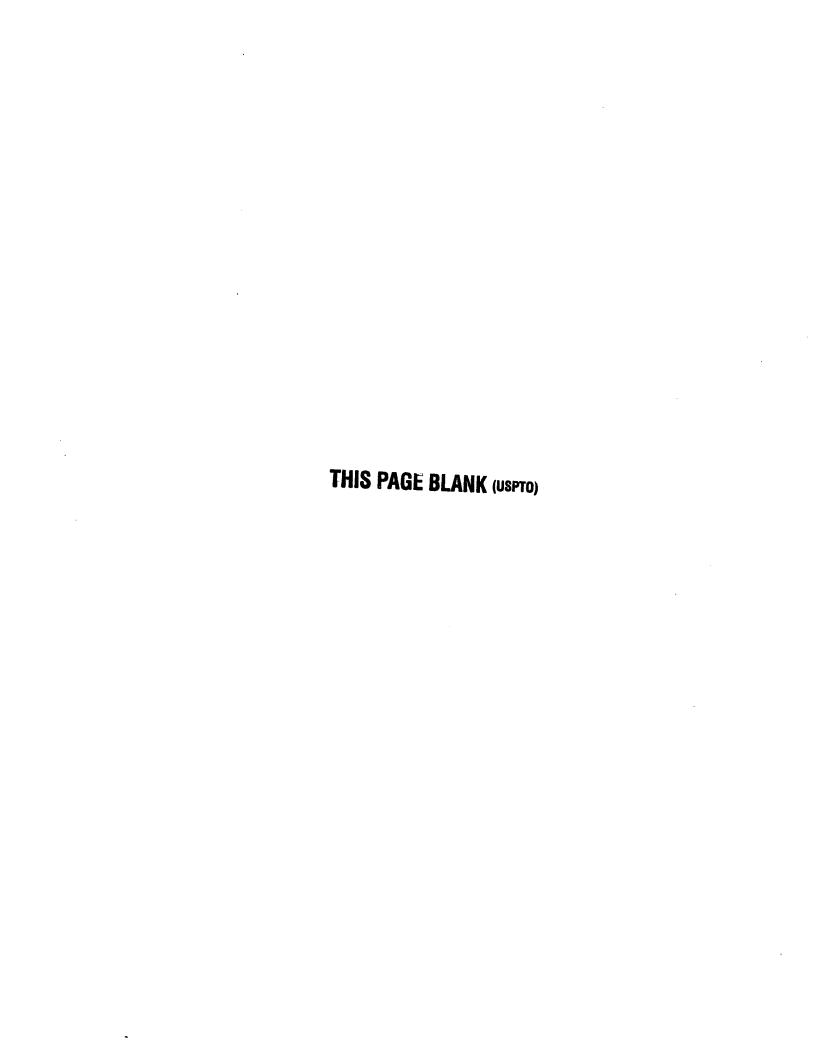
Align seg 1/1 to: R20026 from:

to: 973

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                   J03262484-A.
22-NOV-1991.
14-MAR-1990;
14-MAR-1990;
                                                                                                          Claim 1; Fig 1; 18pp; Japanese.

The sequence was deduced from the DNA sequence determined from clone isolated from a library prepd. from mRNA extracted from horse atrium tissue. The sequence is one of four similar ones provided which all have the same sequence up to residue 809 at which point they diverge, having different C-termini. The different termini are created by deletions in the last portion
                                                                                                                                                                                                                                           obtd.
                                                                                                                                                                                                                                                        \ensuremath{\text{N-PSDB}}\xspace , \ensuremath{\text{Q20198}}\xspace . coding for peptide C terminal amidation enzyme
                                                     DNA (see feature table). See also R20025-28. Sequence 973 AA;
                                                                                                                                                                                                                                                                                               14-MAR-1990; JP-063306.
(SHIS ) SHISEIDO KK.
WPI; 92-012701/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 GluLysTrp 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 snSerGlyProPheSerPheSerValIleAspLysProProGlyMetAla 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                674 CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCA.....GTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 IleAsnAspAsnCysProThrLeuIleGluProValGlnThrIleCysHi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equus caballus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-terminal amidation enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R20026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R20026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           630 CATAAATGG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 sAspAlaGluTyrValAsnValThrAlaGluAspLeuAspGlyHisProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 spTyrProArgLysThrIleThrGlyThrValLeuIleAsnValGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                              region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerValThrSerGluIleLysLeuAlaLysLeuProAspPheGluSerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.....TATGAAATTTTGGATGGTGGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG...CCAGTATGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTT.....GATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AT....AAAACAGTTAGTGCACAG....ATTGAGGTATCTGAA
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                                                                                                                                                                                                                                           from horse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                         063306
                                                                                                                                                                                                                                                                                                                                                                                                                                  829.
                                                                                                                                                                                                                                                                                                                                                                                                               /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 973
                                                                                                                                                                                                                                                                                                                                                                                                               deleted in R20027 and R20028'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
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406	AAATATGCGGATCGATCACAGCTTTTCTATCAATGC	441
9	spileThralaSerGluAspGlyThrValTyrValGlyAspAlaHisT	80 -
. 4	ATTTAA ATTCCCTGAACAACATAACTTACTATTAC	7
476 782	ATGGATGTGCTCTTGATAAAATATTTGCTAAATAATTTGGAATATCCAAC	525 772
	ValMetAsnPheSerSerGlyGluIleIleAspValPhe	G
526	TGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCT	575
758	AspGlnLysProValGlnGlyPhe	751
576	GGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT	625
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626	AACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAA	675
737		734
676	TTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA	725
w	argGluIleLysHisAlaSerPheGlyArgAsnValPheAlaIleS	سر
726	PAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC	775
717	AsnGlyArgIleGlnCysPheLysThrAspThrLysGluPh	701
776		۰
823 700	TTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT ::::::::	864
684	rpGlyGluGluSerSerGluSerAsnProLysProGlyGlnPheArgV	667
865		865
667	erArgIleValGlnPheSerProThrGlyArgPheIleThrGl	652
866	ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC	915
651	Cys	651
916	AGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC	965
650		642
966	GACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG	_
41		ω c
1016	TGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA	1065



78.50 1 78.50

78.50 78.50 114.96 114.71 2 128.39 128.39 96 2.71

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Database length: 13297546
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                                                                       alignment_block:
US-09-323-427-5/rev x US-07-707-367-2
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; MOLECULE TYI
US-07-707-367-2
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; Sequence 2, Application
                                                                                                                                                                alignment_scores:
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/cgn2_6/ptodata/1/iaa/PCTUS9_COMB.pep:PCT-US98-03916-67 - 
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-819-288-3 - 78.5 
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-261-8228-3 - 78.5
                                           Align seg 1/1 to: US-07-707-367-2 from: 1 to: 935
                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
 1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kangawa, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 19910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: C.L. 7 Skyline
                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 10-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                  Quality:
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seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-07-707-367-2
                                                                                                                                                                                                           TELEFAX: (919)541-868
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 141678/90
PRIOR DATE: 01-JUN-1990
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (914)785-7120
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 3 FILING DATE: 30-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                  Villamizar, JoAnn
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                                                                                                                         TYPE: protein
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Nishikawa, Yoshiki
Kawahara, Takashi
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                                                                                                                                                                                                                            (919)541-8689
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                                                                                                                                       CAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT
                                         GCA.....GAACCGGAGAATATCATT...GATGTACGAAC 227
                                                                                           alGluLysGlnThrGlnGluLysGlnGlnLys.....GlnLysAsnSer
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                                                                                                                                                                                                                                                                                 HisArgSerValLysLysAlaGlyIleGluValGluGluIleThrGluTh
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AlaGlyValSerThrGlnGluLysGlnAsnValValGlnGluIleAsnAl
                                                                                                                                                                                     rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV
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seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-070-301-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16,
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                                                                                                                           FILING DATE: 26-MAK-1330
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 2-106412
                                                                                                                                                                                                        APPLICATION NUMBER: JP 1-181933 FILING DATE: 31-OCT-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: JP 1-209687

FILING DATE: 15-AUG-1989

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL THILE OF INVENTION: AMIDATION, AND METHOD OF PREPARING NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     840
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                               ATTORNEY/AGENT INFORMATION:
                                                                                         APPLICATION NUMBER: JP 2 FILING DATE: 24-APR-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 24-MAY-1991
                                                                           APPLICATION NUMBER:
                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C.
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NAME: Player, Willi
REGISTRATION NUMBER:
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OKAMOTO, Hiroshi
KISHIMOTO, Jiro
IFUKU, Ohji
KATO, Ichiro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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TAJIMA, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAMINUMA, Toshihiko
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                     William
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                                                                           JP 2-205475
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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US-09-323-427-5/rev x US-08-070-301-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1015 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                              751
                                                                                                                                                                                                                                                                                                                                                                                   778 AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   679 nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 679
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                                                                                                            631 TCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                                                                                                                                      681 GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 632
                                                                                                                                                                                                                                                 744 laValSerTyrAlaPro.....Gly
                                                                                                                                                                                                                                                                                                731 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            696 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
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                       581 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTA 532
                                                               762 rGly......AspSerThrProValGlnGlyPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                  713 AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl 728
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TELEX: 440706
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TOPOLOGY: li
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                                                                                                                                                         Gly......ValLeuTyrAlaValAsnGlyLysProTyrTy
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43.103
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alignment_block:
US-09-323-427-5 x US-08-477-451-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 8, Application US/08477451
Patent No. 5928865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                745 IleValPheCysArgIlePheGluLeuValTyrArgLeuLeuIleAlaLy 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3200 amino aci
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
774 alAsnPheLeuSerGlnPheLeuIleProLysProTyrLeuThrGluIle
                                       203 CTAATTTCAAGGGTGTTGATATC....AGTTCGTACATCAATGATATT 246
                                                                              761 sLysThrCys......PheSerPheTyrArgLeuIleGluIleV 774
                                                                                                                       153 GCAGAAGTGCACGGTGACGTAAATCAACTGGCAAAGCTTGATTATCATCG
                                                                                                                                                                                                       112 ATTTTGTACTGCAGCAAGTAT.....TACAGGTTGTCCATTATGTT
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TELEPHONE: 510-655-3542
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CITY: Emeryville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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1037 AAATTGATTGTTATTGAAGTTGGTCCACATTCAAT...TTCTGGCTCACC 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      873 uAspValArg......LysValPheArgLysSerCysGlyPheC
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                                                                                                                                                                 CATAAAGACCTTTCACATAAACATGTCCTTCGAATGCATTACGTGTATTA 1036
                                                                                                                                                                                                                                                                           AATTCCGGCAACTTGACGTCCACCTTCATCATTACGGCAACCTTCTTGAT 986
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  ysVal...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAATGGATGAAACGAAATGACAACAGTTGTTACCAAAAATACCACGT
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                                                                                                                                                                                                                                                                                                                                                                                    GGATTCAGAGATCGTGTACGCGCAACATTGCATGAATCAAATGGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                          ....TyrLeuLeuIleAspAspHis.....IlePheAsnGlyIleP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....GATTTCAGATACCTCAATCTGTGCACTAACTGTTTTATCAGC
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                                                                                                                                                                                                                     .....LeuIlePheAlaIlePheGluPh
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...PheAsnPheAsnProPheTrpIle...
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                                                                                                              ..SerCysIleL
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alignment_block:
US-09-323-427-5/rev x US-07-906-349A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-07-906-349A-6
                                                                                                                                                                                                  Align seg 1/1 to: US-07-906-349A-6
                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020 uAlaGlu 1022
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                                                                                                                  573 ThrThrAlaAlaThrCysAlaCysThrGlyCysThrGlyCysThrCy
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC COMPUTER: POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/906,349A
FILING DATE: 30-JUN-1992
                                                                                                                                                          346 ACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 18-JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
AATATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGA 197
                                                                             CTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAG
                                   sCysThrCysThrThrThrCysCysCysThrCysCysThrThr....
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                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                       Ratio:
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801 amino acids
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A NOVEL EXPRESSION-CLONING METHOD FOR IDENTIFYING TARGET PROTEINS FOR EUKAR
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                                                                                                                                                                                                                                                                                                  Percent Identity: 28.571
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                                                                                                                                                                                                    to:
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                                                                               247
                                                                                                                    589
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; NAME/KEY:
; NAME/KEY:
US-08-415-751-35
                                    alignment_scores:
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                                                                                                                                                                                                                                                                      TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GUT, JIRI
TITLE OF INVENTION:
                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1,193
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hana Dolezalova REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/415,751 FILING DATE: 03-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: Wordperfact
                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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Quality:
Ratio:
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: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEECH, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PETERSEN, CAROLYN
                                                                                                                                                                 Cryptosporidium parvum
                                                                                                            Positions coded by nonsense codons identified as Xaa.
                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                          (415) 324-1677
                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette - 3.5 inch, 1.44 Kb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLYPEPTIDES BINDING ANTI-
                                                                                                                                                                                                                                                                                                                                                                                                             30,518
                                                                                                                                                                                                                                                                                                                                                                                           480.19-2 (HHD)
Length:
Gaps:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/08325071 Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                             APPLICANT: RIDING, G
APPLICANT: RAND, Kei
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 n 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 uCysCysCysGlyCysCysSerLysIleTrpAspAsnCysCysCysSerL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 .....TyrGly......CysCysCysCysCys***LeuTrpTyrAs 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 GCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACA.... 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 GTTTACTCAAGAAAAGAT.....CTGCAGAACCGGAGAATATCATTGAT 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 AATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                               COUNTRY:
                                                                                                                  STREET: 3000 K St. CITY: Washington,
                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....LeuValGlu*****LeuGlnLeuArgLeuValValLeuLeu* 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yMetArgAsn***ProHisArgGluLeuLeuHisGlüLeuValValLysG
                                                                               20007-5109
                                                                                                                          E: Foley & Lardner 3000 K Street, N.W. ashington, D.C.
                                                                                                                                                                                                                                                                                              RIDING, George Alfred RAND, Keith No. 5587311man
                                                                                                                                                                                                                                                                                                                                              KEMP, David Harold
SRISKANTHA, Alagacone
                                                                                                                                                                                                                                                                                                                                                                                               WILLADSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                        JOHNSON, Law Anthony York
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                                                                                                                                                                                                                           DNA Encoding A Cell Membrane Glycoprotein Of A Tick Gut 71
                                                                                                                                                                                                                                                                                                                                                                                                    Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 25.828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
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alignment_block:
US-09-323-427-5/rev x US-08-325-071-67
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-325-071-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-325-071-67 from: 1
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APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephan a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA: 05-08/062,109
FILING DATE: 17-WAX-1993
PRIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-WAX-1993
PRIOR APPLICATION DATA: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: 07/242,196
FILING DATE: 06-UUL-1988
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/AU87/00401
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-WOV-1987
PRIOR APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION NATA: APPLICATION DATA: 
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INFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1024 TGCATTCGAAGGACATGT.....TTATG 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
TOPOLOGY: linear
200 yProAspGlyGlnCysLysAsnAlaCysArgThrLysGluAlaGlyPheV 217
                                                                                                                                                                              187 ProProAlaAspSer..
                                                                                                                                                                                                                                                                 901 ACGATCTCTGAATCCACGTGGTATTTTTGTAAC.........
                                                                                                                                                                                                                                                                                                                                                    173 rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                951 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 sGluLysAsnLeuLeuGlnArgAsp......SerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFORMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI2570
FILING DATE: 19-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.00
0.612
40.947
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Percent Identity: 21.727
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671 283 621 290 571 303 303 350 484 484 484 484 484 484 484 484 484 48	51 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
712 266	758 AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG :: :: ::	
233 759 250	849 TTTCATCCATTACTTTCTACCAAAGTTCATCGCATATCGAGTACAATGG	

seq_documentation_block:
; Sequence 61, Application US/08325071
; Patent No. 5587311

seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-61

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alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                                                                                                             LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-325-071-61
                                        alignment_block:
US-09-323-427-5/rev x US-08-325-071-61
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/AU87/00401
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION NUMBER: AU PI2570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/111
TELECOMMUNICATION:
TELEPHONE: 202 672 5300
TELEPKX: 202 672 5399
TELEX: 904136
INFORMATION: CHARACTERISTICS:
Align seg 1/1 to: US-08-325-071-61 from: 1 to: 549
                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
DEFICE DATE: 06-JUL-1988
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APPLICANT: COBON,
APPLICANT: MOORE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3000 A C. CITY: Washington, D.C.
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MOORE, Joanna Terry
JOHNSON, Law Anthony York
                                                                                                              89.00
0.614
40.390
                                                                                                            Length: 359
Gaps: 22
Percent Identity: 22.284
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1024	TCCATTCGAAGGACATGTTTATG	1002
1001	TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGAAGGTGGAACGT	
82	::::: ::: ::: 	92
951	CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGGTAC	902
. 92	rgCysCysGlnGlyTrpAsnThrAlaAsnCysSerAlaAla	105
901	ACGATCTCTGAATCCACGTGGTATTTTTGTAACAAC	866
106	ProProAlaAspSerTyrCysSerProGlySerProLysGl	119
865	AACTGTTGTCATTTCG	850
119	yProAspGlyGlnCysIleAsnAlaCysLysMetLysGluAlaGlyPheV	136
849	TTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATG	800
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799	CTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG	759
152	sProArgGlyPheThrValAlaGluAspGlyIleThrCysLysSerIleS	169
	AGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATG	712
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7	TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA	
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620	CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC	571
209	hrCysIleSerAspCysValAspLysLysCysHisGluGlu	222
570	TTTGTCGATGATGGT	556
223	PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr	239
555	AACGGTGATACTGTGGAAATTCTAAATGCTGATGGAT	519
239	pLysSerArgLysProGlyProAsnValAsnIleAsnGlyC	253
518	GTGCTCTTGATAAATATTTGCTAAATAATTTGGAA	00
483 270	TATCCAACAGATTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC :: :: :: PhaAspSerAsp	434 279
433	GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG	384
279	uAspArgValLeuGluAlaIleArgThrSerIleGlyLysGluV	294
383	AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC	334
294	alPheLysValGluIleLeuAsnCysThrGlnAsp	305
. ω . ω	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA ::: :::	8
306	IleLvsAlaArgLeuIleAlaGluLvsProLeuSerAsnHisVa	320

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AGG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AGG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AGG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
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Patent No.
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                                                                                APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrar
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: WE COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/242,196 FILING DATE: 06-JUL-1988
                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: AU PI4912 FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/AU87/00401 FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: AU PI2570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yGlnAsnLysCysValLysValAsp 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etTyrProLysLeuIeuIleLysLysAsnSerAlaThrGluIleGluGlu 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-325-071-63
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5587311 ·
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SRISKANTHA, Alagacone
RIDING, George Alfred
RAND, Keith No. 558731lman
RAND, Keith No. 558731lman
Company of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOORE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOHNSON, Law Anthony York
                                                                                                                                                                                                                                                                                                                                                          19-JUN-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart Gary
                                            60042/111 BIAU
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alignment_block:
US-09-323-427-5/rev x US-08-325-071-63
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    Quality:
    Ratio:
Percent Similarity:
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy 163
320 pLysSerArgLysProGlyProAsnVal....AsnIleAsnGlyC 334
                                                                                                                                                                                                                                                     620 CATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGC 571
                                                                                                                                                                                                                                                                                                                                                       670 TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 621
                                                                                                                                                                                                                                                                                                                                                                                                      267 GluAspCysArgValHisLysGlyThrValLeuCysGluCysProTrpAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    711 CCAGTATGCCGTTATGAA.....ATTTTGGATGGTGGACCAACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 sProArgGlyPheThrValAlaGluAspGlyIleThrCysLysSerIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 rgCysCysGlnGlyTrpAsnThr.....AlaAsnCysSerAlaAla 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 sGluLysAsnLeuLeuGlnArgAsp......SerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 erHisThrValSerCysThrAlaGluGlnLysGlnThrCysArgProThr 266
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TYPE: amino acid
TOPOLOGY: linear
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                                              .....AACGGTGATACTGTGGAAATTCTAAATGCTGATGGAT 519
                                                                                                  PheMetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 320
                                                                                                                                                   TTTGTCGATGATGGT.....
                                                                                                                                                                                                    hrCysIleSerAspCysValAspLysLysCys......HisGluGlu
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202 672 5399
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORM
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,332
FILING DATE: 25-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19076CA
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DN:
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICANT: RAMBOSEK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: REEVES, CHRISTOPHER D. APPLICANT: DAVIS, CHARLES R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 uAspArg.....ValLeuGluAlaIleArgThrSerIleGlyLysGluV 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 ysLeuLeuAsnGluTyrTyrThrValSerPheThrProAsnIleSer
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CITY: F
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: CHRISTINE E. CANAL
STREET: 126 E. LINCOLN AVENUE, P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alPheLysValGluIleLeu.....AsnCysThrGlnAsp......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etTyrProLysLeuLeuIleLysLysAsnSerAlaThrGluIleGluGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HENDRICKSON, LEE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VINCI, VICTOR A.
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                                                                                                                                                                                   Version
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alignment_block:
US-09-323-427-5/rev x US-08-450-332-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3038 amino aci
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                                                                                                                                                                                                                   1313 Ile.....ArgSerPheLeuSerGlnLeuThrLeuGluGluArgGl 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1263 ProProAspAlaSerThrAspHisAlaMetPheAlaArgTrpSerTrpGl 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1279 yProLeuThrProAspSerLeuLeuAspAsnProGluTyrTrpAlaThrA 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  921 TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTT..
                                                        701 GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT 652
                                                                                                                                                                                                                                                                         792 ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 743
                                                                                                                                                                                                                                                                                                                                                                              827 AAGTTGATCGT......GCATATCGAGTACAATGCTTTTAC 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                AACTGCT.....TTTCAAACTCAAATTGTCCCGATGCCAGTATGCC
.....GlnValLeuAlaSerAlaLysGluGlyArg......
                                                                                                           nGlnAlaAlaPheHisLeuGlnLysGlnIleGluTrpLeuGlu.....
                                                                                                                                                                                                                                                                                                                           laGlnAspLysGluAlaIleProIleIleGluArgIleValTyrPheTyr 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....GTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTT...CCATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3038 amino acids
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908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.481 \\ 38.347
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Percent Identity: 19.703
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                                                                                                                                                                702
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seq_documentation_block:
                                                                                                                                 seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-637-640-2
Sequence 2, Application US/08637640 Patent No. 5849541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1542
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1575 gCysThrGluProPhe 1580
                                                                                                                                                                                                                                                                                                                                   1559 PheIlePheGlyLeuPheAlaAspTrpTrpAlaGlyValAspAspGlyAr 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1496 euAspIleArgArgSerProAlaGluGlnGlyPheGluPro...HisAla 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1479 nAlaArgGluGlnPheAlaProPheGluAspArgMetValPheGluProL 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1463 GlyPheAsnSerTyrThrTyrThrAspIleSerThrGlyPhePheGluGl 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1442 IleLeuGluIle..... 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1426 laArgGluLeuValAla...GlnIleAlaHisArgTyrGlnSerMetAsp 1441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1394 ArgSerAsnGlyAsnProPheAspLeuLeuAspHisAspGly...LeuLe 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1377 roHisValArgLeuValGlnArgValGlyGlnHisLeuLeuProThrVal 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1360 nAspThrGluAlaGlnIleGluHisLeuCysThrAlaAsnSerTyrHisP 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 CTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 AAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 CGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 CAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGAT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 TGATAAATATTTGCTAAATAAT................TTGGAATATC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT..... 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT 602
                                                                                                                                                                                                                                                                  CTGCATGTCACCATTT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAACCTGTAATACTT......127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrAspLeuIleIleAlaSerAsnValLeuHisAlaThrProAsp..... 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \dotsLeuGluLysThrMetAlaHisAlaArgSerLeuLeuLysProGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTTTGCCAGTTGATTTACGTCAC...CGTGCACTTCTGCAACATAATG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....ThrGlyGlyAlaThrLysTyrValLeuAlaThrProGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                         .....GCTGCAGTACAAAATGGAAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......CGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATC
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alignment_block:
US-09-323-427-5/rev x US-08-637-640-2
                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM:
US-08-637-640-2
                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-637-640-2 from: 1 to: 3038
                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VINCI, VICTOR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 1907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 908-594-4720 INFORMATION FOR SEQ ID NO:
                                                 1200 isValAspArgIleThrLeuValProSerLeuCysLeuAlaThrAlaGlu 1216
                                                                                                                                              1096 CAATGGTGTCGAAGGTGAGCCAGAAATTGAATGT.....GGACCAACTT 1053
                                                                                                                                                                                              1175 ValAlaPheGlnThrValIleGlyAla.....TyrSerSerPro..... 1187
                                                                                                                                                                                                                                 1146 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGA 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3038 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: REEVES, CHRISTOPHER D. APPLICANT: DAVIS, CHARLES R. APPLICANT: HENDRICKSON, LEE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 07065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
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                  .....ACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 1010
                                                                                                                    .....GlyAspArgArgLeuArgCysLeuTyrValProThrH 1200
                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3038 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPKS Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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38.347
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2:
                                                                                                                                                                                                                                                                                                                                                  Length: 472
Gaps: 24
Percent Identity: 19.703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
#1.25
                                                                                       1048
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1479	lyPheAsnSerTyrThrTyrThrAspIleSerThrGlyPhePheGluGl	1463
280		280
280 1462	IGCTGCAGCTGCGCAACTT ::: LeuAlaThrProGlnLeu	329 1449
4		-4-
330	GTTCGACCACAATGTTCAGAACCACAAGGATTCGGAG	379
1445		1442
380	AGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACC	429
430 1441	TATGCGGAT SerMetAsp	479 1426
480 1426	CTAAATAATTTGGAATATC ::: ::: hasnThrLeuSerPheGlyProAlaLeuHisTyrA	511 1409
512 1409	ACTGTGGAAATTCTAAATGCTGATGGATGTGCTCT ::::: ::: ProPheAspLeuLeuAspHisAspGlyLeuLe	558 1394
1393	uValGlnArgValGlyGlnHisLeuLeuProThrVal	1377
559		559
559 1377	TTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT ::	601 1360
1360	ALIGNICANGLIIRICATAAATGGACATGCGATTCTGAAACCGF 	
- ω	.GlnValLeualaSerAlaLysGluGlyArg	1341
52	TTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT	. 0
702 1340	.TTTCAAACTCAAATTGTCCCGATGCCAGTATGCC ::: ::: sLeuGlnLysGlnIleGluTrpLeuGlu	742 1326
743 1326	GATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC :::::: ::: ::: ArgSerPheLeuSerGlnLeuThrLeuGluGluArgGl	792 1313
793 1312	GCATATCGAGTACAATGCTTTTAC :: ::	827 1296
828 1296	ACTGTTGTCATTTCGTTTCATCATTATTTGTTACCA ::::::: :::::::::::::::::::::::::	7
874 1279	ATGCAATGTTGCGCGTACACGAGTCTCTGAATCCACGTGGTATTTTT : : : : : : : : :	921 1263
922 1262	GTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT ::: ::::: ::: hrLeupheGinValGluAsnileThrPheLysPropheSer	968 1247
969 1246	CTTTATGATCAAGAAGGTTGCCGTA :::::: leValValPheAspAlaGlu	ω
N N	SerGlyCySGluLySvalAlaPheAsnThrIleAsnThrTyrAspLySGl	1009

); 12:	
. 0	TELEFAX: 617-861-9540
240	TELEPHONE: 617-861-6240
SER: WHI94-03A2	BER:
227	ER: 32,2
TON:	; ATTORNEY/AGENT INFORMATION:
1994	FILING DATE: 25-MAR-1994
US 08/218, 265	us o
1995	FILING DATE: 21-AUG-1995
IIS 08/521	08
۲	CLASSIFICATION: 424
US/08/540,804	CATION NUMBER: US/08
6	CURRENT APPLICATION DATA:
/MS-DOS	SYSTEM:
disk patible	; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatib
:	ADABLE FORM
	; COUNTRY: USA ; ZIP: 02173
	TATE:
Drive	wo Militia D
Brook, Smith & Reynolds, P.C.	amilton,
.9	NUMBER OF SEQUENCES: 39
Canscription and Methods of Use Therefor	Tran
M. SOLOSSES TACTOR Which Wollies Con	o, David M
raig	ICANT: Thompson, Craig
+ O:	Richard A
	GENERAL INFOR
JS/08540804	ocumentation_block: uence 12, Application US/085
/iaa/5B_COMB.pep:US-08-540-804-12	<pre>seq_name: /cgn2_6/ptodata/1/iaa/5</pre>
	158
	. 106 CTGCATGTCACCATTT 91
laAspTrpTrpAlaGlyValAspAsp	aAs
GCTGCAGTACAAAATGGAAT 107	:
LuIleThrHisLysGluHisThrArgLeuGly 1558	yGlnMetValIleLeuGluIl
	:
AlaArgSe	P
CGTGCACTTCTGCAACATAA	CCAGTTGATTTACGTCA
	1512 TyrAspLeuIleIleAlaSerAsn
ATTAG	TACGAACTGAT
COAlaGluGlnGlyPheGluProHisAla 1511	1496 euAspIleArgArgSerProAlaG
AAAAGATCTGCAGAACCGC	TTTACTO
aProPheGluAspArgMetValPheGluProL 1496	1479 nAlaArgGluGlnPheAlaProPh
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-540-804-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-323-427-5/rev x US-08-540-804-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1048 AACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1098 GACAATGGTGTCGAAGGTGAGCCAGAATTGAATGTGGACCAACTTCAAT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1148 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT 1099 :::::: ||||::: ||||||::: |||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445
560 eIleTyrLysLysValLeuLysGluLysAspValProAlaTyrAsnValT 577
                                                                                                           545
                                                                                                                                           641 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA.. 597
                                                                                                                                                                                                                   528 luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe 544
                                                                                                                                                                                                                                                                                                                               511 ePheLysTrpIleGluPheIleValTyrHisGlnLeuLeuSerAspIleG 528
                                                                                                                                                                                                                                                                                                                                                                                            708
                                                                                                                                                                                                                                                                                                                                                                                                                                                      495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              752 CTGAAATCACAACTGCTTTTC.....AAACTCAAATTGTCCCGATGCCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784 TG.....ATAAAACAGTTAGTGCACAGATTGAGGTAT 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 834 GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 yrAspValLysPheTyrGluIlePheAsnPheAspGlnLeuValGluIle 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 ACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTG..... 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 ValGlnLeuLeuIleAsnLeuLysIleSerProLeuMetLys..... 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     998 AAGGTCTTTATGATCAAG...AAGGTTGCCGTAATGATGAAGGTGGACGT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 ...SerSerGlyLeuLeuTyrLeuGlnAspSerAsnAspLysPheValHis 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 eIleLysValProThrTyrIleArgLysLeuIle........... 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 MetMetProSerLeuTyrArgLeuLeuAsnIleLeuIleThrTyrGlyIl 374
                                                                                                  ATTTGCTA.....TCATTGGTC 642
                                                                                                                                                                                                                                                                                                                                                                                            GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euSerHisLeuCysSerGlyIleLeuSerSerValAsnArgThrValLeu 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrGluGlnIleLysMetArgIleLeuSerAsnAspIleThrAsnLeuGl 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....TTGTCATTTCGTTTCATCCATTATTT 835
                                                 .........SerGlnTyrAsnMetValLeuArgAsnValMetGluT 428
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0.457
47.949
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Gaps: 13
Percent Identity: 19.744
                                                                                                           560
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	REFERENC TELECOMMUN	
	REGISTRATION NUMBER: 32,227	
	ATTORNEY/AGENT IN	
	FILING DATE: 25-	
	CURRENT APPLICATION DATA:	
	COMPUTER: IBM PC compatible	
	COMPUTER READABLE I	
	ZIP: 0217:	
	; STATE: MA	
	CITY: Lexington	
:'	ADDRESSEE: Hamilton,	
	NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:	
e Th	TITLE OF INVENTION: Transcription and Methods of Us	
ifv Gen	APPLICANT: Thompson, Craig M. TITLE OF INVENTION: No. 5922585el Factors Which Mod	
	APPL:	
	GENERAL INFORMATION:	
	ence	
5-12	seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-218-265	
	lelleArgLe	
	205 TAGCGATGATAATCAAGCTT 186	
LyL 727	710 uIleSerLeuLysLeuLeuThrPheGluValThrGlnAsnValLeuGl	
AAAT 206	ACGAACTGATATCAACACCCTTG	
Le 710	heThrAsnLysAsnLeuIleGln	
243	ACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATA	
1et 693	${\tt nValMetLeuLeuIleAlaThrAsnLeuLysGluTyrIleLysPh}$	
CGC 285	GGTGCCGCAGCAAAACCTGCTGCAGCTGC	
snA 677	lnLysAlaArgAs	
ATT 335	GAACCACAAGGA	
1Se 660	eProGluValPheGlnValAsnIleArgPheLeuLeuHisAsn	
351	NGCGAATGTGTTCGACCACAAT	
rp 643	SValTyrSerMetIleAsnAsnSerAsnGlnAlaValGlyGlnThrT	
378	CCAGATCAGTATTACCATTAAAGAACCAA	
eul 627	610 pGluLysLeuLysThrGluLysLeuLysAsnAspLysSerGluValLe	
3GC 460 AS 610	509 ATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAAATGGCTG :::::::::::::::::::::::::::::::::	
Val 593	577 hrSerPheMetProPheTrpLysPhePheMetLysAsnPheProPheV	
, <u>v</u>	59 TGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATG	

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alignment_scores:
Quality:
Ratio:
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-218-265-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-218-265-12 from: 1 to: 1226
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TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1098 GACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAAT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1148 TTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1048 AACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGA 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 ... SerSerGlyLeuLeuTyrLeuGlnAspSerAsnAspLysPheValHis 401
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                             641 AGCCAGTTTATCATAAATGGACATGCGATTCTG...AAACCGTTGATA.. 597
                                                                                                                                                                                                                         511 ePheLysTrpIleGluPheIleValTyrHisGlnLeuLeuSerAspIleG
                                                                                                                                                                                                                                                                                                                                         495 LeuLysIlePheLysIlePheCysIleAspLeuGluValPheHisHisPh 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998 AAGGTCTTTATGATCAAG...AAGGTTGCCGTAATGATGAAGGTGGACGT 952
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        545
                                                                                                               528 luSerLeuGluAlaLeuMetAspIleLeuLeuCysTyrGlnLysLeuPhe
                                                                                                                                                                                                                                                                              708 GTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCA 659
                                                                                                                                                                                                                                                                                                                                                                                           752 CTGAAATCACAACTGCTTTTC.....AAACTCAAATTGTCCCGATGCCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              784 TG.....ATAAAACAGTTAGTGCACAGATTGAGGTAT 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 nLeuSerLysThrProLeuSerIleLysIleMetValAlaGluTrpTyrL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           834 GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 ThrGluGlnIleLysMetArgIleLeuSerAsnAspIleThrAsnLeuGl 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 yrAspValLysPheTyrGluIlePheAsnPheAspGlnLeuValGluIle 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 ACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTG...... 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 CAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC 902
                                                                                                                                                               ATTTGCTA.....TCATTGGTC 642
SerGlnPhe...IleAsnAspHisIleLeuPheThrLysThrPheIlePh 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                            euSerHisLeuCysSerGlyIleLeuSerSerValAsnArgThrValLeu 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....TTGTCATTTCGTTTCATCCATTATTT
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0.457
47.949
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Gaps: 13
Percent Identity: 19.744
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	APPLICATION NUMBER: US/08/480,604A FILING DATE: 07-JUN-1995	·· ··
	ICATION DATA:	
	SYSTEM: PC-DOS/MS-DOS	. ~.
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	·· ··
	Ď.	٠. ٠.
	·	· · · ·
	NIGOMEKI SIKEET,	
	RESSEE: MEDLEN & CARROLL, LLP	٠.
	SEQUENCES: 32 DENCE ADDRESS:	~. ~.
5	OF INVENTION:	٠. ٠
e P	N: VACCINE AND ANTITOXIN FOR TREATME	
	ANT: FIRCA,	·· ··
	ANT: THALLEY, BRUCE	٠. ٠
	atent No. 5736139 GENERAL INFORMATION:	
	documentation_ quence 6, Appl	~ · · · · · · · · · · · · · · · · · · ·
	eq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-480-604A-6	Ç0
	7 euGluTyrIleIleArgLeu 73	
t		
727	0 uIleSerLeuLvsLeuLeuThrPheGluValThrGlnAsnValLeuGlvL	
206	TACGAACTGATATCAACACCCTTGAAAT	
710	94 SerIlePheLeuLysArgLysAspPheThrAsnLysAsnLeuIleGlnLe	
_	A CALCULATOR A DE VOLTA DE VERTE E E E E DE CALCULA DE LA	
9	77 snValMetLeuIleAlaThrAsnLeuLysGluTyrIleLysPheMet	
	34 CGGAGCTGTTAAAAAAAAACAGCTGGTGCCGCAAAAACCTGCTGCTAGCTGCCGC	
7	:::: ::::::: 	
335	CACAAGGATT	
660	::: ::: GlnValAsnIleArgPheLeuLeuHisAsnSe	
351	AGCGAATGTGTTCGACCACAATGTT	
643	627 ysValTyrSerMetIleAsnAsnSerAsnGlnAlaValGlyGlnThrTrp	
378	GCCAGATCAGTATTACCATTAAAGAACCAA	
627	::: :::: LysAsnAspLysSerGluValLeuL	
410	AGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCA	
610	594 LeuLysValAspAsnAspLeuArgIleGluLeuGlnSerValTyrAsnAs	
460	AAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTGGC	
593	:::::: :::::::::::::::::::::::::::::::	
510	TGTGGAAATTCTAAATGCTGATGGATGTGCTCTTG	
577		
560	CCTGCTTTGTCGATGA	

CLASSIFICATION:

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alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: US-08-480-604A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 397-83:
INFORMATION FOR SEQ ID NO:
  264 uAlaAlaAlaSerAspIleVal.
                                     333 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 284
                                                                                                                     383 AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC
                                                                                                                                                             232
                                                                                                                                                                                                  433 GGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAG 384
                                                                                                                                                                                                                                           230
                                                                                                                                                                                                                                                                                   483 TATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGC 434
                                                                                                                                                                                                                                                                                                                      533 TAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAA 484
                                                                                                                                                                                                                                                                                                                                                                                                    204 eIleLysSerHisLeuValSerGlu.....T
                                                                                                                                                                                                                                                                                                                                                                                                                                            583 TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 TyrTyrLysSerGlnIleAsnLysProThrValProThrIleAspAspIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 02-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/422,711
                                                                              GlnGluLeuLeuAsnIleTyrSerGlnGluLeuLeuAsnArgGlyAsnLe
                                                                                                                                                           snSerAsnHisGlyIleAspIleArgAlaAsnSerLeuPhe...ThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGOLIA, DIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: US-08-480-604A-6 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2710 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER: US 08/161,907
02-DEC-1993
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0.825
52.551
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Percent Identity: 22.449
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....ArgLeuLeuAlaLeuLysA 278
                                                                                                                                                                                                                                           .....Lys.IleA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2710
                                                                                264
                                                                                                                       334
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; MOLECULE TYPE: US-08-405-496A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-405-496A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08405496A Patent No. 5919665
                                                                                                                           TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino aci
                                                                                                                                                                                                                                                                         FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/329,154 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311
                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 PheLysLeuIleIleGluSerLysSerGluLysSer 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 16-MAR CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 01 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                          TOPOLOGY:
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/429,791
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                                                         amino acid
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                                                                                 2710 amino acids
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16-MAR-1995
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                                                                                                                                                                                                                                 40,027
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seq_documentation_block:
    Sequence 65, Application US/08325071
    Patent No. 5587311
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Quality:
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US-09-323-427-5/rev x US-08-405-496A-6
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                                                                                                                                                               Patent No. 5587311
GENERAL INFORMATION:
                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 pGluMetIleLysLeuGluAlaIleMetLysTyrLysLysTyrIleAsnA
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                                             APPLICANT:
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                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 TGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTC 534
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt snPheGlyGlyValTyrLeuAspValAspMetLeuProGlyIleHisSer}
                                                                                                                                                                                                                                                                                                                                                                                                                                          ..TACGTCACCGTGCACTTC.....TGCAACATAATGGACAAC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....TTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATT.... 174
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                                                                                                                          MOORE, Joanna Terry
KEMP, David Harold
SRISKANTHA, Alagacone
RIDING, George Alfred
RAND, Keith No. 558731
                                                                              WILLADSEN, Peter
                                                                                                    JOHNSON, Law Anthony York
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0.825
52.551
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Gaps: 9
Percent Identity: 22.449
    5587311man
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alignment_block:
US-09-323-427-5/rev x US-08-325-071-65
                                                                                                                                                                                                                                                                       alignment_scores:
Quality:
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                                                                                                                                             Align seg 1/1 to: US-08-325-071-65
                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                   1024 TGCATTCGAAGGACATGT.....TTATG 1002
                                   1001 TGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGT 952
                                                                   117 CysValProThrThrCysLeuArgProAspLeuThrCysLysAspLeuCy
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
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FILING DATE: 06-UUL-1988
PRIOR APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
 133 sGluLysAsnLeuLeuGlnArgAsp...
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-OCT-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-NOV-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DN
TITLE OF INVENTION: G1
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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TELEFAX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: AU PFILING DATE: 19-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0' FILING DATE: 07-AUG-1992
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16-OCT-1987
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14-OCT-1993
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40.669
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250	GAACCG	276
388	_	371
277	Þ	283
7	::: ::: 	UI (
80	GGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCA	333
334	AACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTC 3 :: ::::: :: ::: ::: ::: ::::::	383
345		
884	G	133
330	ء س	321
320	ysLeuLeuAsnGluTyrTyrTyrThrValSerPheThrProAsnIleSer 3	304
184	GTGCTCTTGATAAATATTTGCTAAATAATTTGGAA 4	518
304	PLYSSerArgLysProGlyProAsnValASnIleAsnGluc 3	290
068	MetAspCysGlyValTyrMetAsnArgGlnSerCysTyrCysProTr 2	274
556	TTTGTCGATGATGGT5	570
273	::: SCysIleSerAspCysValAspLys	260
71	GATTCTGAAACCGTTGATACI	520
21	TCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGA 6 : ::::: ::: :::::: ::: ::::: ::::::	570 253
53	pCysArgValGlnLysGlyTh	237
671	CAGTATGCCGTTATGAA	111
36	::: ThrValSerCysThrValGlu	220
12	GGTATCTGAAATCACAACTGCTTTT	58
59	TTTTACATGGAAG ::: erGlySerThrValAlaG	799 203
203	ATCCATTATTTGTTACCAAAGT ::: ::::: SLysHisGlyCys.ArgSerTh	.87
	PIOASPGIYGINCYSHYSASHAIGC	
50	AACAACTGTT	896
70	Ту	57
69	TGGTATTT	10
56	 ysLeuAlaAla 1	43
02	CTTCCATTTGATTCATGCAATGTTGCGCGTAC 9	51

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Search information block:
Query: US-09-323-427-5
Query length: 1161
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pir2:I57940
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pir2:A41519
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pir2:S27799
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       Documentation
                            calsequestrin precursor, cardia hypothetical protein F46Gll.2 - NADH dehydrogenase (ubiquinone)
                                                                                                                                                                                                   probable reverse transcriptase
T16G12 1 protein - Caenorhabdii
DNA-directed RNA polymerase (
                                                                                                                                                                                                                                                                                                                                                                                                         peptidylglycine monooxygenase (
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c-kit-related kinase 1 (XKrk1)
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pir2:A19079
pir2:S61668
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                                                                         TTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCA 641
                            LeuAspGlyGlyProSerGlyGlnProIleGlnPheAlaThrIleGlyGl
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R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P. Dev. Biol. 146, 519-530, 1991
A;Title: cut-1 a Caenorhabditis elegans gene coding A;Reference number: A49772; MUID:91323673
A;Accession: A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
cuticle protein cut-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C;Accession: A49772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-323-427-5/rev x A49772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: A49772 from: 1
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                                                                                                                                                                                              840 TTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACAT
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seq_documentation_block:
    cuticlin 1 - Caenorhabditis elegans (fragment)
    C;Species: Caenorhabditis elegans
    C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
    C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
    C;Accession: S27799
    R;Sebastiano, M; Lassandro, F; Bazzicalupo, P.
    submitted to the EMBL Data Library, July 1991
    A;Description: CUT-1 a Caenorhabditis elegans gene
    A;Reference number: S27799
    A;Accession: S27799
    A;Molecule type: DNA
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A;Cross-references: EMBL:M55997; NID:g156271; PID:g156272
C;Genetics:
A;Gene: CUT-1
A;Introns: 245/3
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alignment_scores:
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N;Alternate names: peptidylhydroxyglycine N-C lyase
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: S17855
R;IWasaki, Y; Kawahara, T.; Shimoi, H.; Suzuki, K.; Ghisalba, O.; Kangawa, K.; Matsuo,
Eur. J. Biochem. 201, 551-559, 1991
A;Title: Purification and cDNA cloning of Xenopus laevis skin peptidylhydroxyglycine N-C
A;Accession: S17855; MUID:92037609
A;Accession: S17855; MUID:92037609
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molacylla truce. mana
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A;Molecule type: mrNA
A;Residues: 1-935 <IMA>
A;Residues: 1-935 <IMA>
A;Cross-references: EXMAL:X62771; NID:g64530; PIDN:CAA44615.1; PID:g64531
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: oxidoreductase
F;131-342/Domain: peptidylglycine monooxygenase I homology <PGM>
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US-09-323-427-5/rev x S17855
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                                                                                                           563 nTrpGlyGluGluThrSerSerAsnValProArgProGlyGlnPheArgI 580
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                                                                                                                                                                                                                                                                                                                                       Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl 563
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Gaps: 18
Percent Identity: 19.437
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	38 TIACCATITCGTITAAATITCGT 16	
840	823 lSerPheValLeuIleIleThrLeuLeuIleTleProIleAlaValLeuI	
823		
	85 TGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAACC 90 lyValSerThrGlnGluLysGlnSerValValGlnGluSerSerAlaGl	
186 790	: TGATATCAACACCCTTGAA : ::: : aGlyValProThrGlnGluLysGln	
227 773	CCGGAGAATATC ::: ::: LysGlnAsnVal	
259 756	8 CAGCAAAACCTGCTGCAGCTGCGCAACTTC : ::	
309 742	358 ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCG ::: ::: ::: ::: 725 rGluIlePheGluThrHisIleArgSerArgProLysThrAsnGluSerV	
359 725	6ATTACCATTAAAGAACCAAAT ;::::: ::: 9 HisArgSerValLysLysAlaGlyII	
397 708	ATGCGGATCGATCACAGCTTTTCTATC :::::::: : lyAspAlaHisAlaAsnAlaValTrpL	
438 692	GGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA::::	
488 675	AATGCTGATGGATGTGCTCTTGATAAATATTTGCT	
532 663	1 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTC : : : : : : : : : :	
582 652	1 TCATAAATGGACATGCGATTC	
632 646	TTGCTATCATTGGTC :: ::: : yralavalasnGlyL	
682 634	731 AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT :::::::::::::::::::	
732 628	778 AACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTC : ::: ::: ::: :	
779 612	. 5	
596	580 leProHisSerLeuThrMetValProAspGlnGlyGlnLeuCysValAla	

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C;Accession: A40970
R;Just, M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripier, D.; Stein, H.; Schuppan, D.
J. Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular management of the fibronectin type in the fibronect
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366
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                                                                                  722 TTGTCCCGATG......CCAGTATGCCGTTATGAAATTTTGGATGGT 682
                                                                                                                                                                        389 uTleAsnGluValGluValAspProIleThrThrPheProLeuLysGlyL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 uThrHisThrAspIleGluLeuSerGlyLeuLeuProAsnThr......
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                                                                                                                                                                                                                               TAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAA 723
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euThrProLeuThrGluTyrThrIleAlaIlePheSerIleTyrAspGlu 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTT 823
                                                                                                                                                                                                                                                                                                                                                      IleAsnGlyTyrArgIle.....ValTyrAsnAsnAlaAspGlyThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....ThrSerArgGln
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0.578
53.086
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Gaps: 19
Percent Identity: 22.222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     847
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681 423	GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCC 638
637 438	AGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCG 588 :::
587 455	CGGTTGTCCATTCCTGCTTTGTCGATGATGGT
555 472	AACGGTGATACTGTGGAAAATTCTAAATGCTGATGGATG 518 :::
517 487	TGCTCTTGATAAATATTTGCTAAATAATTTGGAATATC 480 : : : : : : : : : : : : :
479 503	CAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATAC 442 ::::: :::
441 519	AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGAT 401 : :::
400 536	CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTT 351 ::::::: hrIleValProThrThrSerValThrSerValPheGlnThrGlyIle 551
350 552	CAGAACCACAAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAGCAAAA 301 :::
300 560	CCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGA 254 : ::: ::::! ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
253 577	ACCGGAGAATATCATTGATG 234 :: :::::: InPheArgValThrTyrMet 583
m m	: pir2:T03099
seq_docu mucin, s N;Altern C;Specie C;Date: C;Access R;Eckhar J. Biol	999 #text_change 20-Sep-1999
A;Title: A;Refere A;Access A;Status A;Molecu	The complete cDNA sequence and structural polymorphism of the polypeptide chance number: Z14839; MUID:98070526 ion: T03999 : preliminary; translated from GB/EMBL/DDBJ le type: mrNA
A;Residu A;Cross- R;Eckhar J. Biol.	Residues: 1-13288 <eck> Residues: 1-13288 <eck< 1-13288="" <ec<="" <eckretion:="" eckretion:="" td=""></eck<></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck></eck>
A; Title: A; Refere A; Access A; Molecu	Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal domain nce number: A40009; MUID:91236743 ilon: A40009 lle type: mRNA
A; Residu A; Cross - R; Timpte J. Biol. A; Title:	Residues: 12139-12167,'T',12169-13288 <ec3> Cross-references: GB:M61883; NID:9454837; PID:9164374 Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L. Biol. Chem. 263, 1081-1088, 1988 Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical se</ec3>

hav

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alignment_scores:
Quality:
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A;Residues: 1572-1607 <EC2>
C;Superfamily: pig submaxil
C;Keywords: tandem repeat
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A; Title: Structural properties of porcine submaxillary gland apomucin.
A; Reference number: A92606; MUID: 87280230
A; Accession: B29789
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A;Residues: 12139-12167,'T',12169-12641 <TIM>
A;Cross-references: GB:J03512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: pig submaxillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13030 LysGluIleThrAlaSerProLysValSerSerProGluThrThrAlaG1 13046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13074 GlyGluGluLysSerProGlyAspValTrpThrAlaAsnCysHisLysCy 13090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13124 AspThrCysCysGluIle......GlyHisCysGluLysArgThrCy 13137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13107 erProProThrCysLysThrGlyGluArgLeuIleLysPheLysAlaAsn 13123
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                                                                                                                                                                                                                                                                                                           402 ATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 AAAACAGTTAGTGCACAGATTGAGGTATCTGAA...ATCACAACTGCTTT 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||| ::::::::||||||||||
| SThrCysThrGluAlaLysThrValAspCysLysProLysGluCysProS 13107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACC 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sLeuPheAsnAsnThrAspTyr..... 13144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATG
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                                                                                                  s...GlnAsnThrGlyPheThrAlaValValGlnAsnCysProLysGlnT 13178
                                                                                                                                                                     TTCAGAACCACAAGGATTCGGAGCTGTTAA......AACA 319
                                                                                                                                                                                                                                        ValGlySerSerPheAspAspProAsnAsnProCysValThrTyrSerCy 13162
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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1.089
40.724
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Gaps: 12
Percent Identity: 23.982
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                                   .AGCAAAACCTGCTGC...
   353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-reference: GB:M20191
A;Cross-reference: GB:M20191
C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of p I cand dismutates to glyoxylate and the corresponding desglycine peptide alpha-amide. C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I keywords: copper; glycoprotein; monooxygenase; oxidoreductase; transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG>F;40-385/Product: peptidylglycine monooxygenase II #status predicted <MAT>F;40-385/Product: peptidylglycine monooxygenase II #status predicted <MAT>F;133-344/Domain: peptidylglycine monooxygenase II homology <PGM>F;164-787/Domain: transmembrane #status predicted <TMN>F;365,662,743/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptidylglycine monooxygenase (EC 1.14.17.3) II precursor - African clawed frog N;Alternate names: C-terminal alpha-amidating enzyme II (AE-II); peptidyl alpha-amida C:Species: Xenopus laevis (African clawed frog) C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Jun-1997 C:Accession: A27715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-323-427-5/rev x URXLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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A; Residues: 1-875 < OHS>
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A;Accession: A27715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1015 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1065 TGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 CysGlnProThrAspValAlaValAspProIleThrGlyAsnPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546 lAlaAspGlyTyr.....
584 leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                  nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI 584
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                                                           ....ACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACC
                                                                                                                                                                                                                                                                        Asn...SerArgIleMetGlnPheSerProAsnGlyMetPheIleMetGl
                                                                                                                                                                                                                                                                                                                                    AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGC 916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
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0.945
43.103
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12
21.552
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871

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551

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A; Status, F-2-A, Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1895 <PAUS A; Residues: 1-1895 <PAUS A; Cross-references: EMBL:U00065; NID:g495681; PID:g495684; PIDN:AAA50735.1; A; Cross-references: EMBL:U00065; NID:g495681; PID:g495684; PID:g496684; PID:g4966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
hypothetical protein D1044.3 - Caenorhabditis elegans
c)Species: Caenorhabditis elegans
c)Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
c;Accession: T15881
R;Pauley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-323-427-5/rev x T15881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, June 1994
A;Description: The sequence of C. elegans cosmid D1044.
A;Reference number: Z18423
A;Accession: T15881
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A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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Percent Similarity:
                                                                                                                                                                                                       1149 GlnCysIleAspAsnSerValCysMetAsnGlnMetCysThrCysAsnAs
                                      1165 nAsnTyrArgLeuValTyrGlyTyrCysValProIleThrSerSerIleC
                                                                                                                       866 CAAC......TGTTGTCATTTCGTTTCATCCATTATTT
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alignment_block:
US-09-323-427-5/rev x C70126
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DNA mismatch repair protein (mutL) homolog - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13.Feb-1998 #sequence_revision 13.Feb-1998 #text_change 05-Jun-1998 . C;Accession: C70126 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997 A;Authors: Smith, H.O.; Venter, J.C. A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A;Accession: C70126 A;Accession: C70126 A;Cattus: preliminary; nucleic acid sequence not shown; translation not shown A;Actus type type. NA
                                                                                                                                                                   A;Cross-references: GB:AE001131;
A;Experimental source: strain B31
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-610 <KLE>
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SerGlnCysValGlySerGlnGlnCysLeuSerAsnSerGlnCysIleSe 1323
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B. Vu

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                                                                                                                                                                                                                                                                              283 CysTyrLeuPheLeuGluIleAsnProGluTyrIleAspPheAsnValHi
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                                                                                                                                                                                                                                                                                                                                CTGATGGATGTCTTGATAAATATTTGCTAAATAATTTGGAATATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCT 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erLeuIleAspArgValGlnAsnValTyrGlyAsnValIleGluAsnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .TCTTATTCGATTCCGGTTGACAATGGTGTCGAA.......GGTG 1080
                                                                                                                      ATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGACATGCG...ATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProIleAspGlnLysAspLeuLeu.......GluAlaIleThrAs
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                                                                                                                                                                                                                                                                                                                                                                       .....GlyAsnPheProIle
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                                                                         ....LeuProPheLeuPheLys 315
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C;Accession: T11616
R;Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V. submitted to the EMBL Data Library, October 1995
A;Reference number: Z17300
A;Accession: T11616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) - fission yeast (Sc
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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US-09-323-427-5/rev x Tl1616
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Quality:
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C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2244 <BAR>
A;Cross references: EMBL:254328; NID:g1009451; PID:g1009456
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A; Note: SPAC22G7.06c
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Percent Similarity:
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1039 AlaValArgThrLeuArgAspArgGlyVal......LysThrIleMe
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                              CGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uArgArgTyrAsnSerIleIleGlnAsn.....ArgProThrLeuArgG 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATTGATGTACGAACT...GATATC......AACACCCTTGAAATT
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                                                                                             lyValTyrArgIleGlySerSerValGluPheAspTrpCysAlaValArg
                                                                                                                                             GACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCG 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1216 IleGluLeuAspAlaValAlaArgGluGlyLysMetValMetHisValIl 1232
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                                                                           114 AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGT 70
                                                                                                                                                                                                                               164 GTGCACTTCTGCAACATAATGGACAACCTGTAATACTTGCTGCAGTACAA 115
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                                                                                                                                                   rgAla.....SerArgSerPheProPheValSerLysValIle...
                                                                                                                                                                                                                                                                                                           eGlnPheIleAlaLysAspAsnGluIleLysValIleGluCysAsnValA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....GTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAG 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerTyrValLeuSerGlyAlaAlaMetAsnThrValTyrSerGlnSerAs 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ........................AspThrValGlyTyrProValLeuValArgPro 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATT..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rgLeuTyr...PheGluAsnIleGlyLeuGluThrValLeuAspIleTyr 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGT 769
...GlyValAspMetIleSerMetAlaThrAspValIleMetGly 1325
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alignment_block:
US-09-323-427-5/rev x A36054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
C;Accession: A36054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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A;Molecule type: mRNA
A;Residues: 1-563 <BHA>
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Ratio: 0.612
Percent Similarity: 42.609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101 GTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051 AATAACAATCAATTTTAATACACGT...AATGCATTCGAAGGACATGTTT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 IleGlnThrGlyIleThrGlyThrGlySer.......GlyThrThrSe
644 GTCAGCCAGTTTATCATAAATGGACATGC...GATTCTGAAACCGTTGAT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          954 CGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 rSerProGlyGlyPheAsnAlaGluAlaThrThrPheLysGluHisValA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 rThrSerLysSerAsnArgIleThrThrSerSerArgIlePro.....T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 alserGlyArgValThrGlyValSerGluSerSerProGlyThrSer 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  904 TACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCA 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 rgThrThrGluThrArgIleLeuSerGlyThrThrArgGlyArgSerGly 238
                                                                                                                                                                                      LysThrGlyCysThrThrSerLeuProProProProAlaCysTyr....
                                                                                                                                                                                                                                                                                                                                                                                          ACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATC
                                                                                                                                                                                                                                                             ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGA
                                                                                                                                                                                                                                                                                                                      yrProGluThrThrValValAlaThrGlyGluGlnGlu...ThrGluThr 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rSerThrGlyValGlyArgGln......ThrSerThrAlaValV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGA 955
                                                            .....GlyProLeuGlyGluLysLysSerProGlyAspIleT
                                                                                                                             AATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AAAGTTGATCGTGCATATCGAGTACAATGCTTTT 795
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Gaps: 18
Percent Identity: 20.290
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                                                                   354
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R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Wh. J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium A;Reference number: S72277; MUID:96346169
A;Accession: S72278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
seq_documentation_block:
ATP-dependent Clp proteinase (EC 3.4.21.-) homolog - Plasmodium falciparum plastid C:Species: plastid Plasmodium falciparum
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
C:Accession: S72278; S78483
                                                                                                                                                                                                                                                   A:Cross-references: EMBL:X95276; NID:g1171591; PID:e220210; PID:g1171612 C:Genetics:
                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A; Reference number: S78483 A; Accession: S78483
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X95276 R;Wilson, R.J.M.
                                                                                                                                                A;Note: this apparently degenerate plastid is referred to C;Keywords: hydrolase; plastid; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not
A;Molecule type: DNA
A;Residues: 1-765 <WIL>
                                                                            alignment_scores:
                                                                                                                                                                                                                              A;Gene: clpC
                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-95, 'N', 96-765 <WIW>
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  Ratio:
Percent Similarity:
                                                                                                                                                                                                  Genome: plastid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 TCTGCAGAACCGGAGAATATCATTGATGTACGAAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laTyrCysGluProArgThrCysLeuPheAsnAsnAsnAspTyr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rAspSerThrLysCysCys......TyrThrCysLysProT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGlnAspCysProLysGlnThrTrpCysAlaGluGluAspArgValTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAT.....TTGCTAAATAATTTGGAATATCCAACA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAACGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....AGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....ACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....GluValGlyAlaSerPheAlaAspProLysA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ArgLeuValLysPheLysAspAsnAspThrCysCysGluIleA 401
                                                    Quality:
90.00
0.720
55.556
  Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                         January 1996
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                                                 Length:
                          Gaps:
225
20
27.111
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submitted to the EMBL Data Library, May 1994 A; Description: The sequence of S. cerevisiae A; Reference number: $846691
                                                                                 hypothetical protein YHR102w - yeast (Saccharomyces cerevisiae) C:Species: Saccharomyces cerevisiae C:Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change C:Accession: S48944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-323-427-5/rev x S72278
                                                                 R; Latreille,
                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                 seq_name: pir2:S48944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 TAAATATTTGCTAAATAAT...TTGGAATATCCAACAGATTTAATGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 TyrLeuPheLeuLeuAsnLysLeuTyrGlyTyrAsnIleHisIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      848 TTCATCCATTATTTGTTACCAAAGTTGATC......GTGCATATC..
                                                                                                                                                                                                                                                                                                                                                                                           CAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCACAATGTTCAGAAC......CACAAGGATTCGGAGCTGTTAAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGAAATTTTGGATGGTGGACCAACCGGTCAACCAG.....TTCA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAAACAG......TTAGTGCACAGATTGAGGTATCTG 750
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                                                                                                                                                                                                                                                              nHisIleTyrGlyGlnAsn
                                                                                                                                                                                                                                                                                                         AAGAAAAGATCTGCAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nLysTyrLeuLeuAsnAsnLysIleSerTyr.SerAsnPheAsnTyrLeu
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                                                                                                          24-Sep-1999
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A,Gene: SGD:NRK1
A,Cross-references: SGD:S0001144; MIPS:YHR102w
A,Map position: 8R
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C;Keywords: ATP; serine/threonine-specific protein kinase F:21-276/Domain: protein kinase homology <KIN>F;29-37/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
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A;Molecule type: DNA
A;Residues: 1-1080 <LAT>
A;Cross-references: EMBL:U00059; NID:g529116; PIDN:AAB68860.1; PID:g529127; MIPS:YHR102w
C;Genetics:
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US-09-323-427-5/rev x S48944
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                                                                                                                                                                                                                                                                                                                                                                                      CAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAA 301
CGTCACCGTGCACTTCTGCAACATAAT 145
                                                                                                                                                                                                                                                                                       CCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACC
                                               spTyrIleIleGluAsnAsnIleAsnLeuAspAlaLeuAlaGluAspAsn
                                                                                         AT.....
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Percent Identity: 21.531
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A; Residues: 1-1712 <GAR>
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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743
A;Accession: C71618
A;Status: preliminar; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: C71618
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H.E

90.00 Percent Identity: 19.941

US-09-323-427-5/rev x C71618 0.584 45.161 . 0 1712

1102 MetLysLysLysLysThrGlnGluTyrValAspIleGlu.....Th 1116 rValTyrGluTyrValIleGluLysTyrLysArgValHisValLeuTyrL 1166 tGluLysLeuLysLysAsnTyrIleHisCysIleTyrAspIleSerAspL 642 CAGCCAGTTTATC.....ATAAATGGACATGCGATTCTGAAACCGT 742 AACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA ACGGTGATACTGTGGAAATTCTAAATGCTGATG ATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAA TGATACTTTCTGCGCGGTTGTCCATTCCT...GCTTTGTCGATGATGGTA LysTyrSerPheHisLysLeuArgIlePheTyrGluTyrLysIleGluMe 1166 CATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTAC euGlyArgLeuLeuGlnIleValGluLysLeuPheLysLysTyrIleLeu 1149 euLeuLeuLysGluLysSerAlaTyrGlnAsnHisLeuGlyLysAsnTyr 1238 uSerSerPheIleAsnTyrGlnIleLysThrAsnAspMetLeuTyrAsnLTTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGT ysLeuGluPheLeuIleLysLysLysMetGlnHisTyr..... ATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCAC 743 ${\tt TC...CACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATC}$ ATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAGATGTGCTCTT 511 693 1133 1222 602 793 843 940

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posterior-group Protein tudor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C;Accession: A41519; S19019
R;Golumbeski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.
Genes Dev. 5, 2060-2070, 1991
A;Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes a R;Reference number: A41519; MUID:92038995
A;Accession: A41519
alignment_block:
                                                                                                                                                                                                 A;Cross-references: FlyBase:FBgn0003891
C;Superfamily: posterior-group protein tudor
                                                                                                                                                                                                                                                                                             A;Cross-references: GB:X62420; NID:g8753; PIDN:CAA44286.1; PID:g8754
                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-2515 <GOL>
                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                     A;Gene: tud
                                                                                                                                                                                                                                                                               C;Genetics
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                                               Percent Similarity:
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                                               Percent Identity:
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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2035 AlaAspAspLeuGluPheTyrArgSerArgIleLeuGluValLeuGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1116 TCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGA 1067
                                              2125 rAlaSerProProValValArgLeuThrThrLysAspLysArgSerLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2077 PheThrLeuIle...LysProValAlaGlu.....IleCysSerMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2060 spTyrGlyAsnThrThrValValAspLysLeuTyrGluLeuProGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2018 lnProLysThrGluLysAlaAlaValAspAspMetCysValValGlnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1960 uLeuProLeu.....CysGlnArgLysGluProLysGluAlaSerLysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2051 pAspGlnTyrLysValIle.....LeuIleA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001 sAspSerLeuMetAspIleIleCysGluLysLeuAsnGlySerLysLeuG
                                                                                                        490 TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       784 TGAT.....
                                                                                                                                                                                                           540 GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         984 CAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTC
440 AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...ThrHisValGluAsnThrSerArgIleTyrLeuGlnPheSerGluLy 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerLeuGlnLeuPro...AspAlaTyrIleSerTrpSerProGluAlaGl
                                                                                                                                                      .....LysGlyValValAlaValGluPheValAsnLysSe
                                                                                                                                                                                                                                                            spAlaLeuLeuAspSerCys.....
                                                                                                                                                                                                                                                                                                                   GCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTG 541
                                                                                                                                                                                                                                                                                                                                                                       uProSerAlaIlePheGluLysAsnLysAlaLeuThrLeuThrThrPheA
                                                                                                                                                                                                                                                                                                                                                                                                                      A.....ACCGTTGATACTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uAlaLysPheAlaGluLeuThrGlyGluGlyGluLeuValPheThrThrG
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R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardhois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aithers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Rieference number: A69580; MUID:98044033

A. Staries, nrealinings.
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
C;Accession: H68898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PID:e1185369; PID:g2634290
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1201 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: H69898 from: 1 to: 1201
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-323-427-5/rev x H69898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                 1100 TTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCA 1051
                                                                             1050 ATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGT 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2192 leValLysThrLeuGlnSerLeuLysLysGluLysLeu.....LysLys 2206
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                                                                                                                                                               552 LeuLeuGluLeuGluArgGluLysGlnGluIleArgAlaGlnSerLeuGl 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 ATCATTGATGTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 CAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAAT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 ACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTG 294
n......ValLeuIleThrLysMetAsnSerLysAspValPheSerA 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.50
0.511
44.643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 392
Gaps: 17
Percent Identity: 18.367
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848		839
359	AGAACCAAATAGCGAATGTGTTCGA	408
838	ProAsnileThrTyrAlaAlaValLysAsnSerAsp	827
>	ひきょ ごしきほうじしょ しょうきょうしきょうじんしゅ とうく ちょうく もく そうしょうしょく ひょうしょく しゅうしょく しょうしょうしょく しょうしょう しょうしょく しょくしょく しょうしょく しょくしょく しょうしょく しょくしょく しょくしゃく しょくしゃく しゃんしゃく しゃんしゃく しゃんしゃく しゃんしゃん しゃんしゃん しゃんしゃん しゃんしゃん しゅんしゃん しゃくしゃん しゃんしゃん ゃん しゃんしゃん ゃん しゃんしゃんしゃんしゃんしゃんしゃんしゃんしゃんしゃんしゃんしゃんしゃんしゃんし	л
459 826	NTTTGGAATATCCAACAGATTTAAT :leLeuAsnAsp	502 816
816	rGluThrIleTyrAspPheValValGlnArgAsnLeuTyrGluIleAsnI	799
503	GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGA	552
553 799	ATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAAC::: ::: :::::::::::::::::::::::::::	599 783
600 782	CATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTG ::: ::: erLeuValSerAspGluGluLysIleLysGluLeu	649 771
771	tSerPheThrLeuSerLysTyrLeuAsnLeu	758
650	AAATTTTGGATGGTGGACCAACCGGTCAACCAG	699
758	spIleAlaAspIleIleArgMetAsnLysGluS	744
700	AAACTCAAATTGTCCCGATGCCAGTATGCC	734
743	AsnTyrThrGlnGlnL	727
735	TTGAGGTATCTGAAATCACAA	764
727	erSerLysTrpAspAspPheTrpSe	710
765		765
710	heLysGluArgAlaIleAsnLysAlaAlaF	694
765		765
693	lySerLysGluSerVa	677
765	AGCTGATAAAACAGTTAGTGC	793
677	SerGl	664
794	TTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT	843
664	:::: uValGlyAlaGluPheLysGlnIleGluValLeuAsnPheHisLeu	4
844	TTTTGTAACAACAACTGTTGTCATTTCGTT	893
647	::::::::::::::::::::::::::::::::::::::	631
894		913
631	 	614
914		920
614	: rAsnHisTyrIleThrTyrPheTyrProGl	598
921	CCGGAATTTCACTTCCATTTGATT	950
597	rGluLysLysLe	582
951	GTCTTTATGATCAAGAAGGTTGCC	1000

	883ValLysHisAlaMetIleMetLys 890	883
	214 CCTTGAAATTAGCGATGATAATCAAG 189	214
882	877 uAspLeuAspLysArg 882	877
215	264 AGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACAC 215	264
877	865 GluProGluGluSerPheLeuGluLeuLeuAsnArgGl 877	865
265	TTCGTTTACTCA	311
864	848 spAsnIleAspIlePheValGluLysValLeuThrGluGluIleGlu 864	848
312	358 ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTTAAAACAGGTGGTG 312	358

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SwissProt_38: AMD_BOVIN -
SwissProt_38: PDLG_EC12T -
SwissProt_38: SYM_SYN3 -
SwissProt_38: AMD_RAT -
SwissProt_38: IPDE_DICDI -
SwissProt_38: PDP_BACST -
SwissProt_38: PDF_BACST -
SwissProt_38: PDF_BACST -
SwissProt_38: PTSA_ECOLI -
SwissProt_38: TSA_ECOLI -
SwissProt_38: TSA_ECOLI -
SwissProt_38: UL52_HSV7J -
                                                                                                                                                                                                                                                                                                                                   SwissProt_38:CGE1_CHICK
SwissProt_38:PHY3_AVESA
SwissProt_38:YAOE_SCHPO
SwissProt_38:SRB8_YEAST
SwissProt_38:SRB_YEAST
SwissProt_38:PITA_MOUSE
SwissProt_38:PITA_MOUSE
SwissProt_38:POSA_CLODI
SwissProt_38:YHHT_ECOLI
SwissProt_38:YHHT_ECOLI
SwissProt_38:YHHT_ECOLI
SwissProt_38:YHHT_ECOLI
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SwissProt_38:CUT1_CAEEL
SwissProt_38:YQH3_CAEEL
SwissProt_38:YAY3_SCHPO
SwissProt_38:XY3_SCHPO
                                                                                                                                                                                                                                     SwissProt_38:RMS5_EMENI -
SwissProt_38:RMS5_NEUCR -
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SwissProt_38:NU5M_APILI -
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SwissProt_38:AMD_HUMAN -
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SwissProt_38:NRK1_YEAST -
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SwissProt_38:YLK3_CAEEL -
SwissProt_38:PYR1_SCHPO -
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SwissProt_38:GALU_PSEAE -
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Database length: 29864866
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Query length: 1161
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-DB=SwissProt_38 -QEMT=fastan -SUFFIX=backtrans.rsp
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 LOOPCL=0.000
-LOOPEXT=0.000 -QGAPEXT=4.000 -QGAPEXT=0.050 -XGAPOP=10.000
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-YGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -FGAPOP=50-CALIGN=200
-MINLENSOUNDE2 -TRANS-human40.CG1 -LIST=45 -DOCALIGN=200
-THR_SCORE-pct -ALICN=15 -MODE-LOCAL -OUTFMT=pfs -NORM-ext
-MINLENSOUNDE3 -MODE-100000 -USER=US09323427 -NCPU=6 -ICPU=3
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2515 i p25823 drosophila melanogast
363 i p30938 rattus norvegicus (rat)
974 i P19021 homo sapiens (human)
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861
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7 ! P49707 gallus gallus (chicke
128 ! P06503 avena sativa (oat).

260 ! Q10093 schizosaccharomyces.

427 ! P25648 saccharomyces cerevi
117 ! Q14126 homo sapiens (human).

1025 ! O42611 fugu rubripes (japan
1068 ! P42337 mus musculus (mouse)

361 ! P11704 spinacia oleracea (s
2710 ! P16134 clostridium difficil
2710 ! P16134 clostridium difficil
2710 ! Q39575 chlamydomonas reinha
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P24855 apis mellifera ligust
P21421 plasmodium falciparu
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                                        P36417 dictyostelium discoid
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P09794 schizosaccharomyces
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Q09276 caenorhabditis elegar
Q10211 schizosaccharomyces p
  Q10128 caenorhabditis
P52468 herpes simplex
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seq_documentation_block:
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SwissProt_38:YEW2_YEAST -
SwissProt_38:P11A_HUMAN -
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PIR; A49772; A49772.
                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Dev. Biol. 146:519-530(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: EXPRESSED DURING DAUER LARVA FORMATION. DOMAIN: THE SMALL REPEATS A-A-P-[AVI] ARE ALSO PRESENT IN MANY PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES
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                                                                                                                 nLeuGluTyrProThrAspLeuMetAlaGlyGlnGluAlaHisValTyrL
ysTyrAlaAspArgSerGlnLeuPheTyrGlnCysGlnIleSerIleThr
                                                                                                                                              TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA
                                                                                                                                                                           GlnIleLeuAsnGluGluGlyCysAlaLeuAspLysPheLeuLeuAsnAs
                                                                                                                                                                                            GAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAA 491
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                                                                                                                                                                                                                                                                                             nGlnValTyrHisLysTrpThrCysAspSerGluThrThrAspThrPheC
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A FERRICA COCCOCCE REPORTED TO SOLUTION OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
HYPOTHETICAL 55.1 K
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                           Hypothetical
TRANSMEM
                                                                                                                                                                         WORMPEP;
                                                                                                                                                                                                                       EMBL; Z47067; CAA87330.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULSTON J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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heGlyGluAsnGluGlyIleLeuAspValArgValGluIleAsnThrLeu
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                                                                                                               protein;
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ein; Transmembrane; ATP-binding.
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35, Last sequence update)
35, Last annotation update)
KD PROTEIN C43C3.3 IN CHROMOSOME
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TRANSMEM NP_BIND SEQUENCE

495

AA;

WW. ATP POTENTIAL. POTENTIAL.

TP (POTENTIAL).
09C77468 CRC32;

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alignment_block:
US-09-323-427-5/rev x YQH3_CAEEL
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                                                                                                                                                                                                                                               LysIleThrPhe.....ValGlnGlyGlyCysProValAsnGlyMetAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAA 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....ACACGTAATGCATTCGAAGGACATGTTTATG 1002
PheArgThrPheArgPheGlyAsnGlnSerThrValPheValHisCysGl
                                       GCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCA 404
                                                                              ...IleIleAspProLeuAlaAsnValAsnAspGlnIleTyrPheSerLys
                                                                                                                                                          nAsp.....
                                                                                                                                                                                                          CGGTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAAT 504
                                                                                                                                                                                                                                                                                                                                ysGluCysThrPheSerAspArgGluAspIleSerAlaProAspAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrAspSerGlyLysThrLeuGlnAlaAlaArgGluAsnGluPheValGl
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                                                                                                                       .....ACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAA 554
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Ratio:
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Gaps: 19
Percent Identity: 22.647
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alignment_block:
US-09-323-427-5/rev x YAY3_SCHPO
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                                                                                                    Align seg 1/1 to: YAY3_SCHPO
                                                                                                                                                                                      Ratio:
Percent Similarity:
1039 TTTTAATACACGTAATGCATTC.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPAC4H3.03C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Transmembrane TRANSMEM 265 285 POTENT: TRANSMEM 564 584 POTENT:
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Q10211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                 36 LeuAspGlySerValGluMetMetCysTrpPro.....
                                                                 GTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCAA 1040
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                                              TrpIleArgAspSerAlaPheThrIleTyrAlaLeuAlaGlnLeuGlyPh
                                                                                                                                  erLeuProGluAspLeuGlyGlyValArgAsnTrpAspTyrArgPheThr
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MEDLINE; 97248516.

MEDLINE; 97248516.

GERKEN T.A., OWENS C.L., PASUMARTHY M.;

"Determination of the site-specific O-glycosylation pattern of the "Determination of the site-specific O-glycosylation pattern of the porcine submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:galnac transferase peptide binding site.";

J. Biol. Chem. 272:9709-9719(1997).

-I- FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE THE ALL TO ANY CANTTY AND TO PROTECT IT FROM THE EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                        ECKHARDT A.E., TIMPTE C..., DHNSON W.C. JR., HILL R.L.;
JOHNSON W.C. JR., HILL R.L.;
"Structural properties of porcine submaxillary gland and properties of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosylated domain.";
J. Biol. Char
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Cetartiodactyla; Suina; Suidae; Sus.
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TIMPTE C.S., ECKHARDT A.E., ABERNETHY J.L., HILL R.L.;

"Porcine submaxillary gland apomucin contains tandemly identical sequences of 81 residues.";

J. Biol. Chem. 263:1081-1088(1988).
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01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                 CARBOHYDRATE-BINDING SITES, TISSUE=SUBMAXILLARY GLAND;
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                                                                                                                                                                                                                                                                                                                                                                                  AND SEQUENCE
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SIMILARITY: CONTAINS 1 CWFC DOMAIN.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE
DOMAIN: CONTAINS TANDEMLY REPEATED, IDEN
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PS01225; CTCK_2; 1.
PS01208; VWFC; 1.
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1057 ThrCysLysSerSerCysLysProSerProValAsnValThrValArgTy 1073

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alignment_block:
US-09-323-427-5/rev x GALU_PSEAE
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01-NOV-1997 (Rel. 35, Last annotation update)
UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE
PYROPHOSPHONYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE
URIDYLYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 10145;
CHANG H., LEE C., PE
Submitted (DEC-1993)
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01-NOV-1997 (Rel. 35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
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                                                                   GGT...TGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACT
                                                                                                                                        GTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAA
                                                                                                                                                                                                         AGAAATTGAATGTGGACCAACTTCAATAACAATC...AATTTTAATACAC
TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTG
                              AsnGlnIleLysGlyThrAspLysGluLysTyrLeuValGlyIleArgLy
                                                                                                     ysArgAlaLeuGluAspHisPheAspIleSer....TyrGluLeuGlu
                                                                                                                                                                         uAlaLeuAspAlaGlyLeuAsnGluIleSerIleValThrGlyArgGlyL
                                                                                                                                                                                                                                              LeuProValValAsnLysProLeuIleGlnTyrGlyVal.....GluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PROKARYOTIC UDPGP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MAY PLAY A ROLE IN STATIONARY PHASE SURVIVAL (BY
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Ratio:
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seq_name: SwissProt_38:AMD2_XENLA
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                  Biochem. Biophys. Res. Commun. 150:1275-1281(1988).
-!- FUNCTION: C-TERMINAL ALPHA-AMLDATION OF BIOLOGICAL PEPTIDES.
-!- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + O(2) =
PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O.
(THE PRODUCT IS UNSTABLE AND DISMUTATES TO GLYOXYLATE AND THE
CORRESPONDING DESGLYCINE PEPTIDE AMIDE).
                                                                                                                                                                                                                                                                                                                                                           01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE II PRECURSOR
(EC 1.14.17.3) (PEPTIDE C-TERMINAL ALPHA-AMIDATING ENZYME II) (AE-II).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
                                                                                                                                                                                                                       OHSUYE
                                                                                                                                                                                                                                          MEDLINE; 88134244.
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                                                                                                                                                          enzyme having a putative membrane-spanning domain from
                                                                                                                                                                                                      MATSUO H.
                                                                                                                                                                                                                                                                 TISSUE-SKIN;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                       K., KITANO K., WADA Y., FUCHIMURA K., TANAKA S., MIZUNO K.,
                                                                                                                                                                                                                                                                                                                                            Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511
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  COPPER,
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AND ASCORBATE
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alignment_block:
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DOMAIN
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PIR; A27715; URXLA2.
PROSITE; PS00084; CU2_MONOOXYGENASE_1;
PROSITE; PS00085; CU2_MONOOXYGENASE_2;
                                                                                                                                                                                                        567
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                                                                                                                                                                                                    \verb"nTrpGlyGluGluThrSerSerAsnLeuProArgProGlyGlnPheArgI"
                                                                                                                      leProHisSerLeuThrMetIleSerAspGlnGlyGlnLeuCysValAla
                                                                                                                                                                                                                                                                                                                        AATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTA....
AACAGTTAGTGCACAGATTGAGGTATCTGAAATC...ACAACTGCTTTTC
                                     AspArgGluAsnGly...ArgIleGlnCysPheHisAlaLysThrGlyGl
                                                                                AAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MONOOXYGENASE FAMILY.
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Gaps: 12
Percent Identity: 21.552
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Seq_documentation_block:

ID YIK3_CABEL STANDA
AC P41951;

DT 01-NOV-1995 (Rel. 32,
DT 01-NOV-1998 (Rel. 32,
DT 15-DEC-1998 (Rel. 37,
DE PUTATIVE SERINE/THREO
DE (EC 2-7.1.-).
GN 01044.3.

OC RADIOLEY A, WATERSTON
R. STRAIN-BRISTOL N2;
RA PAULEY A, WATERSTON
R. STRAIN-BRISTOL WITH
CC -1- SIMILARITY: CONTY
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      Hypothetical protein; T
ATP-binding; EGF-like of
DOMAIN 431 703
NP_BIND 437 445
BINDING 461 461
ACT_SITE 569 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAULEY A., WATERSTON R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3
(EC 2.7.1.-).
                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROCETTE: DS50011: PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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                                                                                                                                                                                                                                  PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS01186; EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00065; AAA50735.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institumodified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASES.
-!- SIMILARITY: CONTAINS ? EGF-LIKE DOMAINS.
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                                                                                                                                                                                                        PF00069; pkinase;
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      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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32, Created)32, Last sequence up39, Last annotation
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    THE PROCESS AND DESCRIPTION OF THE PROCESS CONTRACTOR OF THE PROCESS C
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PFAM;
PFAM;
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URA1 OR SPAC22G7.06C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                       PF00289; CPSase_L_chain; 2.
PF00744; Dihydrooratase; 1.
PF00988; CPSase_sm_chain; 1.
                                                                                                                                                                                                                                                                                                                                    PF00117; GATase; 1. PF00185; OTCace; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X81841; CAA57433.1;
Z54328; CAA91130.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P00968; lJDB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-2244 FROM N.A
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00097; CARBAMOYLTRANSFERASE;
PROSITE; PS00442; GATASE_TYPE_I; 1.
PROSITE; PS00866; CPSASE_I; 2.
PROSITE; PS00867; CPSASE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "As in Saccharomyces cerevisiae, aspartate transcarbamoylase is assembled on a multifunctional protein including a dihydroorotase-like cryptic domain in Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BADCOCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH Submilted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: THIS PROTEIN IS A "FUSTON" PROTEIN ENCODING THREE ENZYMATIC ACTIVITIES OF THE PYRIMIDINE PATHWAY (GATASE, CPS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORTHOPHOSPHATE + GLUTAMATE + CARBAMOYL PHOSPHATE.

CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE =

ORTHOPHOSPHATE + N-CARBAMOYL-PHOSPHATE + ASPARTATE =

ORTHOPHOSPHATE + N-CARBAMOYL-SPHOSPHATE + ASPARTATE =

ORTHOPHOSPHATE + N-CARBAMOYL-SHOPHATE STED IN PYRIMIDINE BIOSYNTHESIS.

PATHWAY: FIRST AND SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.

PATHWAY: PROSPHATE SYNTHASS PORM TOOFRANSFERASE) AND CPSASE

(CARBAMOYL PHOSPHATE SYNTHASS PORM TOOFRANSFERASE) STEP THE

GLUTAMINE-DEPENDENT CPSASE (GD-CPSASE) (EC 6.3.5.5).

MISCELLANEOUS: IN EUKARYOTES EC 6.3.5.5 IS SYNTHESIZED BY TWO

PATHWAY-SPECIFIC (ARGININE AND PYRIMIDINE) UNDER SEPARATE CONTROL.

SIMILARITY: THE CPSASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE

SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND ATCASE) (BY SIMILARITY).

CATALYTIC ACTIVITY: 2 ATP + GLUTAMINE + CO(2) + H(2)0 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligase; Transferase; Multifunctional enzyme.
GATASE (GLUTAMINE AMIDOTRANSFERASE)
(BY SIMILARITY).
                                                                                                                               BOUNDARY BETWEEN ENZYMATIC DOMAINS (BY SIMILARITY).

CPSASE (CARBAMYUL-PHOSPHATE SYNTHASE (BY SIMILARITY).

BOUNDARY BETWEEN ENZYMATIC DOMAINS (BY SIMILARITY).

DEFECTIVE DHOASE DOMAIN
(BY SIMILARITY).
BOUNDARY BETWEEN ENZYMATIC DOMAINS
(BY SIMILARITY).
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alignment_block:
US-09-323-427-5/rev x PYR1_SCHPO
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GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA 473
                                                                                                                                                                                                                      hrSerProGluMetIleAspGlyAlaGluAsnArgPheLysPheSerArg
                                                                                                                                                                                                                                                                                                                                                               GluGlnGluSerSerGlyIleIleIleAlaMetGlyGlyGlnThrAl 1101
                           .....AspThrValGlyTyrProValLeuValArgPro 1170
                                                         TCGATGATGGTAACGGTGATACTGTG.....GAAATTCTAAATGCTGAT
                                                                                          rPheAspGlu...AlaAspLysPheCys...........
                                                                                                                CGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTG
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                                                                                                                                                           MetLeuAspAspIleGlyValAspGlnProLysTrpLysGluLeuThrSe 1151
                                                                                                                                                                                            CCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATG
                                                                                                                                                                                                                                                                                                                                                                                                GCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATT..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tValAsnTyrAsnProGluThrValSerThrAspTyrAspGluAlaAspA 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTTCGTTTCATCCATTATTTGTTACC.....AAAGTTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lyValTyrArgIleGlySerSerValGluPheAspTrpCysAlaValArg 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCG
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                                                                                                                                                                                                                                                            GTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGT 769
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GIC -> RYF (IN REF. 1).

CAVRA -> LQFAQ (IN REF. 1).

EL -> DV (IN REF. 1).

G -> E (IN REF. 1).

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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SUBMAXILLARY MUCIN-LIKE PROTEIN.
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                             entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGT 70
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PROSITE; PS01225; CTCK_2; 1.
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ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCCGTTATGA
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seq_documentation_block:
ID NRK1_YEAST STAN
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                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
SERINE/FHREONINE-PROTEIN KINASE NRK1 (EC 2.7.
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J., DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J., DU Z., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y., LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L. NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.
                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470
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                                                                                                                       STRAIN=S288C
                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                               Submitted (MAY-1994) to
                                                                                                                                                                                                                     STRAIN=DC-5;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 P38692;
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                                                                                                   MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGCAGAACCGGAGAATATCATTGATGTACGAAC 227
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RAPE TERMINATION OF THE TERMINAT

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alignment_scores:
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US-09-323-427-5/rev x NRK1_YEAST
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EMBL; U00059; An-
PIR; S48944; S48944.
PIR; 524941; 1A01.
P24941; 1A01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 265:2077-2082(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      732 CAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGG
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VIII.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGACCA.....ACCGGTCAACCAGTTCAATTTGCTA
CAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTT
                                         {\tt ArgTyrLeuLeuPheArgAspLysAsnLysBnLysTyrLysIleGluGlug1}
                                                                                                                                                                                                                                                                  TGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATT
                                                                                                                                                                                                                                                                                                                            LysGluPheIleAlaLeu.....CysLeuAspGluAspProLys..
                                                                                                                                                                                                                                                                                                                                                                          GATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGG
                                                                                           CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGAT
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                                                                                                                                         leArgAlaHisLysAlaThrProThrSerIleLeuLysGluLeuIleSer
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PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00107; PROTEIN_KINASE_ATP;
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23 276 PROTEIN KINASE.
29 37 ATP (BY SIMILARII
52 52 ATP (BY SIMILARII
144 144 BY SIMILARITY.
                                                                                                                                                                                                                                . {	t GluArgLeuSerAlaAspAspLeuLeuLysSerLysPheI}
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117061 MW;
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Percent Identity: 21.531
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ATP (BY SIMILARITY).
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Gaps:
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alignment_scores:
Quality:
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 Percent Similarity:
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                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOLUMBESKI G.S., BARDSLEY A., TAX F., BOSWELL R.E.; "Tudor, a posterior-group gene of Drosophila melanogaster, encodes novel protein and an mRNA localized during mid-oogenesis."; Genes Dev. 5:2060-2070(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation updat
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                                                                                                                                                                                  PIR; A41519; A41519
                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                               Developmental protein
SEQUENCE 2515 AA; ;
                                                                                                                                                FLYBASE; FBgn0003891;
PFAM; PF00567; TUDOR;
                                                                                                                                                                                                         EMBL; X62420; CAA44286.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATERNAL TUDOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                          PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION
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                     Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
 0.552
44.414
                                      90.00
                                                                                                             285236
                                                                                                                                                10.
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                                                               rAlaSerProProValValArgLeuThrThrLysAspLysArgSerLeuL
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                         AATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC
                                                                                                             TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA 441
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seq_documentation_block:
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                   EMBL;
                                                                                         the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
SOMATOSTATIN RECEPTOR TYPE 5 (SS5R).
                                                                                                                                                                                                                                                                                                                          "Molecular cloning, functional characterization, and chromosomal localization of a human somatostatin receptor (somatostatin receptor type 5) with preferential affinity for somatostatin-28.";

Mol. Pharmacol. 45:417-427(1994),
11- FUNCTION: RECEPTOR FOR SOMATOSTATIN-28. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBIT ADENYLYL CYCLAS:
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'CARROLL A.-M., LOLAIT S.J., KONIG M., MAHAN L.C.; "Molecular cloning and expression of a pituitary somatostatin receptor with preferential affinity for somatostatin-28."; Mol. Pharmacol. 42:939-946(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANETTA R., GREENWOOD M.T., WARSZYNSKA A., DEMCHYSHYN L.L., DAY
NIZNIK H.B., SRIKANT C.B., PATEL Y.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93125499.
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                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: PROMINENT IN THE PITUITARY AND SMALL INTESTINE. LOW LEVELS IN ISLETS AND SPLEEN. NOT DETECTED IN KIDNEY, PANCREAS, CEREBELUM, OR CORTEX.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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U01152; AAC09011.1;
X74828; CAA52825.1;
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GCRDB;

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Multigene family; Lipoprote:
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PROSITE; PS00237; G_PROTEIN_RECEPTOR;
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                                                           oLeuLeuValPheAlaAspValGlnGluGlyTrpGlyThrCysAsnLeuS
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                                                                                                                         LysMetAlaSerAlaAlaValTrpValPheSerLeuLeuMetSerLeuPr
                                                                                                                                                                                                                     TTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCG
                                                                                                                                                                                                                                                                               C...AATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGA
                                                                                                                                                                                                                                                                                                             GlySerPheLeuCysArgLeuValMetThrLeuAspGlyIleAsnGlnPh
erTrpProGluProValGlyLeuTrpGlyAlaAlaPheIleThrTyrThr
                              TTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACA
                                                                                                                                                                                      alValHisProLeu..
                                                                                                                                                                                                                                                eThrSerIlePheCysLeuMetValMetSerValAspArgTyrLeuAlaV
                                                                                                                                                                                                                                                                                                                                         .....ATGGTGGACCAACCGGTCAACCAGTT
                                                                                                                                                                                                                                                                                                                                                                           lyLeuProPheLeuAlaThrGlnAsnAlaValValSerTyrTrpProPhe
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Ratio:
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1.114
51.974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
111
133
155
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                                                                                                                                                                                      .ArgSerAlaArgTrpArgArgProArgValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 152
Gaps: 6
Percent Identity: 24.342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
BY SIMILARITY.
PALMITATE (POTENTIAL).
A0DDD650 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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7 (POTENTIAL).
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2 (POTENTIAL
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                                                                                          AATATTTGCTAAATAA
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                              441
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alignment_scores:
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                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 169:551-558(1990).

-!- FUNCTION: C-TERMINAL ALPHA AMIDATION OF PEPTIDES.

-!- CATALYTIC ACTIVITY: PEPTIDYELIXCINE + ASCORBATE + O(2) =
PEPTIDYE(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O.

(THE PRODUCT IS UNSTABLE AND DISMUTATES TO GLYOXYLATE AND
CORRESPONDING DESGLYCINE PEPTIDE AMIDE).

-!- SUBCELLULAR LOCATION: SECRETORY GRANULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human peptidylglycine alpha-amidating monooxygenase: and functional expression of a truncated form in COS of Biochem. Biophys. Res. Commun. 169:551-558(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTLDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE
(EC 1.14.17.3) (PAM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
                                                             METAL
METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205
                                                                                                                                                               DOMAIN
                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                        Oxidoreductase;
                                                                                                                                                                                                                                                  PFAM; PF01082; Cu2_monooxygen; PFAM; PF01436; NHL; 4.
                                                                                                                                                                                                                                                                          PROSITE; PS00084; CU2_MONOOXYGENASE_1; PROSITE; PS00085; CU2_MONOOXYGENASE_2;
                                                                                                                                                                                                                                                                                                    MIM; 170270;
                                                                                                                                                                                                                                                                                                              EMBL; M37721;
PIR; A35477; U
                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAUDER J., RAGG H., RAUCH J., ENGELS J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=THYROID CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MONOOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE COPPER TYPE II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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                                                                                                                                                                                                                          Phosphorylation;
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                                     AΑ;
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                                                                                                                                                                                                                                       Monooxygenase;
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240
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361
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762
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                                      WW;
                                                                                                                                                                                                                                                                                                                                                                 agreement (See http://www.isb-sib.ch/announce/
                                                             COPPER
COPPER
                                                                                    COPPER
COPPER
                                                                                                              COPPER
                                                                                                                          COPPER (POTENTIAL)
                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                     PEPTIDYL-GLYCINE ALPHA-AMIDATING
                                                                                                                                                                                                    PROBABLE
                                                 POTENTIAL
                                                                                                                                                               INTRAGRANULAR (POTENTIAL).
                                                                                                                                                                           MONOOXYGENASE
                                                                                                                                                                                                                          Copper; Vitamin Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                     05A75C07 CRC32;
                                                                                    R (POTENTIAL)
R (POTENTIAL)
R (POTENTIAL)
                                                             (POTENTIAL)
                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                           Usage
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                                                                                                                                                                                                                                       Transmembrane;
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cells.";
                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration -
MBL outstation -
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Quality:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-323-427-5/rev x AMD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1015 AGGACATGTTTATGTGAAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631 CysGlnProThrAspValAlaValAspProGlyThr......
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TAMAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTT
                                                    ValLysLysAlaGlyIleGluValGlnGluIleLysGluAlaGluAlaVa
                                                                                                          AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGT
                                                                                                                                                                 hrAsnThrValTrpLysPheThrLeuThrGluLysLeuGluHisArgSer
                                                                                                                                                                                                                        CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT
                                                                                                                                                                                                                                                                            sAspIleValAlaSerGluAspGlyThrValTyrIleGlyAspAlaHisT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ValMetAsnPheSerAsnGlyGluIleIleAspIlePhe.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCA 676
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                                                                                                                                                                                                                                                                                                                                   AGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT
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45.652
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Percent Identity: 18.944
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alignment_scores:
    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: SwissProt_38:CGE1_CHICK
Align seg 1/1 to:
                                US-09-323-427-5/rev x CGE1_CHICK
                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P49707: Q91032;

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

G1/S-SPECIFIC CYCLIN E1.
                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                            PFAM; PF00134; cyclin; 1.
Cyclin; Cell cycle; Cell division.
                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIH., LAHTI J.M., VALENTINE M., HOUSTON J., KIDD V.J.;
SUBMILTED (JUN-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE (START) TRANSITION. INTERACTS WITH A MEMBER OF THE CDC2/CDK PROTEIN KINASES FAMILY TO FORM MPF (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN E SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as modified and this statement is not removed. U
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U28982; AAA81647.1; J
U28983; AAA81647.1; J
L; U28983; AAA81647.1; J
U28984; AAA81647.1; J
L; U28986; AAA81647.1; J
L; U28986; AAA81647.1; J
U28987; AAA81647.1; J
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L -> S (IN AAA81647).
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Gaps: 16
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SEQ_documentation_block:
ID PHY3_AVESA
AC PO6593;
AC 01-JAN-1988 (Rel. 06, Creat Of 01-JAN-1988 (Rel. 38, Last DT 01-JAN-1999 (Rel. 38, Last DT 15-JUL-1999 (Rel. 38, Last DT 16-JUL-1999 (Rel. 39, Last DT 16-Jul-1999 
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                                                                                                                                                                                             PROSITE; PS00245; PHYTOCHROME_1; PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as modified and this statement is not removed. U
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Nucleic Acids Res. 13:8543-8559(1985).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHYTOCHROME A TYPE 3 (AP3).
                                                                                                                                                                                                                                                                                        MENDEL; 1305; AVESa; PhyA; 1
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S Lett. 234:497-499(1988).

FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT AREA REFURESIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE REGION OF THE SPECTRUM AND THE PEFF FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
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              PF00360; phytochrome; PF00512; signal; 1. PF00989; PAS; 2. PF01590; GAF; 1.
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981	981 nValLeuIleThrCysGlnGlyLysGlyIleArgIleSerCysAsnLeuP 998	w
95		
998	998 roGluArgPheMetLysGlnSerValTyrGlyAspGlyVal 1011	11
66	66 AGCATTGCATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCG 17	
1012	1012 ArgLeuGlnGlnIleLeuSerAspPheLeuPheIleSerValLysPheSe 1028	28
16	16 TCCA 13	
1028	1028 rPro 1029	

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sp_invertebrate:Q93177 1363.50 28

sp_invertebrate:Q93VW7 725.50 11

sp_invertebrate:Q93VW7 725.50 11

sp_invertebrate:Q21808 654.50 11

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-Q=/cgn2_1/USPTO_spoo1/US09333427/runat_14042000_170514_19920/app_query.fasta.
-DB=SPTREMBL_12 -QEMT=fastan -SUFFIX=backtrans.rspt
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -MINMATCH=0.100 -XGAPOP=10.000
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sp_human:O94829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_invertebrate:096440
sp_virus:Q66951 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
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Q93115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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91.50 1
90.50
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alignment_scores:
Quality: 1653.50
Ratio: 4.593
7-4-41arity: 92.784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: Q93115 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                us-09-323-427-5/rev x Q93115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIMINOUNI M., BAZZICALUPO P.; "cut-1-like genes of Ascaris Gene 193:81-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ascaris lumbricoides (common roundworm).
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Ascaridida;
Ascaridoidea; Ascarididae; Ascaris.
                                          AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG
                                                                                                                                                                   GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
                                                                                                                                                                                                                                                                                                                                                 TGGACGTCAAGTTGCCGGAATTTCACTTCCACTTTGATTCATGCAATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTC
gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaTyrValLysGlyLeuTyrAspGlnGluGlyCysArgSerAspGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aIleProValAspAsnGlyValGluGlyGluProGluIleGluCysGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y {\tt GlyArgGlnValAlaGlyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerLeuProPheAspSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnValAlaglyIleSerCysAsnVa
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17 385
385 AA; 42408
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Percent Identity: 80.155
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CUT-1-LIKE CUTICLIN PROTEIN.
; BDEB1169 CRC32;
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30 2.63
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seq_name: sp_invertebrate:Q19707
_documentation_block:
Q19707 PRELIMIN
Q19707;
O1-NOV-1996 (TrEMBLr:
O1-NOV-1996 (TrEMBLr:
O1-JAN-1999 (TrEMBLr:
F22B5.3 PROTEIN.
                                                                                                                                                                                       381
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTTCTGCAACAT...AATGGACAACCTGTAATACTTGCTGCAGTACAA
                                                                                                                                                                                                                                                                                                                                                                          AATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAA 409
                                                                                                                                                                                                                          CAAATCAGAAGGCA 1
                                                                                                                                                                                                                                                                aValAlaLeuAlaAlaValValValValValSerPheLysLeuArgP
                                                                                                                                                                                                                                                                                                     CATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAATTTCGTC 15
                                                                                                                                                                                                                                                                                                                                     GluGlyIleCysMetSerProPheGlyPheSerIlePheMetGlyLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uAspIleSerAspArgAspGluAlaLeuProMetAspLeuArgHisArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlyAspTyrAspAsnThrLeuAspValArgThrAspPheSerAlaLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt ACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC.}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA
                     (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 09,
                                                                                               PRELIMINARY;
                      Last annotation
                                          Last sequence update)
                                                           Created)
                                                                                                 PRT;
                                                                                               389
                     update)
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RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONEIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA GRADNER A., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HANKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
PR EMBL; 250044; CAA90355.1;
RE EMBL; 250044; CAA90355.1;
SEQUENCE 389 AA; 42983 MW; 56B9543C CRC32;
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US-09-323-427-5/rev x Q19707
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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hrGlnValValProMetProIleCysLysTyrGluIleLeuAsnGlyGly
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: 4.177
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629179579196

CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCA

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Seq ID AC AC DT DT DT DT DT OC OC OC
                                                                                                                                                        seq_name: sp_invertebrate:018479
                                           O18479
O18479;
O1-JAN-1998
O1-JAN-1998
O1-NOV-1998
CUTICLIN-1.
                                                                                                                 _documentation_block:
O18479 PRELIMINARY;
MTCUT-1.
Meloidogyne artiellia.
Eukaryota; Metazoa; Nematoda;
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8 (TrEMBLrel.
8 (TrEMBLrel.
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                                                           05,
                                                        Last sequence update)
Last annotation update)
                                                                                       Created)
  Secernentea; Diplogasteria; Tylenchida;
                                                                                                                  PRT;
                                                                                                               433 AA
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alignment_block:
US-09-323-427-5/rev x 018479
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Ratio: 4.042
Percent Similarity: 77.751
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DE GIORGI C., DE LUCA F., DI VITO M., LAMBERTI F.;

"Modulation of expression at the level of splicing of cut-1 RNA
infective second-stage juvenile of the plant parasitic nematode
Meloidogyne artiellia.";

Mol. Gen. Genet. 253:589-598(1997).

EMBL; X96677; CAA65452.1; -.
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    Q9XVM7 PRELIMINARY;
    Q9XVM7;
    Q9XVM7;
    O1-NOV-1999 (TrEMBLrel. 12, L. O1-NOV-1999 (TREMB
MEDLINE; 9
BURTON J.;
"2.2 Mb of
                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi.
Rhabditina; Rhabditoldea; Rhabditidae; Peloderinae;
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIKEN L., ROOPAA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VANDERAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.1 Mc of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
[2]
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EMBL; Z81088; CABO3124.1;
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                                                                                                hrCysThrTyrGlnIleLeuSerGlyGlyProPheGlyGluProValGlu
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LeuLeuCysLeuTyrArgGluSerGlnValThrValAlaAsnAsnIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                         TCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGA::||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACC
{\tt PheGlyLeuIleGlyGlnGlnValTyrHisGlnTrpLysCysAspAsnAs}
                                                TTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGA
                                                                                                                                                TATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAA
                                                                                                                                                                                              {\tt rValAspGluIleSerThrIleSerTyrAsnValAsnLeuThrMetProTect} \\
                                                                                                                                                                                                                                                                                                                                             GTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGA
                                                                                                                                                                                                                                                                                                                                                                                               hrIleSerPheHisProTyrPheIleThrLysValAspArgThrTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uArgGlnArgValLeuAsnProLysGlyLeuAlaValArgThrThrIleT
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D 09XYU9

C 09XYU9;

C 09XYU9;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

DE CUTICULIN-1 (FRAGMENT).

OS Wuchereria bancrofti.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spi

Pilarioidea; Onchocercidae; Wuchereria.
                                                                                                                                                                                                                                                                          alignment_block:
US-09-323-427-5/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAMZY R., HELMY H., ADELY M., CURTIS K., WEIL G.;
"Wuchereria bancrofti L3 cuticulin-1 cDNA partial sequence.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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                  456
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                                                              {\tt ThrValAspThrPheCysAlaValHisSerCysPheValAspAspGlus}
                                                                                                                                                                                         ACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCTTTGTCGATGATGG
                                                                                                           yAsnGlyAspLysValGluLeuLeuAsnAlaAspGlyCysAlaLeuAspL
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                GAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATG
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                                               ysPheLeuLeuAsnAsnLeuGluTyrProThrAspLeuMetAlaGlyGln
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Quality:
Ratio:
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4.064
86.364
                                                                                                                            22602 MW;
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alignment_block:
US-09-323-427-5/rev
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
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LEWIS E.K., HUNTER S.J., TETLEY L., PAVIA NUNES C.,
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the cuticle.";
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GTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCG
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17

gValGlnCysPheTyrMetGluAlaAspLysThrValSerThrGlnIleG

34

17

ValIleSerPheHisProLeuSerValThrLysValAspArgAlaTyrAr AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTG

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alignment_block:
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                                                                     Percent Similarity:
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Q21808 PRELIMINARY;
Q21808; PRELIMINARY;
01-NOV-1996 (TrEMBLrel. 01
01-NOV-1996 (TrEMBLrel. 01
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., CALLAGHAN M.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULISTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
EMBL; Z49207; CAA89068.1;
SEQUENCE 290 AA; 33215
                                                                                                                                                                                                                                                                                                                                                                        "2.2 Mb of contiguous nucleotide sequence
elegans.";
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Ratio:
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(TrEMBLrel. 01, Last seq
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3.306
69.965
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                                                   Length: 283
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Percent Identity: 45.230
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US-09-323-427-5/rev x Q21808
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:::||||||||||:::|||
4 SerProArgGlyLeuPheLeuSerThrAsnValValValAlaPheAsnPr
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                                                                                                                                                                                                                                                                                                                     ThrAlaIleAlaAlaHisIleGluTyrGlu.AspSerGluIleIleSerA
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                                                                                                                    GTACGAACTGATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTT 185
                                                                                                                                                                                                                                        {\tt spTyrIleIleProAsnAspAspIleIleSerLeuAsnTrpLeuGlnArg}
                                                                                                                                                                                                                                                                                                                                                                                                                                        CA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTAAAGAACCAAATAGCGAA...TGTGTTCGACCACAATGTTCAGAAC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCCAGTTTATCATAAATGGACATGCGATTCTGAAAACCGTTGATACTTTC
                                     GCCAGTTGATTTACGTC.....
                                                                                                                                                         AsnPhe.....AspMetArgIleSer....
                                                                                                                                                                                                 AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGAT
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                                                                                                                                                                                                                                                                              roProArgArgArgSerAsnThrLeuProAlaProAspAspAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt rValLysGluProGlyLeuAspTyrCysAspValProSerCysProAspP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lys \verb|TyrAlaAspArgAspAsnMetTyrPheAspCysGlnIleSerIleTh|
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seq_name:

sp_invertebrate:Q21540

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alignment_scores:
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Q21540;
Q1-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1999 (TREMBLrel. 1
M142.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                _documentation_block:
                                                                                                                                                                                                                                                                                                  1033 TACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATC
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BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRETILE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VAUGHAN K., WATERSTON R.,
WELNSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.;
"2.2 M. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
EhAbditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
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EMBL; Z73428; CAA97806.1; -.
PFAM; PF00092; vwa; 1.
PRINTS; PR00453; VWFADOMAIN.
795
                            310
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                                                                                                                                                                                                                          244 rThrLysGlnProPheGluGlyAsnValPheValMetAspHisTyrHisA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MCMURRAY A.;
                                                                                                                                                                                                                                                                                                                               GlyThrProGluIleIleCysGlyProAspArgIleGlyValLysAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                                            ATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTT
                                                                                    GCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATC
                                                                                                                                                                                                          spGluGluCysArgAlaGlyProGluLysPheProAspSerArgSerIle
TACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAAT
                           isSerLeuPheMetThrLysThrAspGlnThrValLysValGlnCysPhe
                                                                                                                    TCTGAATCCACGTGGTATTTTGTAACAACAACTGTTGTCATTTCGTTTC
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Ratio:
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2.953
67.550
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Percent Identity:
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Last sequence update)
Last annotation update)
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seq_documentation_block:
ID Q19053 PRELIMINARY;
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MEDLINE; 9415
WILSON R., AI
BONFIELD J.,
                                                                                              SEQUENCE
MCMURRAY
                                                                                                                                                                                                                                                                                                                                                                                             213
                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernen
Rhabditina; Rhabditoidea; Rhabditidae;
                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1999 (TrEMBLrel. 09,
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                               SEQUENCE FROM N.A. MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                     Q19053;
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                                                                                Submitted (OCT-1995)
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yrGlyAspArgValAspIleLeuAspSerAsnGlyCysGlyLeuAspAla
                                                                                                                                                                                                                                                                                                                                                              LeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAGAACCGGAGAATATCATTGATGTACGAACTGAT...ATCAACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATT
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 AINSCOUGH
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                 R.,
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CONNELL M., COPSEY
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                                                                              EMBL/GenBank/DDBJ
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                                                                                                                                           Secernentea; Rhabditia; Rhabditida;
oditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                    PRT;
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BAYNES C. OPSEY T.,
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                С.,
                                                                                databases
 COOPER J., COULSON A.,
                 BERKS
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alignment_scores:
    Quality:
    Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HISTER N., JIER M., JOHNSTON L., JOHNSTON L., JOHNSTON L., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., RODERA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER B., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; "2.2 MD of contiguous nucleotide sequence from chromosome III of C. elegans."; Califolia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1033 TACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
EMBL; 266496; CAA91280.1;
SEQUENCE 484 AA; 53325
  194
                                            536 TTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG
                                                                                                                                                                                                                                                                                                                                                                                    128
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                                                                                                                                                                                       TyrHisLysTrpThrCysValAlaGluLeuGluAsnValTyrCysMetLy
alIleAspAlaAsnGlyCysSerValAspGlyValIleLeuGlnAsnLeu
                                                                                                                                      TGTCCATTCCTGCTTTGTCGATGATGGT...AACGGTGATACTGTGGAAA
                                                                                                                                                                                                                TATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGT
                                                                                                                                                                                                                                                                                      luAla...GlyGlySerProIleLysTyrAlaArgIleGlyAspGlnVal
                                                                                                                                                                                                                                                                                                                                     GTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCT 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyGluProGluValValCysGluThrAlaSerIleSerLeuLeuPheLy
                                                                                         {\tt sValHisSerCysThrValTyrAspGlyGlnGlyGlyProProValThrV}
                                                                                                                                                                                                                                                                                                                                                                                  uLeuGluSerGluThrGlnLeuProValCysArgTyrGluIleLeuAsnG 145
                                                                                                                                                                                                                                                                                                                                                                                                                               TCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrLysLysValHisAsnHisValAspIleSerAlaLeuThrThrGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leThrLysIleAspArgAlaTyrArgValSerCysPheTyrValGluGly 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                luProSerCysMetThrValGlyAspGlyLysThrGlyHisArgPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sThrArgAsnSerPheAsnGlyLysValPheValLysGlyTyrValSerG
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3.199
74.104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6AEFC669 CRC32;
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alignment_block:
US-09-323-427-5/rev x Q93532
                                                                                                                                                                                                                                                                                                          alignment_scores:
    Quality:
    Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_invertebrate:Q93532
                                                                                                                                                                                                  Align seg 1/1 to: Q93532 from: 1
                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                     1152 CGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCC 1103
                  1052 CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTAT 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILSON R., AINSCOUGH R., ANDERSON K., BAXNES C., BERKS M.,
BONFIELD J., BUTTON J., CONDELL M., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DUBLIN R., FAVELLO A., FULTON L.,
CRAXTON M., DEAR S., DU Z., DUBLIN R., FAVELLO A., FULTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MCRIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.;
"2. 2 M. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
EMBL; Z78542; CAB01742.1;
SEQUENCE 315 AA; 35785
                                                                                                                                                                                                                                                                                                                                                                                                                                                         elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATSON A., WEINSTOCK L., WILKINSON 2.2 Mb of contiguous nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F20D1.8
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                                                                                                                            30
                                                    41 nIleAspAsnGlyLeuGlnGlyGluProLeuIleArgCysGlySerGluS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gln 261
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94150718.
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                                                                                                                                                                                                                                                                                         578.50
3.029
67.972
                                                                                                                                                                                                                                                                                                                                                                                                      35785
                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                         Percent Identity: 40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                    CD2B4B3D CRC32;
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seq_documentation_block:
ID Q22164 PRELIMINARY;
AC Q22164;
DT 01-NOV-1996 (TrEMBLrel 01)
DT 01-NOV-1996 (TrEMBLrel 01)
DT 01-JAN 1999 (TrEMBLrel 09)
DE T04F8.4 PROTEIN.
GN T04F8.4 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemato
OC Rhabditina; Rhabditoidea;
RN [1]
RP SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                seq_name: sp_invertebrate:Q22164
                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 sLeuAsnAspProSerThrGluGluArgIleSerTyrAsnValProLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AlaPheAlaThrValGlyGlnIleValTyrHisGluTrpSerCysGluAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 GluGlyGlyThrValSerHisThrThrGlyAspGlnLysLysLeuHisLy 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 lnArgSerSerAsnProLysGlyIleMetMetThrAlaThrIleIleIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   952 TCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTA 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 uSerGlnValAsnLeuThrValSerTyrSerAlaCysAspValIleArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt aProGlyGlnAsnGlnThrSerProPheCysValThrValHisSerCysA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T......GAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCTGCT 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTAT 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nCysPheTyrAlaGluAlaGlnLysThrValThrGlnGlnLeuAsnValA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACA
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                                                                                                                                                                                                                                                                                                                                                                                 uThrGlyGlyGlnLeuSerGlnValCysSerTrpThrValArg
                                                                                                                                                                                                                                                                                                                                                                                                                           AATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTT
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                                                                                                                                                                    (TremBLrel. 01, Created)
(TremBLrel. 01, Last seq
(TremBLrel. 09, Last ann
                                                oda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470
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alignment_block:
US-09-323-427-5/rev x Q22164
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WILSON R., ALNSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

WALLSON R., ALNSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

AN JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,

PARSONS J., PERCY C., RIFKEN L., ROPPRA A., SAUNDERS D., SHOWIKEEN R.,

AN JONES J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON J.,

THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: 022164 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1099 TGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAA 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
EMBL; 266565; CAA91480.1; -.
SEQUENCE 384 AA; 43964 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1995) to
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AGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCG
                                                                                                                                              laIleAspValSerAsnLeuProThrGluSerValGlnSerAspLeuPro
                                                                                                                                                                                                                                                                                                                                                                       ACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTTGTAACAACA 865
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                                           MetProThrCysSerTyrThrIleArgArgAspGlnLeuAspGlyProIl 176
                                                                                              ATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACC
                                                                                                                                                                                            AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
                                                                                                                                                                                                                                                                                           ATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCAC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                         \verb|snMetAspArgGlnArgMetIleAlaProGluGlyMetMetPheSerThr|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pGlnPheGlyArgProValGlyGlyIleLysLeuAsnHisGlyAlaCysA
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                                                                                                                                                                                                                                             aTyrHisIleArgCysMetTyrLysGluAlaAlaArgThrValThrAlaA
                                                                                                                                                                                                                                                                                                                                           ValLeuIleIleSerPheHisProLeuPheLeuThrArgMetAspLysAl
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Ratio:
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2.240
61.929
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Gaps: 9
Percent Identity: 31.218
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615
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seq_name: sp_invertebrate: Q9XVN2
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SEQUENCE FROM N.A. MEDLINE; 94150718. WHITE S.; "2.2 Mb.of contiguo"
                                                                                                                                                                                     O9XVN2 PRELIMINARY;
O9XVN2;
O1-NOV-1999 (TrEMBLrel. 12,
O1-NOV-1999 (TrEMBLrel. 12,
O1-NOV-1999 (TrEMBLrel. 12,
                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
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                                                                                                                                                      F53B6.6.
                                                                                                                                                                        F53B6.6 PROTEIN.
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                                                                                               Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              argPheGlnCysGluIleArgLeuCysLeuLysAsp...AspGlyGlyCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTA...A
                                                                                                                                                                                                                                                                                                                                                             alValValTyrHisArgTyrCysLysAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eLeuLysTyrAlaLysValGlyAspGlnValValHisArgTrpGlnCysA
                                                                                                                                                                                                                                                                                                                                                                                                                                          aValThrPhePheThrPheIlePheValLeuPheValThrThrIleLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrPheLysProLysAspAlaAsp.....MetPheSerGlnThrVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAspGlyGluGlyGluLysGlnMetTleTleAspGluArgGlyCysHi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTCTGAAACCGTTGATACTTTCTGCGCGCGTTGTCCATTCCTGCTTTGTC 565
                                                                                                                                                                                                                                                                                                                                                                                                 TTACCATTTCGTTTAAATTTCGTCCAAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...LeuAspProGlnThrIleCysLeuAlaProLysLeuLeuValValAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGCAGTACAAAATGGAATCTGCATGTCACCA.....TTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        luIleArgGlu.....
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                                                                                           Nematoda; Secernentea; Rhabditia
pidea; Rhabditidae; Peloderinae;
   nucleotide
                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     PRT;
   sequence
                                                                                                                                                                                                                                                                     610
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 from
                                                                                                                 Rhabditia; Rhabditida;
   chromosome
                                                                                               Caenorhabditis.
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     III
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9XVN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-323-427-5/rev x Q9XVN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1040 ATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
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JONES M., KERSHAW J., KIRSTEN J., LAISTER N., CALLAGHAN M.,
LIGHTNING J., LOVD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
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SMALDON N., SMITH A., SONHAMMER E., STADEN R., WATERSTON R.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
EMBL; 281086; CABO3116.1;
SEQUENCE 610 AA; 68585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 yValValGlyLysProGluValPheCysGlyIleAspThrIleArgValL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGATCAAGAAGGTTGC.....CGTAATGATGAAGGTGGACGTCAAGT 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTACACTTATTGCATTGTCTTATTCG.....ATTCCGGTTGACAATGG 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrLeuHisProArgGlyIleSerPheSerPheThrMetIleThrSerPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HisProPhePheValThrGlyMetAspArgAlaPheSerIleArgCysPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTT
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TGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATA
                                                                                                  HisLeuLysAsp...GlyIleGluGlyHisValLeuArgPheAlaGlnVa
                                                                                                                                                                                               GAAATTTTGGATGGACCAACCGGTCAACCAGTTCAATTTGCTATCAT
                                                                                                                                                                                                                                                                                           eu \verb|AlaProGlnHisValAspGlnGluTyrSerLeuProValCysAlaTyr|
                                                                                                                                                                                                                                                                                                                                                                                                   TCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ePheLeuGluSerIleLysGlyLeuAsnAlaGluIleAspValGlyThrL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCA 1041
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Identity: 37.407
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                       WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
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PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      באגייט.
Caenorhabditis elegans.
Caenorhabditia; Rhabditiqa;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditiqa;
באראלודיוחא: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Q93967; Q94405;
01-FEB-1997 (TrEMBLrel. 02,
01-NOV-1998 (TrEMBLrel. 08,
01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                  Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOBSON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                           LENNARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAATGTTCA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnLeuCysTyrLysHis...AspGlyGlyCysGluGlyIleThrProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATAATTTGGAATATCCAACAGAT...TTAATGGCTGGCCAAGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oGlnCysSer 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTATTACCATTAAAGAACCAAATAGCGAATGT......GTTCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isValPheLysTyrAlaAspLysValGlnLeuTyrPheThrCysThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uProGlnIleGluTyrGluHisGlyAlaIleSerAlaTyrThrAsnAlaH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt LysPheGluLeuValAspAspArgGlyCysSerThrAspProPheLeuLe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_invertebrate:Q93967
Quality:
                                                                                                            440 AA;
     477.50
                                                                                                              49299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                            3F2BBBA2 CRC32;
Length:
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US-09-323-427-5/rev x Q93967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1005 TATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                914 ATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleProGlyCysThrTyrSerIleHisArgSerThrIleAspGluLeuAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yAsnGlnLysThrArgLysProHisPheAspLeuGlnPheGlyAlaCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTT
CATTAAAGAACCAAATAGCGAATGT.....GTTCGACCACAATGT.
                                                   LysPheAlaAspLysProGlyValTrpPhePheCysGlnValGlnMetCy
                                                                                                      AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC
                                                                                                                                                         leArgTyrSerSerAspLeuGlnArgAlaTyrAlaGluSerSerValPhe
                                                                                                                                                                                                               TGGAATATCCAACAGATTTAATG...GCTGGCCAAGAAGCTCACGTATAC
                                                                                                                                                                                                                                                                     pValIleAspAspLysGlyCysProIleAspProIleLeuIleThrGlyI
                                                                                                                                                                                                                                                                                                                           AATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT
                                                                                                                                                                                                                                                                                                                                                                              ValLeuIleAsnAsnCysTyrValThrAspGlyPheGlyLysLysAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rgValLeuHisGlnTrpHisCysAsnAspGln.....MetTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTGGA...CCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCAGTATGCCGTTATGAAATT.....TTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         luLeuGlyValSerMetIleProThrThrGluLeuGluAlaArgHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrValValValSerPheHisProLeuPheIleThrLysValAspGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lyMetLysSerLeuArgSerValAspProArgGlyMetTyrTyrGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTCAAGTTGCC......GGAATTTCACTTCCATTTGATTCATGCA 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spGluIleArgIleTrpValLysThrArgLysIlePheAlaGlyArgIle
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217

200 589

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170 686 153 120 815

715 137 765 865

87

103

70

956 53 1006 37

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Ratio:
2.296
65.000
Percent Identity:
       Gaps:
33.438
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sMetLysLys...HisGlyMetCysAspGlyIleThrProProSerCysG

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alignment_scores:
Quality:
Ratio:
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US-09-323-427-5/rev x Q23097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURFON J., CONNELL M., COPERY J., COOPER J., COULSON A.,
RA BONFIELD J., BURFON J., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GRADNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA THIERRY-MIEG J., THOMAS K., VANDIN M., VAGHAN K., WATERSTON R.,
RA WATSON A., WEILSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTON C.L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTON C.L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTON C.L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTON C.L., WILKINSON-SPROAT J., WOHLDMAN P.,
RA WATSON A., WEILSTON C.L., WILKINSON P.,
RA WATSON A., WEILSTON C.L., WEILSTON C.L., WILKINSON P.,
RA WATSON A., WEILSTON C.L., 
                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
Q23097 PRELIMINARY;
                                                                                                                                                                                                                                                                 1077 CCAGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACG 1028
                                                                                                                                                                      1027 TAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313
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                                                         977 GTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCA 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILKINSON J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W01A8.3 PROTEIN. W01A8.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 lySerMetSerArgValIleSerValGlyGlyGluAspAsnGlyGlyPhe 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditina; Rhabditoidea;
      81
                                                                                                                     64
                                                                                                                                                                                                                                     48
                                                                                                               rLysProPheArgGlyAsnIlePheValLysGlyArgAlaLysAspLysS
erCysArgGlnSerTyrAlaAsnAsnGlyThrAsnSerTyrSerLeuPro
                                                                                                                                                                                                                                  ProLysValIleCysAlaGluAsnAspLeuAlaLeuAspIleValThrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rProLysPro 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAGAACCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGluGluLysAlaProSerSerArgArg.....LysThrTh 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....TCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCC
                                                                                                                                                                                                                                                                                                                                                     to: Q23097 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476.00
2.235
59.167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 31.389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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6
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   97
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351	laProSerProPheCysValProArgLeuLe	336
58	CATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAGCAT	107
335	<u> </u>	334
108	ATAATGGACA	157
ω i	. ::: : ubeuValLeuAspProAlaAspArgG	324
CT .	TTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGC	207
323	luAlaAspArgSerAspTyrGluIleAspValAlaThrSer	307
208	agaaccggagaatatcattgatgtacgaactgatatcaacacccttg <i>a</i>	257
307		304
258	GTTTACTCAAGAAAAGATC	307
303	euLeuSerGluAl	295
308	TCAGAACCACAAGGATTCGGAGCTGTTAAAA	351
294	MetCysGlnGluValThrProProAsnCysGlyValLysL	278
352	CCAAATAGCGAATGTGTTCGACCACAATG	383
278	AspSerAsnGlnLeuTyrPheThrCysGlnIleArgLeuCysGl	261
384	TCAATGCCAGATCAGTATTACCATT	433
261	Ĥ	245
434	CAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATG	480
244	spPheAspG1yCysAlaThrAspProPheLeuLeuSerGluLeuSerTyr	228
481	TGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTTGGAAT	530
531 228	> ര്	580 211
211		198
581	AAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTT	630
197	ProThrLe	181
631	ACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTT	680
8	:::: rAspSerMetValMetProLysCysGluTyrSerValArgArgAs	
681	CCCGATGCCAGTATGCCGTTATGAAATTTTGGATGC	730
164	GluIleValThrGlnAsnIleAspValSerMetIleProThrThrGluLe	148
731	AAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTT	780
147		131
781	CAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCT	830
131	:::	114
831	TTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGT	877
114	LeuGlyLysCysGlyMetGlnArgLeuArgSerAlaAsnProArgGlyVa	9 1
878	AATCCACGTGGT	927

57

TTGATTGCTGCCGTCATTATTACCATTTCG

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alignment_block:
US-09-323-427-5/rev x Q22680
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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Q22680 PRELIMINARY;
                                                                                                                                                     1009 TGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAG 960
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                                                                                                                                                                                                                                                                                                               1109 CGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGA 1060
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MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILLSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A. BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A. BONFIELD J., BURTON L., DURBIN R., FAVELLO A., FULTON L., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JOHNSTON L., JOHNSTON L., CONSES M., KERSHAW J., KIRSTEN J., LAITEILLE P., CALLAGHAN M., LIGHTNING J., LLOYD C., MCMURRAY A., MORFIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., PROMES K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; "2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z49071; CAA88879.1; -. HSSP; P03000; lTIF. SEQUENCE 609 AA; 68882 MW;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                         959 GTGGACGT.....CAAGTTGCCGGAATTTCACTTCCATTT...GAT 922
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Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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T22C8.7.
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                                      73
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                                                                                                                                                                                                                                                                                                                                                      20 AspAsnSerAsnTyrAsnPhe...TyrTyrThrHis......me
                                                                                                              CCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACA 1010
TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGT
                                  ysThrArgLeuThrAsnArgProIleValMetAspLeuProPheArgGly
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65.854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 287
Gaps: 11
Percent Identity: 37.282
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Rhabditidae; Pelc
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Peloderinae; Caenorhabditi
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872
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188
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285 ProIleLys
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                                                                                                                                                                                                          ATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAA
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                                                                                                                                                                                                                                                                                                                  GATTTAATGCCTGGCCAAGAAGCT...CACGTATACAAATATGCGGGATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTT 772
                                                                                         snGlyCysGluGlyIleSerProProIleCysArgProMetAspLeuGly
                                                                                                                                    ATAGC...GAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGA
                                                                                                                                                                                  nValMetValHisPheSerCysGlnIleThrThrCysGlnLysGlnGluA
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Title:
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Maximum
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Gapop 10.0 , Gapext 1.0
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1161
1 tgccttctgatttggacgaa.....gcaataagacgaatcatcat 1161
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Copyright (c) 1993 - 2000 Compugen Ltd
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45: gb_htg7:*
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49: em_hum5:*
50: gb_pl3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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)0 Helicoba	Euglena	Homo sap	AF044022 Eurytides	0	repto	67 Homo	Homo sap	Dictyost			Chartenant Cachornan	2 5	⊃ !	79	0 Arabidops	Caenorha	575	Z66565 Caenorhabdi	1 Homo sap	Z98551 Plasmodium	Z49071 Caenorhabdi	/608 Caenorha	18 Caenornabo	UZ3449 Caenornabol	ALUUGGGU CAENOFNAD	100880 Cacacata			7/0011 Caenorhabdi	II41264 Caenorhabdi	Z71267 Caenorhabdi	Z81143 Caenorhabdi	273428 Caenorhabdi	Continuation (4 of	Caenorhabd	Caenorhabd	aenorhabd	Caenorhabd	8 Brugia	617 Bruqia m	7 M.artiel	5 As	25580 Wucherer	5997 C.elegans	125 Caenorhabd	044 Caenorh	Description	

RESULT 1
CEF22B5
LOCUS
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

CEF22B5 25823 bp DNA INV 02-SEP-1999 Caenorhabditis elegans cosmid F22B5, complete sequence. 250044 250044.1 GI:899234 Edition factor; GTP-binding ADP-ribosylation

ALIGNMENTS

745. 745. A EST	Current sequence fliishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both dye primer and dye terminator reaction, from distinct subclones Exceptions are indicated by an explicit note. IMPORTANT: This sequence is NOT necessarily the entire insert the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a sequence, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone F22B5 is at 24607 in sequence 265522. The true left end of clone F22B5 is at 16002 in sequence 265523. The true left end of clone F22B5 is at 16002 in sequence right end of clone F12B5 is at 4610 in this sequence. The start of this sequence (1101) overlaps with the end of sequence 265523. The end of this sequence (2572325823) overlaps with the star Location/Qualifiers Location/Qualifiers **Corporison** Capacity Sequence** Ca	O'Callaghan, M. Parsons, J., Percy, C., Ricken, L., Roopra, A., Saunders, D., Shownkeen, R., Smildon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P. TITLE 2. Mb of contiguous nucleotide sequence from chromosome III of C elegans Nature 368 (6466), 32-38 (1994) MEDLINE 94150718 REFERENCE 10bases 1 to 25823) AUTHORS Sims, M. Direct Submitsion Solinetted (13-UL-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, usin predictions from Genefinder (P. Green, U. Washington), and other available information For a graphical representation of this sequence and its analysis bin/display?db-wormace&class=Sequence &object=F22B5	factor; Phenylalanyl-tRNA synthetase; RNA binding. SOURCE Caenorhabditis elegans. Caenorhabditis elegans Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditoidea; Rhabditidae; Peloderinae; Cae REFERENCE 1 (bases 1 to 25823) AUTHORS Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J. Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Fave Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L. Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, Latreille, P. Lighting, T. Lloyd C. Mawarray A. Mort
.1127,12161471) protein; cDNA EST yk390d8.5 yk499d6.3 comes from this	ria for the C. elegans genome Il bases are either sequenced r on a single strand with both a action, from distinct subclones. Illicit note. necessarily the entire insert of shorter because we only sequence oper because we arrange for a small missions. The entire insert of clone F22B5. Y sequence overlapping sections ge for a small overlap between is at 24607 in is at 25723 in this sequence. The at 4610 in this sequence. The overlaps with the end of sequence .25823) overlaps with the start of	ifken,L., Roopra,A., mith,A., Sonnhammer,E., Thomas,K., Vaudin,M., instock,L., from chromosome III of C. instock,L., in	ns. ns. ns. ns. ns. Nematoda; Secernentea; Rhabditia; Rhabditida; pidea; Rhabditidae; Peloderinae; Caenorhabditis.), R., Anderson, K., Baynes, C., Berks, M., J., Connell, M., Copsey, T., Cooper, J., M., Dear, S., Du, Z., Durbin, R., Favello, A., N., Green, P., Hawkins, T., Hillier, L., Jier, M., M., Kershaw, J., Kirsten, J., Laister, N., M., Kershaw, J., Kirsten, J., Laister, N., M., Kershaw, J., Kirsten, J., Laister, M.,
. gene	gene CDS	gene CDS	gene CDS
1157811832,119171215 1157811832,119171215 /gene="F22B5.5" /codon_start=1 /protein_id="CAA90357.1" /protein_id="CAA90357.1" /db_xref="G1:3876229" /db_xref="G1:3876229" /db_xref="G1:3876229" /db_xref="G1:3876229" /translation="MNGCKQSASKVF" EQIKQFQKLVCDFNIKLLKETMEDN SDSTYLSGTQKITYKSLNRSIPDFQT GGCVDSKYAAVWRKVLHTKVRGFTYY YDNSIFPYERKEVILAKFKNGVGRVA AAQAIFQSIIQDLPMKDLKDVLVRCS PDGLNFSKVFVSSNPSNAPC" complement(1224014032)	/db_xref="spTrEMBL:019707" /tanslation="MARYSLGLGLCL" TRNAFEGHYYVKGLFDQOECRNDEGG VVSFHPQFYTKVDRAYRVQCFYMEAD GGPTGEPVQFATIGQQVYHKWTCDSE DKFLLNNLEYPTDLMAGGEAHYYKKJ 10234 FEAVKQANQTAQFFRULKKRSAPVME REIGEDSFRQELCISSFHISVVTVFL 9691. 10234 /gene="F22B5.4" /join(9691. 9890,9940. 1.0 /gene="F22B5.4" /ootc="cDNA EST yk304c8.3 yk304c8.5 comes from this from this gene" /codon_start=1 /protein_id="CAA90356.1" /db_xref="GTREMBL:019708" /translation="MSLSKAPKKTMF SRNWSRDPFFWKVAIQKGDTPYOFLV KAEIWLGRSNSKAPWDWERLRDTYWK RGTR" Complement(10849. 12154) /gene="F22B5.5"	//bb_xref="GI:3876255" //db_xref="SUISS-PROT:0197 /translation="MGFLKILKRQRY EPTLGFDIKTVHFRDF0LMLWDVGGG SEELKKLLGEERLAGASLLVLANKSI HSIKSHHWKIFSCCALSGDRLVQAMY complement(383.4393) /gene="F2285.3" /gene="F2285.3" /gene="F2285.3" /gene="F2285.3" /gene="F2285.3" /gene="F2285.3" /gene="F2285.3" /gene="F2285.3" /gene="F2285.3" /gene-"F2285.3" /gene-"F2385.3" /gene-"F238	/translation="MAPAPEVVSWAE VVTOPKVINKKVPKVVADRKKWVKFG ILDVQEDKQTAKTTSREHCRHCKGNL MRPDGRQIDRNNSDENTCRVTNLPQE FAFVTFESRDDAARAIAELNDIRMYH 18702668 18702668 join(18702158,220923 join(18702158,220923 /gene="F22B5.1" /note="similar to GTP-bind /codon_start=1

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ene="F22B5.3"
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b_xref="GI:3876225"
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in(1870. .2158,2209.
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"TQfkvInkrvpkvvadrkkwvefgsckgepagdvattyvaeevbmoftrnrageq
DVQEbKQTaktTsrehgchgkokwsthcpvkvmygldebadadkotebavamg
(PDGRQIDrnrsdentcrvtnlpQemnedelrdlfgkIgrvIrIfirardkvtglpkg
                                                                                                                 IKSHHWKIFSCCALSGDRLVQAMTWLCDDVGSRLFILD"
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note="similar to cuticulin; cDNA EST EMBL:T01970 comes rom this gene; cDNA EST CEESX90RB comes from this gene; bNA EST EMBL:T00412 comes from this gene; cDNA EST EMBL:T00412 comes from this gene; cDNA EST k386c7.3 comes from this gene; cDNA EST y886c7.5 comes rom this gene; cDNA EST y886c7.5 comes rom this gene; cDNA EST y890cb12.3 comes from this gene; cDNA EST x652bB.3 comes from this gene; cDNA EST x652bB.3 comes from this gene" ID_xref-"Sptrembl.Q19707"

ID_xref-"Sptrembl.Q19707"

Lyans Lation="MarySlGLGLCLLVASVSAIPVDNNVEGEPEVECGPTSITVNFN

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om this gene"
codon_start=1
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b_xref="GI:3876228" in(9691. 9890,9940. 10234)
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sote="cDNA EST yk304c8.3 comes
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ITAGNS! Action="MNGCKQSASKVFKLVGGFNKASSRCFSSEKLIPKDLKIVKNPTS

ITAGNS! Action="MNGCKQSASKVFKLVGGFNKASSRCFSSEKLIPKDLKIVKNPTS

ITAGNS ITAGNE ACTION nplement(12240. .14032)

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TTGATAGAAAAGTTGAGAACGATCAGCGTATTTGTAGACGTGAGCCTCTTGTCCAGCCAT
                                                                                                                    AGAGCACGTTGGGCGAGCACACTCCTCATTTGGTTCCTTAACAGTAATGGAAATCTGGCA
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ROLDLVPAKQPKGFIKAVVPVFGKLTGDADQDVREASLQGLGAVQRIIGDKNVKNLL
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LDPKANYGALVERLOKVLEKDANINVAALAANCITGIANGLRTKFQPFAVSVTPIIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="limited similarity with the elongation factor EF-3 (Swiss Prot accession number P25997); cDNA EST EMBL:C12588 comes from this gene; cDNA EST y349b7.5 comes from this gene; cDNA EST y442b2.5 comes from this gene; cDNA EST EMBL:M89075 comes from this gene; cDNA EST EMBL:M89075 comes from this gene; cDNA EST y421d3.3 comes from this gene; cDNA EST y421d3.5 comes from this gene; cDNA EST y442ld3.5 comes from th
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20672. .21000,21677. .21812)
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/db_xref="GI:3876232"
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Pred. No. 4.1e-70;
""" matches 233;
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ACGTGTCCCTCGAAGGCATTACGTGTGTTGAAGTTTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggattcagagatcgtgtacgcgcaacattgcatgaatcaaatggaagtgaaattccggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttggtaacaaataatggatgaaacgaaatgacaacagttgttgttacaaaaataccacgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGTGACAAATTGGGGATGGAAAGAGACGACGACAGTTGTGGTAACGAAGACTCCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAACCTTCAAGAAGCATTCCTTAAAAATTACAGAAGTTTCATAGTCTTACCGATCAACC
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Caenorhabditis
Z49125
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                                                                                                                                                                                                                                                                                                                                                   HTG; Cuticulin; Fork he Caenorhabditis elegans Caenorhabditis elegans
Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernent Rhabditina; Rhabditoidea; Rhabditidae;
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TITLE

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Mb of contiguous nucleotide sequence from chromosome III of C

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AUTHORS
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IMPORTANT: This sequence is not the entire insert of clone C47G2. It may be shorter because we arrange for a small overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-APR-1995) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The true left end of clone T24F1 is at 34731 in this sequence. The true right end of clone T05B9 is at 12750 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighbouring submissions.
The true left end of clone C47G2 is at 1 in this sequence. The true right end of clone C47G2 is at 6388 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available information.
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15433. .17108
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join(15433. .157
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LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGICLTP
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                                                                                                                  IGFASFLGIGTIVATALSATIFYVARPTSHKH"
                                                                                                                                                                                                                                KFLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKDPGSECARPTCSEPQGF
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/gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="cut-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:6239"
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   .15770,16205.
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   .16531,16772.
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gene CDS

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/codon_start=1

from this gene; cDNA EST yk486d7.5 comes

from this gene"

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EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 comes from this gene; cDNA EST EMBL:C11456 comes from this gene; cDNA EST EMBL:C1331 comes from this gene; cDNA EST EMBL:C1331 comes from this gene; cDNA EST yk358b10.3 comes from this gene; cDNA EST yk30164.3 comes from this gene; cDNA EST yk301f4.3 comes from this gene; cDNA EST yk301f4.5 comes from this gene; cDNA EST yk301f4.5 comes from this gene; cDNA EST yk305f2.3 comes from this gene; cDNA EST yk305f2.3 comes from this gene; cDNA EST yk305f2.5 comes
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RVYWSAQLLTWLLLPLQSYVTAGNFTILGKIRAVVINNALYYAIYSLCFLAILIYA
MFKGVSINIENLKVIVVSASNTWGLFLLVVLLGHGLVELPRSLWHHGNRHYRLRKTYF
DIEKLASEKSEABENVKDIYKKVRVLFNSMKNDSNGQRKVRFILLSKYSDDVIDNLFP
SRQVIDNAHLDESGPCSEAKLISLHKKTIYAPQTLNNATAOMKVLVDRALFLENLAFS
ESNGYNLELSRNTCVPIGVRFWYTRLQTPFCXILGIVTVFMTFFVLFSCTTFFVVSY
TLSPAAFVTEYASTRFHYKYTQFVAFGIIVLITSAYFTIFRQTYKYYHLDPNGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(24417. .24975,25043. .25176,25237. .2552
25668. .25907,25967. .26054,26106. .26227,26277. .26608,
26681. .26785,26846. .26914))
/gene="C47G2.4"
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FEYYKEKFPAMQNSIRHNLSLNDCFVKVARGPGNPGKGNYWALDPNCEDMFDNGSFLR
RRKRYKKNSDTYHEMMSHHPMPFPPFLPQGMPFPPRMMHPMANIPMLGHPMNPRAVPN
MPAFFIPQNIDSQKLLSMMASRIMPMDAPVSSGQKRTSSSSSPNENGSSAVSDKLSA"
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/note="cDNA EST CEMSB75F comes from this gene; cDNA EST EMBL;C13621 comes from this gene; cDNA EST yk27d8.5 come from this gene; px257e7.5 comes from this gene; cDNA EST yk257e7.5 comes from this gene; cDNA EST yk319c4.5 comes from this gene; cDNA EST yk335b12.5 come; yk331d4.5 comes from this gene; cDNA EST yk335b12.5 come;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENSILFSAILLCRLTPPICLNFLGMIHMDSHISMAKSFGIETQFTKLMGHLDVIPILA
KGINIYLPICIILLCAIHYYRVGAYVLHNIGFDQFVEADEMTNDMINSGRSLVQIERN
SIKRSNDRSQRTQNWTNSFGSSNAGNGSTTSKFKRSNKNDEERPMLEDDDEEVEESST
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/db_xref="GI:3875032"
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/db_xref="GI:3875031"
                                                                                                                                                                                                                                    /gene="C47G2
                                                                                                                                                                                                                                                                          join(30076. .30134,30184. .30492,31050. .31274,31321. .31480,
31534. .31653,31701. .31835,31889. .32104,32160. .32570,
2639. .32935,32998. .33215,33263. .33651,33802. .34049)
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/translation="MLFSMESILSSTKPKLEPPPKLEPEVTINEQVVDLPRSNTRLSE
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              cDNA EST yk335b12.5 comes
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CDS

BASE CO

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REFERENCE
AUTHORS
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SOURCE
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ACCESSION
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Best Local
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hes 409;
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                                                                                                                                      C.elegans
M55997
                            Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Ca
1 (bases 1 to 2310)
Sebastano, M., Lassan
                                                                                    C.elegans DNA.
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MDETILKI IADNILIVEEGCPAEELYKKSALISASAKILEAF INFVSNAPAQOLEEI
ERNLIEERHYSYGLMRCOMDNDYEHSYQDDERIVESILANKLPNILOYLRDIEAN
GSVWQPLLRLIIELCNTNCMSTHEKIAVAFRSLPFINLIKAAKMLPRASVLHCLLVKV
VILLLIBSTPCDELSPAAEYLLTEGGLLONIVDTATSENPGSSVACSGLRSFNONLGD
AINRAKKAGIPNQKLLAILSADNTWTELEDIIIHLYNLKHRQMQHDFNDSSVVSSIRN
DSHGFNDSEWTDASTKRAEMDATSSAKQAFSGTSSPERNMQRFSDFEGQFDDTPDE
DEFRKLCSERANSSSCAGISFTSPIKWPGEAEKTSEKASEPPSVVASTYPQQTNGNQ
DEFRKLCSERANSSSCAGISFTSPIKWPGEAEKTSEKASEPPSVVASTYPQQTNGNQ
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WADFSSFPTISPTAAANSASSSSSDAWPGSDIHLQGEASDWPLNNSHESKASDPVMVG
LAASISHPGDSSEA"
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Pred. No. 1.8e-66;
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Bazzicalupo, P
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nes 393; Conserv
                gaccaatgatagcaaattgaactggttgaccggttggtccaccatccaaaatttcataac 701
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 GTCCGATGGTGGCGAACTGGATTGGTTGTCCGGATGGTCCTCCGTCAAGGATCTCGTATT
                                                                                                                                         catcagcatttagaatttccacagtatcaccgttaccatcatcgacaaagcaggaatgga
                                                                                                                                                                                     TTTGGCATTGATAGAAGAGTTGGGAGCGATCGGCATATTTGTAGACGTGAGCTTCTTGGC 154:
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                                                                           caaccgcgcagaaagtatcaacggtttcagaatcgcatgtccatttatgataaactggct 641
                                                                                                                          CTTCTTCGTTAAGAATCTGAACGGTGTCGCCATTACCATCATCGACAGTGCAAGAGTGAA
                                                                                                                                                                                                                                                                  tctggcattgatagaaaagctgtgatcgatccgcatatttgtatacgtgagcttcttggc 461
                                                                                                                                                                                                                                                                                                              GTGGCTCTGAGCAAGTTGGACGGCACATTCGCTTCCTGGGTCCTTGATGGTGATGGAGA 1601
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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GGPSGQPIQFATIGQQVYHKWTCDSETTDTFCAVVHSCTVDGKGDTVQILNEEGCAL
DKFLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKDPGSECAPETCSEPQG
FGAVKQAGAGGGAHAAAAPQAGVEEVQAAPVGAAPVAAAAAAAAPAVPRATLAQLRL
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567 c 433 g
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/protein_id="AAA27995.1"
/db_xref="GI:156272"
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join(1186. .1920,1971.
/gene="cut-1"
join(1186. .1920,1971.
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/strain="N2"
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75.1%;
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Pred. No. 2e-64
0; Mismatches
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TITLE
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                                                                                                                                                                                                                                                     97
                                                                                           agctccgaatccttgtggttctgaacattgtggtcgaacacattcgctatttggttcttt
                                CAATACTCTAAATGCAGCAGCTTGTCGTGATGCAGCTGCAACACCATTGCGCGTTTTAAT
                                                       gagtaaacgaagttgcgcagctgcagcaggttttgctgcggcacca---cctgttttaac 327
                                                                                                                                                            TAACAATGATGATCGATGACGTAGCGCATTTGGTAATGAGGTAAACTCTTCATTTATATC
                                                                                                                                                                          ---cagaagtgcacggtgacgtaaatcaactggcaaagcttgattatcatcgctaatttc 210
                                                                                                                                                                                                                                                                                                        aataatgacggcagcaatcaatgcaatgcttaaacccataaacattgagaagccaaatgg 96
                                                                                                                                                                                                                                                  tgacatgcagattccattttgtactgcagcaagtattacaggttgtccattatgttg--- 154
                                                                                                                                                                                                                                                                                      AATTGTAGCAACAGAAACAATAACAAATATTAGCATACCGGCAAGTGTAAAAACCGGTTAT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACATACATATACCTTGTGTCATTGTTGCAACAATTACCGGATGACCATTCTCATGTGC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tctgtgcactaactgttttatcagcttccatgtaaaagcattg 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGTGTGGACACAGTCTTGTCGGACTCCATGTAGAAGCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-FEB-1999) Research & Training Center on Vectors of Diseases, Ain Shams University, Abassia Square, Cairo, Egypt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Filarioidea: Onchocercidae; Wuchereria.

(bases 1 to 724)

Ramzy, R., Helmy, H., Adely, M., Curtis, K. a
Wuchereria bancrofti L3 cuticulin-1 cDNA
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AF125580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wuchereria
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ASRQAAAFRVLKKRDVBDENIVDVRTDLAALDINEEFTSLPNALRHRSSLLAHENGHP
VIVARNTOGICMSITGETLAGMLIFVIVVSVATIVAITLLRSHSTKV"
112 c 128 g 236 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Wuchereria bancrofti"
/db_xref="taxon:6293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD28743.1"
/db_xref="GI:4741875"
/translation="TVDTFCAVVHSCFVDDGNGDKVELLNADGCALDKFLLNNLEYPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="cuticulin-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="L3 larvae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to Ascaris lumbricoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /country="Egypt:
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Ascaris l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Timinouni, M. and Bazzicalupo, P. cut-1-like genes of Ascaris lum Gene 193 (1), 81-87 (1997) 97390131
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-OCT-1996) GA3, I.I.G. NA 80125, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ascut-1) gene, complete cds U73005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Timinouni, M. and Bazzicalupo, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ascaris lumbricoides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 5792)
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lumbricoides
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           FHPLFITKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQTQIVPMPVCRYEILDGGP
TGQPIQFATIGQQVYHKWTCDSETVDTFCAVVHSCFVDDGSGDTIQILNEEGCALDKY
LLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQITITIKEPNSECPRPTCSEPQGFGA
                                                                                                                          /note="cuticlin gene; ASCUT-1; proteins of other nematodes" /codon_start=1
                                                      /translation="mCravsflalfglaaaipvDngvEgEpEiECGPTSITvnfnTrn
pfEGHAYVKGLYDQEGCRSDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVIS
VRPGGSTAPKKQRRCQLRLTKKSGGDYDNTLDVRTDFSALDTSDRDEALPMDLRHRAF
                                                                                 /product="CUT-1-like cuticlin protein
/protein_id="AAB66646.1"
/db_xref="GI:1657625"
                                                                                                                                                                     join(882. .954,2851.
/gene="ascut-1"
                                                                                                                                                                                               /gene="ascut-1"
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                                                                                                                                                                                                                                           /gene="ascut-1"
                                                                                                                                                                                                                                                                                                                                                                                        /variety="suum"
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Ascaris lumbricoides"
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                                                                                                                                                                                                                                                                      'gene="ascut-1"
                                                                                                                                                                                                                                                                                                   /gene="ascut-1"
/product="CUT-1-like
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                                                                                                                                                                                                                                                                                                                                             'gene="ascut-1"
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CUT-1-like
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                                                                                                               precursor"
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BASE COUNT
ORIGIN
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x96677
Biologia Molecolare, Via Orabona 4, 70126, Bari, ITALY 2 (bases 1 to 2584)
De Glorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.
Modulation of expression at the level of splicing of cut-1 RNA
                                    Direct Submission
Direct Submission
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
Submitted (15-MAR-1996) C. De Giorgi, Dipartimento di Biochimica
                                                                                                                                    Eukaryota; Metazoa; Nematoda; Secernentea; Diplogasteria; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae;
                                                                                                                                                                 Meloidogyne artiellia.
Meloidogyne artiellia
                                                                                         1 (bases 1 to 2584)
De Giorgi,C.
                                                                                                                      Meloidogyninae; Meloidogyne
                                                                                                                                                                                               cuticle protein;
                                                                                                                                                                                                             X96677.1 GI:2648040
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/gene="ascut-1"
a 1254 c 1213
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/gene="ascut-1"
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join(930. .954,2851. .3239,3583. .4083,4499. .4690)
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No. 7.7e-49;
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polyA_signal
BASE COUNT 761
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Best Local Similarity
Matches 581; Conserv
                                                                                                                                                             gcgcagctgcagcaggttttgctgcggcaccacctgtttttaacagctccgaatccttgtg
CTTCGTTCAAAATTTGCACGGTGTCCCCATTGCCATCATCCACCACACAGCTGTGCACAA
                     cagcatttagaatttccacagtatcaccgttaccatcatcgacaaagcaggaatggacaa
                                                                               CAGTCAAATCGGTTGGGTATTCCAAGTTGTTGAGCAAGAACTTGTCCAGGGCACAGCTTC
                                                                                                  ccattaaatctgttggatattccaaattatttagcaaatatttatcaagagcacatccat
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2518. .25
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/protein_id="CaA65452.1"
/protein_id="CaA65452.1"
/db_xref="G1:2648041"
/db_xref="SPTREMBL:018479"
/translation="MRKLLFAIGVFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV
NENTRNPEEGHYVKGLEDQAGCRSDEHGRQVAGIELPFDSCNVARTDAEPKGVFVST
TVVISFHPQFVTKVDRAYRVQCFYMEADKTVSAQLEVSEITTQFQTQVVPMPVCKYEI
LEGAALGQP1QFATIAQQVYTSGTCDSGTIDTFCAVVHSCVVDDGNGDTVQILNEGSC
ALDKFLLNULEYFDLTAGQEAHYKXADRSQLEVSGEITIKEPHSECARPKCAES
SGFNAYKVGAGGAGGAPPPAAAAATPPPAAAPPAPIPAFIPARVQRLRTRQIRLLRK
SGFNAYKVGAGGAGGAPPPAAAAATPPPAAAPPAPIAPAIPARVQRLRTRQIRLLRK
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/gene="Mtcut-1"
467. .2052
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CMSSFRANHLLRYGHCNGCSHWWVHSTYCLFIVVFFSNEIK"
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/db_xref="taxon:42426"
/clone_lib="lambda7-2(1)"
/clone="pUc(3000)"
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<467. .943
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E., Veterinary Parasitology, Road, Glasgow, G61 1QH, UK

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTGAGCATCTTAAACGTTGGGTAAGGAAGCAAAATGTTGAAATTAAACCACTCGATT 1008
                   cut-1-like genes are present in the fi
pahangi and Brugia malayi, and, as in
components of the cuticle
                                                                                                                                         Brugia malayi cut-1 gene,
AJ012617
AJ012617.1 GI:3858954
 Mol. Biochem. Parasitol. 99339397
                                                                          Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 637)
                                                                                                          Brugia malayi
                                                      Devaney, E
                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                      Brugia malayi.
                                                                                                                                cut-1 gene; cuticlin.
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                                                                                                                                                                                                                                                     1111
                                                                Lewis, E., Hunter, S.J.,
                                                                                                                                                                                                                                  529
                                                                                                                                                                           637 bp
                                                               Tetley, L., Nunes, C.P.,
                                                                                                                                                                           DNA
          101 (1-2),
                                                                                                                                                              partial
           173-183 (1999)
                              filarial nematodes, in other nematodes,
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                                                               Bazzicalupo, P. and
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                                                                                               Spirurida;
                                        Brugia
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                               Matches 334;
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                                                                                                                                                                                                                                                                                                                              TCAAAAAATTCAAAAAGACATGCCTCGTATCGACAAACAGGCATGGGGACAATTTGAGTT
                                                                                                                                          CAGAATTTCCACCGTATCACCGTTGCCATCATCCACAAAGCAGGAGTGGACAACTGCGCA
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Submitted (06-NOV-1998) Devaney
University of Glasgow, Bearsden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devaney, E
                                                                                                                                                                                                                                                                                                                                                                        Similarity
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a 136 c
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266. .484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAAI0074.1"
//db_xref="GI:385955"
//db_xref="SPTRKMBL:096775"
//translation="VISHPLSVTKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQT
QIVPMPVCRYEILDGGPTGQPIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDTVEILSADGCALDKYLLNNLEYP"
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                                                                                                                                                                                                                                                                                                                                                          Score 190.6; DB 34;
Pred. No. 4.5e-35;
Pred. No. 4.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                            134
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BPA012618/c
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                                                                                                                                                                    Matches
                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                          CAGAATTTCCACCGTATCACCGTTGCCATCATCCACAAAGCAGGAGTGGACAACTGCGCA
                                                                                                        GAAATTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-NOV-1998) Devaney University of Glasgow, Bearsden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pahangi and Brugia malayi, and, as in other nematodes, code for components of the cuticle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cut-1-like genes are present in the filarial nematodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brugia pahangi.
Brugia pahangi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brugia pahangi cut-1 gene, partial.
AJ012618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devaney,E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cut-1 gene; cuticlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BPA012618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devaney, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99339397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lewis, E., Hunter, S.J., Tetley, L., Nunes, C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 358)
                                                                                                                                                                                                                                                           110
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Parasitol. 101 (1-2), 173-183 (1999)
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                                                                                                                                                                                                                                                                                                                                                                 LNADGCALDKYLLNNLEYPTDL"
                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA10075.1"
/db_xref="GI:3970656"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(<1. .191,350. .>356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(<1. .191,350. .>356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Brugia pahangi"
/db_xref="taxon:6280"
                                                                                                                                                                                                                                                                                                                                     /gene="cut-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                        'gene="cut-1"
                                                                                                                                                                                                                                                                                                                     'number=]
                                                                                                                                                                                                                                                                                                                                                                              'db_xref="SPTREMBL:096776"
'translation="PIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="unnamed protein product"
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87.7%;
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                                                                                                                                                                  0;
                                                                                                                                                                             Score 156.6; DB 3
Pred. No. 4.7e-27;
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                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                              DB 34;
                                                                                                                                                                  24;
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MEDLINE
REFERENCE
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Z81088.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. This sequence is the entire insert of clone F53F1. The true right end of clone M04G12 is at 21759 in this sequence. The start of this sequence (1..101) overlaps with the end of sequence Z81103. The end of this sequence (39379..39478) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the energy of the entire of the entire of the entire of the energy of the entire of the en
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Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
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Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Sah, Sonnhammer, E., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence AL021448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the specified clone.
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                                                                                                                complement(join(14923. 16033. .16271,16318. ..
                                                                                                                                                                                                                                                                                     complement(14923. .16486)
'note="predicted using Genefinder;
                                                          /gene="F53F1.1"
                                                                                                                                                                                                                                           /gene="F53F1.1"
                                                                                                                                                                                                                                                                                                                                                            /clone="F53F1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contiguous nucleotide sequence from chromosome III of
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CDNA EST EMBL:D72018 comes from this gene; CDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C11739 comes from this gene; cDNA EST EMBL:C12451 comes from this gene; cDNA EST EMBL:C12451 comes from this gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST EMBL:C10189 comes from this gene; cDNA EST yk506b3.3 comes from this gene; cDNA EST yk437e9.3 comes from this gene; cDNA EST yk437e9.5 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h10.3 comes from this gene; cDNA EST yk311h6.5 comes from this gene; cDNA EST yk300g2.3 comes from this gene; cDNA EST yk300g2.3 comes from this gene; cDNA EST yk300g2.3 comes from this gene; cDNA EST yk314b3.5 comes from this gene; cDNA EST yk310g2.5 co
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/gene="F53F1.4"
join(21582. .21670,21781. .22009)
/gene="F53F1.4"
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QSLTALDRGQHYIRCTGWLVK"

18714. .20251

/gene="F53F1.3"

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eesloslototidmylvhypkndsdnddvnnaeyrkiayevleeakaagkvrsigvs
nyeivhleelktyakvppcanQleyhphfariploxyckekniffqafsslarhepkl
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/gene-"similar to aldehyde reductase; cDNA EST yk473d8.3
/note-"similar to aldehyde reductase; cDNA EST yk473d8.3
comes from this gene; cDNA EST yk473d8.5 comes from this
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KYYNNEKEIGDALEILLPKHANKREDIFITTKHHPNTYENVKKUDESLSLLKTSYID
MYLHYPKSSPOYGDODPMNKTILTATWNDLMSCKNAGKIRSVGVSSFEIRHLEBLKD
GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEIITRLAEK
                                                                                               25572. .26408
/gene="F53F1.5"
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19919. 20008.20072. .20251)
/gene="p5311.3"
/note="similar to aldehyde reductase"
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IILIKEDSFCMVVHTCSVDDGRGETSFLIDSNGCSIDKFLLSNLEYPGNLLAGQEAHV
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AFLEIEIGLCGALRQRVLNPKGLAVRTTITISFHPYFITKVDRTYNLLCLYRESQVTV
join(25572. .25660,25850. .26408)
/gene="r53r1.5"
                                                                                                                                                                                                                                                                              LPPLQLPRFELPRLSLPSFGGGGCGGPAPCGGAAPAYVAPPPAAGYAAPPPAGGYATA
                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB03125.1"
/db_xref="GI:3877457"
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/db_xref="GI:3877460"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB03124.1"
/db_xref="GI:3877456"
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                                                                                                                                                                                                                                                                                                                                 translation="MQKIVIFFAAIAVSQAFLLPSGGGGGGGCGCAPPPPPPPPCGCGGPS
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gene CDS

CMMBL.D7448 comes from this gene; cDNA EST EMBL.D7326 comes from this gene; cDNA EST EMBL.D7326 comes from this gene; cDNA EST EMBL.D7326 comes from this gene; cDNA EST EMBL.D7327 comes from this gene; cDNA EST EMBL.D7337 comes from this gene; cDNA EST EMBL.D7332 comes from this ge yk537c8.3 comes from this gene; cDNA EST yk540g5.3 comes from this gene; cDNA EST yk545b10.3 comes from this gene; cDNA EST yk557b11.3 comes from this gene; cDNA EST yk562b11.3 comes from this gene; cDNA EST yk564011.3 comes from this gene; cDNA EST yk566f10.3 comes from this gene; cDNA EST yk596a10.3 comes from this gene; /note="predicted using Genefinder; similar to cuticlin; cDNA EST EMBL:T01107 comes from this gene; cDNA EST EMBL:D7966 comes from this gene; cDNA EST EMBL:D71580 comes from this gene. yk596e11.3 comes from this gene; cDNA EST yk614f1.3 comes from this gene; cDNA EST yk618d8.3 comes from this gene; cDNA EST yk620c8.3 comes from this gene; cDNA EST comes from this gene; cDNA EST yk622e4.3 comes this gene;

Query Match
Best Local Similarity
Matches 171; Conserv Conservative 9.3%; 61.7%; 0 Score 107.4; DB 3 Pred. No. 2.1e-15; Mismatches 106; DB 34; Indels Length 39478; 0; Gaps

0

В 15074 GCTCCACCGCCTTCTACATCTTCACATATTGGTCTCACGCATTCCTGGTCTGGCTCTTTG 15133 gctccgaatccttgtggttctgaacattgtggtcgaacacattcgctatttggttcttta 388

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TITLE
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                                                                                                                                                                                                                                                                                           current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone E04D5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Zu, Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hiller, L., Jier, M. Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lighthing, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Saunders, R., Sulston, J., Thierry, Mieg. J., Thomas, K., Vaudin, M., Vallaghan, R., Sulston, J., Thierry, Mieg. J., Thomas, K., Vaudin, M., Vallaghan, R., Sulston, J., Thierry, Mieg. J., Thomas, K., Vaudin, M., Vallaghan, R., Sulston, J., Thierry, Mieg. J., Thomas, K., Vaudin, M., Vallaghan, R., Sulston, J., Thierry, Mieg. J., Thomas, K., Vaudin, M., Vallaghan, R., Sulston, J., Thierry, Mieg. J., Thomas, K., Vaudin, M., Vallaghan, R., Sulston, J., Thierry, Mieg. J., Th
                                                                      neighbouring submissions.

The true left end of clone E04D5 is at 1 in this sequence. The true right and of clone E04D5 is at 2110 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-CCT-1995) Louis, MO 63110, USA. E-mail: Jes@sanger.ac.uk or rw@nematcode.wustl.edu Coding seguences below are predicted from computer an predictions from Genefinder (P. Green, U. Washington)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elegans
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Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson, R., Ainscough, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans cosmid E04D5, complete sequence.
                                                                                                                                                                                                                    It may be shorter because we only sequence overlapping once, or longer because we arrange for a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bin/display?db=wormace&class=Sequence &object=E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMurray,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2 Mb of contiguous nucleotide sequence from chromosome III of
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                                       The true
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a graphical representation of this sequence and its analysis
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   of clone ZK673 clone T09F3 is
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at 31437
11412 in
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U. Washington), and other
in this sequence. Th
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249070.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yk454d9.5 comes from this gene; cDNA EST yk350b11.3 comes from this gene; cDNA EST yk450b11.5 comes from this gene; cDNA EST yk413f5.3 comes from this gene; cDNA EST yk402d12.3 comes from this gene; cDNA EST yk402d12.3 comes from this gene; cDNA EST yk402d12.3 comes from this gene; cDNA EST yk402d12.5 comes from this gene; cDNA EST yk402d12.5 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk375c1.3 comes from this gene; cDNA EST yk374f8.3 comes from this gene; cDNA EST yk374f8.5 comes from this gene; cDNA EST yk374f8.5 comes from this gene; cDNA EST yk3568e.3 comes from this gene; cDNA EST yk365e8.3 comes from this gene
complement(join(8619. .8761,8813. .8988,9895. .1 10089. .10283,10330. .10614,10730. .10935,11582.
                                                                                                          EQERKAFQLKKKVEEIKVLKQRVANGDQLQPNQMEKIQRENEYLSELSKLTI"
complement(8619. .11718)
/gene="E04D5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVRVYSLADGKHVSTFSAPKEASWEPQFSDDESLAARMVGSEVFFYTINMSFDRYDHKL
VEKGATNFALSPGPAPNHVAVYVPAVGSTPARVRVHRVSESFPVVGNRTFFKSDKAVM
TWNQRGQSLLILASVEVDKTNQSYYGEQSLYLINIQSGESVVVPLEKKGPIYAAKWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QINKMGDNLVYAVRSSEGFYLKRGLGKDAVTVFEQNKTSRDVACNVFAYSNNGQLFAY
CDNQVTRVFEIATNKEILCVELKRTRKILFSPKDNFLLTFEPWAVYGPKTAENQKPEP
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                                                                                                                                                                                                                                                                           MEFWDVETKKEIISIEVPNTTLFDWAPDGQHFVTCTTAPRLRIDNSYRFWHYTGRMLA
ETHFESPKELWEVRWRPMTGYNKFAIKELTKTDKMAAGLPIRKKDASHPLNNVPAGAV
RQAGAYIPHLRKPLGGGGSAGPPSAAAPTPGNQNQRPAQPRANGNGNAPQPFRPQOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA91279.1"
/db_xref="GI:3875451"
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6750. .6930,7003. .7283,7337. .8179,8228. .8326)
/gene="E04D5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGREFAVCYGYMPAKVTFYNPRGVPIFDTIEGPRNDVFYNAFGNIVLICGFGNIAKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MPAPNTTPSRDSNFFVISSSFSNFLLLPEKFKTFSFFRLSQTLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q19052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yk640h2.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5082. .8326
/gene="E04D5.1"
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/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene;
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.10028,
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10089. .10283, 11691. .11718)

/protein_id="CAA91282.1" /db_xref="GI:3875454"

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/IVPVFFIAKVVQFAIPFILILITFERYLWTCTERKRFGITFQVLTLSLSFRKAFSAI

gene

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27861 AAGTTCAGCAACGCAAGTCCATTTGTGATAGACTTGATCTCCGATTCGAGCGTACTTAAT 27802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 acattcgctatttggttctttaatggtaatactgatctggcattgatagaaaagctgtga 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y match 7.2%;
Local Similarity 56.1%;
                                                                                                                                                                                                                                                                                                tggttgaccggttggtcca 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGATTCTGAAGGATCACCCCATCTACAGAACATCCATTGGCATCAATGACAGTTACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caaattattagcaaatatttatcaagagcacatccat---cagcatttagaattttccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATCCATAATTTACGTCTTTGATTGTTAATTGAATTTGACAATTGAAATAAAGCCCAGC 28042
                                                                                                                                                                                                                                      AGGTGATCCACCGGCTTCA 27783
                                                                                                                                                                                                                                                                                                                                                                                                                                      ggtttcagaatcgcatgtccatttatgataaactggctgaccaatgatagcaaattgaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTCCACCTTGTCCATCATAAACCGTACATGAGTGAACTTTCATACAGTACACATTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agtatcaccgttaccatcatcgacaaagcaggaatggacaaccgcgcagaaagtatcaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGTCAGCAAATTTGAAGACTGGTGCGAGTTTTCCAGCTGAAGTCAGAGGTGTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179;
   CEF53B6 32412 bp DNA INV 02-SI
Caenorhabditis elegans cosmid F53B6, complete sequence
281086
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a 5592 c
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VSEPSCMTVGDGKTGHRFEVRHDSCGVRRQREINGVVISATVIISFHSIFITKIDRAY
RVSCFYVEGTKKVHNHVDISALTTQLLESETQLPVCRYEILNEAGGSPIKYARIGDQV
YHKWTCVAELENVYCMKVHSCTVYDGQGGPPVTVIDANGCSVDGVILQNLEYTSDLTA
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28158. .28410,28491. .28811,29092. .29213)
/gene="E04D5.3"
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YPYDSHESGYPTRPANYPVASSRYPIPTTQAPASYPSSPAPPPPGADIDNGYPEPQPI
YIAETPENAYDGIVGFNDTEQPFTTSAAYTEDGVYSRLIKRNVVESTEQINASNKKRP
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/db_xref="GI:3875452"
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/gene="E04D5.3"
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LERFDPSYLYESTDRMQSSTFYIVLSDTVSICYMASSAIRIFIYAKCNPKLRQEITDY
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YDFHVITAIQMMFPFVVLLLLNLTIIKRLVAEKRENMYPILRGAGTTTEVKKASFVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSSSFFYETTTASTCADDPNTDCTQYTFLCSNAKYTPLLQQFCAKTCGFCGSGSTAAP
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/translation="MWSINLTVHIILLVTFSVSHVVTTAVTKATGETTVRGAGQDLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA91281.1"
/db_xref="GI:3875453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=
                                                                    32412 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .29840,31127. .31214,31267.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83.8; DB 34
Pred. No. 7.8e-10;
0; Mismatches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 31536;
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REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence Z81523.

Sequence Z81523.

The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a smale coverlapping sections once, or longer because we arrange for a smale coverlapping sections once, or longer because we arrange for a smale coverlapping sections once, or longer because we arrange for a smale coverlapping sections once, or longer because we arrange for a smale coverlapping sections once, or longer because we arrange for a smale coverlapping sections once.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using computer analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions.
The true left end of clone F53B6 is at 1 in this sequence. The true right end of clone F53B6 is at 5116 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor associated protein; Thrombospondin like Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone F53B6 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence &object=F53B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281086.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditina; Rhabditoidea; Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 32412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 32412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end of this sequence (32306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cuticulin; Human platelet tetraspan antigen like;
                                                                                                                                                       1480. .3649

/gene="F5386.1"

join(1480. .1638.1707. .1

3205. .3308.3430. .3649)

/gene="F5386.1"
                                                                                                platelet-endothelial tetraspan antigen
/protein_id="CAB03120.1"
/db_xref="GI:3877452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:1627952
                                                                                                                                                                                                                                                                                                                                   /clone="F53B6"
                                                                                                                                                                                                                                                                                                                                                                     /chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                 codon_start•J
                                                                                                                           note="predicted using Genefinder; Similarity to Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secernentea;
                                                                                                                                                                                                                                  .1946,2437. .2628,2969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .32412) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baynes, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhabditia; Rhabditida;
oderinae; Caenorhabditis.
                                                                                                   (SWLPET3_HUMAN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berks, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initiation
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BASE COUNT ORIGIN

gene

Best

RESULT 11 CEF53B6

DEFINITION

ACCESSION Snoor 멍 δÃ Вþ δõ

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27981

28041

427

gene

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/note="predicted using Genefinder; similar to thrombospondin like; cDNA EST EMBL:214404 comes from this gene; cDNA EST EMBL:2171 comes from this gene; cDNA EST SEMBL:2171 comes from this gene; cDNA EST yk195c9.5 comes from this gene; cDNA EST yk28697.3 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk28697.5 comes from this gene; cDNA EST yk353hl.3 comes from this gene; cDNA EST yk353hl.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4270. .15311)

/gene="F53B6.2"

/gene="F53B6.2"

complement(j0in(4270. .4339,4493. .4547,5071. .5295,

complement(j0in(4270. .4339,4493. .4547,5071. .5295,

5368. .5662,5891. .6148,6204. .6752,6818. .7287,7546. .767

8104. .8184,12576. .12775,13246. .13384,13931. .14132,

14183. .14294,14341. .14457,14994. .15155,15198. .15311))

/gene="F53B6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMSRTVECVAVNPISSAPIKLPMSECODOEOPKLFESCEVRSCPLQEDSKLSEDEAPY
UMSRTVECVAVNPISSAPIKLPMSECODOEOPKLFESCEVRSCPLQEDSKLSEDEAPY
OWRYGDMSCCSASCLGGKQKAALKCIOVSTGKSVQWSQCDARRAPEKSRPCNOHPCP
PFWLTSKYSDCSMSCGSGTARRSVKCAQTVSKTUGADAHIULEDDRCHEKKPOPETEIC
NVVACPATWVSSLNKRHNKIKLNKLKTAQWTECSRSCDSGERRRQVWCEIRDSRGKTQ
NVVACPATWVSSLNKRHNKIKLNKLKTAQWTECSRSCDSGERRRQVWCEIRDSRGKTQ
RRPDVECDANTKPQTVEVCSFGSCSRPELLSNRVFEQNAEQKKLTLGIGGVATLYQGT
SIKIKCPAKKFDKKIYMKKNGKKIKNDAHIKVSANCHRVFHARMEDAGVYEFFDD
SIKIKCPAKFDKKTYMKKNGKKIKNDAHIKVSANCHVEYBACHNCHARMEDAGVYEFFDD
LOGNVTLNEKYRDFPASRVDLAPKPQIPSTKNRQRVQVSKEDVLREQASVLHKMNVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTENASIATION="MKCSYTVVFLLFYLLIASFHVDALSWAAWSPWSSCTKTCGGGVS
RQLRRCLTSKCSGESVERKVCAQKTCESKSRLAEDTICGGEEIYSRGQCEVCGRSRLT
GANELWRVDDGTPCQAATSRAVCSKGSQOIVGCDGLIESSFRFDACGYCGGRGDTDU
GKFIWKVSEEYTACASNCDDIVDWSGAGRSIASTSQPIVVCVNAITGRVVPEKLCADK
LRFKVBARPCPWLICPSRWMAADWTECVPHCGEGTRKBVYCVGTAHNVTVHVPDTFC
ENGTRPAAEBNCVSTSCGRWBAKWSKCTASCGGGVRRRHVACVGGSDCDCDGGRPRQE
ETTCYAGIPCSIATNSLDWNDRAYLDGNTFGSMDNHNDWQAPRLVAGEWSTCSSTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                    comes from this gene; cDNA EST yk193h3.5 comes from this gene; cDNA EST yk411f5.3 comes from this gene; cDNA EST yk411f5.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(19892. .20022,20241. .20283))
/gene="F53B6.8"
                                                                                     SSKAKHSKRSSKSSKKGTSGKSGKGSSKRGGKSSKSSKSKKVKTATTSGSQVSTVSAA
TGVSDKQSNSSKSSRKSSKSSKSRKNRRLDSDAQKKMEKSGKSGKVALIPKTQQTTGS
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/db_xxef="G1:3877449"
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VPLTAIVTTSLPMVAAIAFCAKNRKTVHAKNKNKNKNKNKSKSKSKSTRGASKSGKSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(20516. .20602,20648. .20953,20999. .21424.
21609. .21818))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(20516. .21818)
/gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(19892. .20283)
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VASWLCITNAIVQVIFVSLKTIKLLNFILLKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKSAIGEEGRKKNOLLKRDFSKLANPLSEESLYREOPD70FLKNRKIKNVDQDGSRLFSLLEKYIFHSLSINLTIYLKALHFOTRVFPFKSFPHFNTLKFTFOLKNGALGDSAYGARGRLIKFSYIVTALISILFSISCICYGIWLLARRSQYAELLVSELYVDVGRILVFISILSILFSISCICYGIWLLARRSQYAELLVSELYVDVGRILVFISILSILFSISCICYGIWLLARRSQYAELVSELYVDVGRILVFISILSILSILNYLICFYAIFKEMRCFVTSCAVASIVIAVMLIIGGCIGLN
YRVNPVYGFAEPRSSVKIDVLRLNGEQKTDKLVLLTANANGSTNPHEAFANQAEHREM
                                                  QVGHSLAEEVNSIKHSKEMNVAPAKLQYQTLGGVNQIELKNTSNERKAYKIKCSDNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGYYQSNYWGKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIKLFHSCDSLEVRQKCCSTCTFVERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {	t TCRFT}{	t NGTSVDIQHCDIT}{	t NRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRL1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GETRNVDNSTCESLASVRPPETRPCHREDCPRWEASQWSECSSQRCVSSMLAQKRRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEALLTAPNDEKAREQLRKYGNELVARWDIGHWSECRQKTCHVAGYQARGISCKVTFH
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/db_xref="GI:4008366"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB54255.1"
/db_xref="GI:5824510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F53B6.8"
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                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="predicted using Genefinder; cDNA EST yk193h3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MDFGILLVFLMAVAGTFAGISVSFSHSHEFPRHGLLGGGGFNPY"
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Best Local Sim
Matches 127;
29798 TGCCTCCGCATATTGCATGCTCCAATTGGAATTG 29831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                           722 atttgagtttgaaaagcagttgtgatttcagatacctcaatctgtgcactaactgtttta 781
                                            gtacgcgcaacattgcatgaatcaaatggaagtg 935
                                                                                                      GGATGAAACGAGGTGATCATTGTGAAGGAAAATGATATTCCACGTGGATGCAGTGTTCGT
                                                                                                                                                     ggatgaaacgaaatgacaacagttgttgttacaaaaataccacgtggattcagagatcgt
                                                                                                                                                                                                               ATTGACTCGAGGAAGAAACATCGAATACTGAATGCTCGATCCATTCCCGTCACAAAGAAT
                                                                                                                                                                                                                                                              tcagcttccatgtaaaagcattgtactcgatatgcacgatcaactttggtaacaaataat 841
                                                                                                                                                                                                                                                                                                                  AATTGATTTAATACTTCAGAGTTAACATACCCAACATCAATTTCCGCGTTCAATCCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB03116.1"
/db_xref="G1:3877448"
/db_xref="G1:3877448"
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/translation="MNLSLFIVKTVYTFYWVVLEKVQLHSFKQYVVALRFESVQFKNP
PILLLLIYNRTFLQSTTILILLSTSSCFEIQMGVVGKPEVFCGIDTIRVKVNTEHPFN
GRIYVDGESDKQHCVQHSADAHSSPQEFTIPIGACNMRRQRTLHPRGISFSFTMITSF
GRIYVDGESDKQHCVQHSADAHSSPQEFTIPIGACNMRRQRTLHPRGISFSFTMITSF
HPFFYTGMDRAFSIRCFFLESIKGLNAFIDVGTLAPQHVDQEYSLPVCAYHLKDGIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(27666.
/gene="F53B6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \text{CVRRGPMEYHPYDMNMPPKLVPRPPLHYKFDPPLTERGQIVSETYGRGLLNAGIRPF EVECSPDMKSYQTAAFILIKGLGLSYTTINIDPALLSYROMLPTBYQEMLLSPKAFFNM GYPINIQYLBSQGFIKABILEDYNLRIQAFFKKNIAKIEQKOVVVISUNWYDLTNEGYPHYDDTLIQCIKKPTCQMNFISLKKGEAQIMDSPILPLTKSLYLVKPFYWTDVPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MILSDQNFLQTQWKEPQTAQSKNTESKCEFHGNSNEVKPIGSLN
GQSIAQCRIHTEKTVFIVKGGEQARMEENEIYAIETFGSTGKGYFHDDMETSHYMKNF
ELADEKIPLRLQKSKGLLNLIDKNFATLAFCRCWIDRLGETKYLMALKGKCSYSTASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(27666. .27862,27919. .27959,28076
28905. .29001,29330. .29417,29467. .29606,29648.
30107. _30301,30478. .30589))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="TTT Lys K-tRNA; predicted using tRNAscan-SE-1.11;
preliminary prediction; similar to tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVPNHPELNON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(26258. .26342,26501. .2
27153. .27288,27334. .27459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Similarity to Rat initiation factor 2
glycoprotein (SW:I2A6_RAT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26276. .26348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/protein_id="CABO3118.1"
/db_xref="G1:8877450"
/translation="MSRESPVSLAQLVERETFNLKVRGSSPLVSHAESMGLIFPNWVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQIEYEHGAISAYTNAHVFKYADKVQLYFTCTVQLCYKHDGGCEGITPPQCSGHSHGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVLRFAQVGQKVTHVWRCDQDASHVYGILIHSCYADDGHGNKFELVDDRGCSTDPFLL
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/db_xref="GI:3877451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="predicted using Genefinder; similar to cuticulin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F53B6.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F53B6.t1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F53B6.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F53B6.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%;
59.3%;
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51
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74.8; DB 34; Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           87;
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KEYWORDS
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CER07E3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bin/display7db-wormace&class=Sequence &object=R07E3
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIONS THIS sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone R07E3. The true right end of clone F41E7 is at 36774 in their sequence. The start of this sequence (1. .115) overlaps with the end of sequence Z68106.

The end of this sequence (39633. .39736) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-MAY-1995) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 21, 1995 this sequence version replaced gi:798823.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M. Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, B., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vanden, R., Sulston, J., Thierry, Mieg, J., Th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cottage, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson, R., Ainscough, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z49207.1 GI:1067021
HTG; ADP,ATP carrier protein; Cuticulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2 Mb of contiguous nucleotide sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 39736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 39736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                          5080. .8873

/gene="R07E3.6"

/gene="R07E3.6"

join(5080. .5246,5409. .5769,5826. .5942,6381. .6905,

6955. .7075,7125. .7448,7495. .7787,7831. .7980,8037.

8222. .8405,8470. .8873)
                                                                            this gene; cDNA EST yk259b4.5 comes from this gene; cDNA EST yk559c11.3 comes from this gene; cDNA EST yk574h3.3 comes from this gene; cDNA EST yk597h8.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL032624.
                                                                                                                                                                                                                       /note="Serine and threonine rich protein, Carboxyl terminus is glycine rich; cDNA EST EMBL:C08296 comes
                                                                                                                                                                                                                                                                                                            /gene="R07E3.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="R07E3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39736 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baynes, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cysteine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berks, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jier, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      using
                                                                                                                                                                                                                                                                                                                                                                                                  .8174,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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RAFSSVIRFHDKENRANKGGICVANHTS9TDVMVLSCCONCYANTGKQAGFLGFTQTT
LSRSSHHIWEFRGFAGORAKVWDRMREHVNDLMKLPIIIFPEGTCINNTSVMMFKKGEN
LSRSSHIWEFRGFAGATAKVWDRMREHVNDLMKLPIIIFPEGTCINNTSVMMFKGEN
EGIGSTIYPJAVKYDTRLTDAFWNSSAQSYGRYLWSMMTSWAIICDVMYLPAMTRGEN
                                                                                                                                                                                                                                                                                                                complement(join(21213. .21359,21654. 22011. .22170,22220. .22335,22428. .23354. .23259))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(17917...18025,18074...18331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEITTTTKAPTTTTQSTTTTTQLPTTTTTEPTTTTTTDPLAENEELEKQAIEVM KSLDDEERIJAEKNVEVOKKROERNAAKKINNELKMKOKAREKKKKPHKETTTSLAT KSLDDEERIJAEKNVEVOKKROERNAAKKINNELKMKOKAREKKKKPHKETTTSLAT EQPKTTTIVASSTETSTVTTDATETTTTAPTTTVATTTKKRSNIPESAEEDEIET EQFKTTTKKTEDGPITTEFPEYIKKRATUTTTAFTTTVAFTTTKKESNIPESASEASAP SENVETAEVAASAAAPVALPEPIAPPOIALPQLTPDQISQFMRPVASIVEDMRPILG SLLQGSSASRARAASVRTYEKTKTPNIRDIMADGYSENSLVGFGSQLAREILNPGILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(17917. .19072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(11510. .14654)
/gene="R07E3.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQLAGRLVQPDMDSGEPESAEDGIDKKKTAEKVDFTTDDNNVSQEADAKPDSTHENGG
EHVSTTPEESITENTTAEVPASTASTKDTKLSVKIRSEDEKREEDKLSDDEKPNYMKK
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/note="~
                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="R07E3.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(21213. .23259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSLRSTGGALIITFYYEFSKYM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCLKKIKASEGVASWYKGLSSALQFVIASRAIFFGIFDSIRTSVEDPKSLNFAACWAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKSD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDS1SFAKRVKRAIAKKGGLIDLEWDGALKRERVSSKLVTLQQKLYFERLARTTTLNA
MLEEKSSDILNIMQGISEEERDELLKQIDEQDDEEEMIRKISSLKPKFKIGDHDADEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ykz/valU.5 comes from this from this gene; cDNA EST yk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="cDNA EST yk278a10.3 comes from this gene; cDNA yk278a10.5 comes from this gene; cDNA EST yk486f8.5 cc from this gene; cDNA EST yk603d8.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(11510. .11773,12101. .12476,12528. .1282
13402. .13542,13587. .13696,13745. .13863,13912. .14026,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDFSFFSSNRKKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAAPVTAPKPVAPAPSPFGGGGFGGGGGGGGGGNRGNGFGGGSGPSVPFDEVEKNSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPQGYVGPLPPAPPPPTTRVAPQVPLPVVQTTQTAPKPTLPPTTLPVLTTNKTPRTKD
EGYEQGRDGVKTTFHGDSGVMTGGGHSAPTFDYLNMPSESFGLAPVAPPAPPPPPATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDKLTRDKAMAAKLEEAKVRNNAVAESMATGAPLDLSGFPQYQQRPVATNSKLPYFIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref~"SPTREMBL:Q21811"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14541.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA89071.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \QISITTSGMVCYPLDTVRRSMMMQSGKQIKQYTSTKDCWKTLYKKDGINGFYRGALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to ADP,ATP carrier protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="R07E3.
                                                                                                                                                                                                                                      'note="similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .14654)
                                                                                                                                                                                                                                                                                                                                                                                                  .21739,21787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .18331,18378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene"
                                                                                                                                                                                                                                                                                                                                                                                                  21886,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comes
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?CMLVHSCFVDDGNGQRVQLLNDKGCALDKYLLTNLEYPTDLMAGREAHVYKYADRDN

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                      22077
                                                                                                                                                                                                                                                                                             22017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                 367
                                                                                                                                                                                                                                                                                         ATAGTCAAGACCAGGCTCTTTGACTGTGATCGAAATTTGACAATCAAAATACATGTTATC 22076
                                                                                                                                                                                                                                                                                                                                                               acattcgctatttggttctttaatggtaatactgatctggcattgatagaaaagctgtga 426
caaattatttagcaaatatttatcaagagcacatc 521
                                                                                                                                                              TCTATCGGCATATTTGTATACGTGGGCTTCCCTTCCCGCCATCAGGTCTGTGGGATACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to cysteine proteinase; cDNA EST EMBL:D69358 comes from this gene; cDNA EST EMBL:D69358 comes from this gene; cDNA EST EMBL:D69358 gene; cDNA EST EMBL:D69368 comes from this gene; cDNA EST EMBL:D69368 comes from this gene; cDNA EST EMBL:D696042 comes from this gene; cDNA EST EMBL:D696042 comes from this gene; cDNA EST EMBL:D696042 comes from this gene; cDNA EST EMBL:C08090 comes from this gene; cDNA EST EMBL:C08041 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q21810"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="R07E3.1"
complement(join(26570. .26749,26841. .26917,27073.
27330. .27815,27863. .27958,28006. .28071,28119. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(29470. .29618,30123.
30963. .31067,31117. .31252))
/gene="R07E3.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHKEAEFIEFIPESLTAKKGESSSPFPDFFDWRDKNVITPVKAQGQCGSCWAFASTAT
VEAAWAIAHGEKRNLSEQTLLLDCDLVDNACDGGDEDKAFRYIHRNGLANAVDLPYVAH
RQNGCAVNDHWNTTRIKAAYFLHHDEDSIINWLVNFGPVNIGMAVIQPWRAYKGGVFT
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TDYISRAFDKMpssihliflfsqcvvlfsfsqlalsllsvktgeevvdteaavtwedm
VVEDTVEVVIWEEDMVAEVTWEEAAMEVAETWEEDTEEVVTADMVATEVADTEEVVIW
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SDYIIPNDDIISLNWLQRNFDMRISELCMTAIGTTLLVFLNAFLFIISLVSIVHVCCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA89073.1"
/db_xref="GI:3878961"
/db_xref="SFTRRMBL:021813"
/translation="MLAVIAGILAVLLILILFFCIRSKDKKQPPSPAEPNRRLPTRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(29470. .31252)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSEYACKNEVIGLHALLITGYGTSKTGEKYWIVKNSWGNTWGVEHGYIYFARGINACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSQESLKRLNAYYNTDENIANWNIQNEHGSAEYGHNDMSDWTDEEFEKTLLPKSFYKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28273. .28295))
/gene="R07E3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(26570. .28295)
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/db_xref="GI:3878962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(23363. .23562,23642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTSPKLEKTKSTML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="R07E3.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA89070.1"
/db_xref="GI:3878958"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 34;
Pred. No. 7.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 39736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 13
CEY39A1_3/c
WPCOMMENT
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AUTHORS
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ORGANISM
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Best Local
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  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82129
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CEY39A1_3
CEY39A1_4
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CEY39A1_0
CEY39A1_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATCCACATAGCAAGAGTGAACTAACATTCCGAAAGTGTCCTTATCAGCACCCTCCACT 82010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tatacgtg---agcttcttggccagccattaaatctgttggatattccaaattatttagc 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGAACACTGTTGTGAT 81873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccggttggtccaccatccaaaatttcataacggcatactggcatcgggacaatttgagtt 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAATGCATTCCCATCTATGATATACACTTTCACCGAGAGTTGCAAAACGGACTATTGGG 81950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTTCAGACATAGTGTTATTTGACACTGATATTGTAGTACCGGGCGGTCCGCGTACTTA 82190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcatcgacaaagcaggaatggacaaccgcgcagaaagtatcaacggtttcagaatc----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCACCGCGTCTAGGCCACAACCATTCGAATCAAGAATATCCACTCTATCACCGTAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197;
                                                   Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Laister, N., Latreille, P., Lightning, J., Lidyd, C., Mchurray, A., Mortimore, B., O'Calladhan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Watson, A., Watson, A., Weinstock, L., Walshan, P., Watson, A., Weinstock, L., Walshan, P., Malkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                     HTG; Cuticulin; Homeobox protein EVX1 like Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEM142
                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans cosmid M142, complete
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                                       .2 Mb of
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|||| |||| |||| |||| ||
                                                                                                                                                                                                                                                                               (bases 1 to 36306)
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368
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                                     contiguous nucleotide sequence from chromosome
(6466), 32-38 (1994)
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310000
410000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bin/display?db=wormace&class=Sequence &object=M142 Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 4, 1996 this sequence version replaced gi:1370039.
Coding sequences below are predicted from computer analysis, usin
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 start of this sequence (1. .104) overlaps with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of clone M142. The true right end of clone C44B9 is at 5059 in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-MAY-1996) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nttp://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end of this sequence (36203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8540. .12501
/gene="M142.2"
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VSEPSQLLRDADVMVYAIGVTNLVNVHOLHQMYGNPVKVFTVESFEQLDRALADSLTW
SMCKTEFREOTPEIICGEDRIGVKASTKOPFESONFVMDHYHDEECRACPEKFPDSRS
SMCKTEFREOTPEIICGEDRIGVKASTKOPFENSLIFMTKTDQTVKVQCFYMEADKHV
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GVGTIDVFTDSVTVLEQEPACQQVTTYSFRFSISTNQKIENS"
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ADRPVLQFQCQITLCLKYDGGCEGITPPQNCKKLPGEDGHHHHHHPEKRRKLVRRLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="cDNA EST yk258a1.3 comes from this gene; cDNA EST yk258a1.5 comes from this gene; cDNA EST yk532a11.3 comes from this gene"
                                                                                               TVPLSVSMITTVFREQIYQMPQCAYTLRKGAPDGPIVRFATLGESVYHRWECIEVEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFCMPNSRNNCEHIYEFPQLSQQLMDDMINNPNETRSDSFYFVENKLVMHNKADYSYD
                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA97806.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA97807.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using Genefinder; similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(3511. .3570,4639. .4750,4821. .5201,5689.
/gene="unc-119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="III"
/clone="M142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="unc-119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36306)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .36306) overlaps with the start of
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for a small
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MEDYASRLMAMHRTSFEPRHANNLANDFSCFANYQTLTEC"

join(34039 . 34101,34448 . 34750,35530 . 36306,
299276.1:105 . 698,299276.1:3364 . 11566,299276.1:1666 . .1772,
299276.1:2495 . 2795,299276.1:3714 . 3928,
299276.1:4056 . 4104,299276.1:5846 . 5958,
299276.1:6478 . 6729,299276.1:7169 . 7338)
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299276.1:16478 . 6729,299276.1:5846 . .5958,
299276.1:6478 . .6729,299276.1:7169 . .7338)
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MPKDNSHNSPOTPPKQPRKKPYMGIPPNRMGYSSDAPPFIESHGQQPPPQFFNSQHL
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RKILDPPLKYRKMTLMFEKVSTCFHYTLKKYMFYVLNTLMFSKRAPTRRARATIPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIEIILSIQSNTHYSSQLWSAVRARGCQFLGPAMQDDVLRLILMTLETGECIARKNLV
MYVVQTLASDYPQVSKTCVGHVQLLYRASCFNVLKRGESSLWGLKEEERTYESLRR
EHBSGIVQLAFESGLRIGPDQWSALLYADQSHRSHMQSIIDKLOSKNSYQGGVEELA
LAGSQTSMLVPAYRYFLTQVIPCLEFFAGIEHEDTSMRMIGDALHQIRILLKLHCSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAPTGQGGQWQEVLCCSICNRHFNETFLPVSLICGHVICRKCAE KPENQTKPCPHDDWKTTHSPSEYPNNVALLSVIFPRKQCMTLSGAVSEAEKRVDQLSI QIAKFFREADSERGTVSSREISRTLQRKVLALLCYQWREVDGRLKTLKWCRGISERV
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DKTLGELTPNLMKSPALSIRGQQAYLQLKRTIIPDTCWCGEDIRVGLVLUHKEYEVSD
VTKDAKATGFDESRAESAVLQVQKILSKPMTEYTARAPLDFTIGAIVANYSSSEMSDT
DDIPQLSADTLAALSWFQAEQQEKIEQLGGIIEKIDEDWGLSQFWYDDETSKKLVAE
GVAAALEGSEARPARIGCVSSPTLVKFFHETEEYKTGQIQLTLFEFDDRFGLKFPTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comes from this gene; cDNA EST yk470a9.3 comes from this gene; cDNA EST yk470a9.5 comes from this gene; cDNA EST yk476b6.5 comes from this gene; cDNA EST yk563c12.3 comes from this gene; cDNA EST yk663c9.3 comes from this gene; cDNA EST yk663c9.3 comes from this gene; cDNA EST yk679e8.3 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/db_xref="GI:3878739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"similar to Zinc finger, C3HC4 type (RING finger); CDNA EST EMBL:D67323 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SWISS-PROT:093899"
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VVSNSLDKIVDVKERISEAQGNASEAENAHLRMELRMAESQMAHLDPYTKNNCLLRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:045962"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA97808.1"
/db_xref="GI:3878737"
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31500. .31763,32933. .33043)
/gene="M142.5"
/note="predicted using Genefinder; cDNA_EST_EMBL:T01774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTSSDDDESKPVNFSNSPSSSSPSPYSTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22840. .23053)
/gene="vab-7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="VAB-7 even-skipped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oin(17427.
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REFERENCE
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ORGANISM
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TITLE
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MEDLINE
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Best Local
                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12191 AATACGTGGTAGGGTTTCGTGGCGAGACGCAGAGAAGTATCGTAGTCCGGAGTTGAGAGA 12132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 tgaaaagcagttgtgat 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tcatcgacaaagcaggaatggacaaccgcgcagaaagtatcaacggtttcagaatc----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaatatttatcaagagcacatccatcagcatttagaatttccacagttatcaccgttacca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATCAGGGGCGCCTTTTCGGAGGGTGTAGGCACATTGAGGCATTTGATAGATTTGCTCA 11892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccggttggtccaccatccaaaatttcataacggcatactggcatcgggacaatttgagtt 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAATGCATTCCCATCTATGATATACACTTTCACCGAGAGTTGCAAAACGGACTATTGGG 11952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----gcatgtccatttatgataaactggctgaccaatgatagcaaattgaactggttga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATCCACATAGCAAGAGTGAACTAACATTCCGAAAGTGTCCTTATCAGCACCCTCCACT 12012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCACCGCGTCTAGGCCACAACCATTCGAATCAAGAATATCCACTCTATCACCGTAGCCG 12072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Nematoda; Secernentea; Rhabditia: Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 36069)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latrellle,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,B., Silsten,I., Philosophy C., Markey, A., Mortimore,B.,
Staden,B., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,B., Silsten,I., Philosophy C., Markey, A., Mortimore,B.,
Staden,B., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,B., Shownkeen,R., Smaldon,N., Smith, Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,B., Shownkeen,R., Smaldon,N., Smith, Shownkeen,R., Smith, Shownkeen
                                                             jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis,
predictions from Genefinder (P. Green, U. Washington), and of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans cosmid ZK265, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M., Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                              available information
                                                                                                                                                                                    Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; Collagen; Cuticulin; Homeobox protein; Human G9A protein like
                                                                                                                                                                                                                                                          Dobson, R
                                                                                                                                                                                                                                                                                                                                           94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z81143.1 GI:1628350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4%;
Similarity 52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               .2 Mb of contiguous nucleotide sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11616 a
                                                                                                                                                                                                                                                                                                    (bases 1 to 36069)
   a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                         368 (6466),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36069 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C
                                                                                                                                                                                                                                                                                                                                                                             32-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62.6; DB 34
Pred. No. 7.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 36306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   III
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                                                                            other
                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                           using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions. The true left end of clone ZK265 is at 1 in this sequence. The true right end of clone ZK265 is at 2412 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone ZK265.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bin/display?db=wormace&class=Sequence &object=ZK265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The end of this sequence (35964. .36069) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 275713.
complement(join(6676. .7754,7804. .7870))
/gene="ZK265.2"
                                                                                                                                                                             /Translation="MPVAKEDSWAFQDIGSPFPEAPVRVPNQNNQYVALWYKHGKPIH
/Translation="MPVAKEDSWAFQDIGSPFPEAPVRVPNQNNQYVALWYKHGKPIH
GRAWNNDGVVECSFPYNKAELKGKLDLGQQIQILQYKGDYNSLGYWYEWLPLKQRHEN
NEGIREIVRCGNSVPVLAKLKGGTDKLGFLDLNTEVALFSNAGTTEK EGGAATANFMT
IFRHLRPPFPGLKVVDDLWYDLRYGDNFPSNAVPADGRALMYETGPHMQYVALWYKHG
DPVFGRSYPSSAGKTMAHFGKNNQENAGPEVSSMQLLTVPEASCMGLEXKWMPLSEGK
SSGWTTVHIGNSAPCILKDDKGLEVLGNLDLTIEKASAGYGGKEKIMTGAAVAKLKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHDYNIKKRVTVGGHTIGADVFKLPNFSFEPSKVSTLEDMIHDYFKRTGNIIRRSVRI
PLHDDLHQPSSSTKPFVGHVPGLLSLVCVPVFNKESSUBVANSRYENLQKMVNLCHNQPE
MFDIHTKNMILLLERWLIDSQTFDSYFLSHFFMKESSRTRIKTCVHNPAFIDLDEQCI
RHMSHSVRSNVSSASADLDDRVHVANIAKIAMLRYNKETISVINPAFNBUFASEDSSC
VYFYPGIKQCRAQRAASSTSQDMRSRLYPLHKAAEDGNAEEIRRFLKIGMDSNLRDDD
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                                                                     complement(6676. .7870)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(492 .736,782 . 1943 . .2076,2124 . .2289,2385 . .
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/gene="ZK265.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDIPFETPRLKLKRNAYATARMEIVTVSIEAVIFINIFDIKKRNQRSYYSDQHY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (TR:G287865)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGEVLDRLAEETQLNREQMNCFALFVYSESMSLQLQPDSLIDGKLKVDKWNTTIRKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASIDVNIQNNEGYRPIDYCGNHPAIQKILELQIFKSKINVDTSIGSFSIKSRSPEEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="predicted using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ZK265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ZK265.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="ZK265"
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EPPPLTHSOENC"
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LTSMCDKGRTLTRAQCSEKEGVWTPGYDISGHCFLMIYSILIITEEAIAYRHYQQVTD
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9879. .9976,12270. .12598,13623. .13818))
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Complement(8777. .13818)
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PGPVGAPGAPGGPGRDGEPGENGQDGQQGPEGPAGADGQPGHPGPDGPSGDVGEVGAP
GADAAYCPCPPRSAEMAATGSSDSQPASYEAPAATKGYDSPAPAA!KGYDAPAPTA
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                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB03516.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ZK265.6"
join(18275. .183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCWFVTYRMLYPAGFLASPIRRTVGRK"
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                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:Q94402"
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                                                                                                                                                                                                                                                                                                                  691 aatttcataacggcatactggcatcgggacaatttgagtttgaaaagcagttgtgatttc 750
                                                                                                                    atatgcacgatcaactttggttaacaaataatggatgaaacgaaatgacaacagttgttgt 870
                                                                                                                                                                                      ACTAACACCCAACTCAGCAGTCAGCCCCTTATTTGCTTCTTCAAAAAAAGCATTTCACATG 35079
                                                                                                                                                                                                                                                                           AATTGAATATGTGCATCCAGGTATTCCATGTCTCGCTTCTAATTCTGTCGTTGGAATCAT 35139
                        tacaaaaataccacgtggattca
                                                                                                                                                                                                              agatacctcaatctgtgcactaactgttttatcagcttccatgtaaaagcattgtactcg
GTAGTACATTCCACGTGGATCCA
                                                                                         ATATGCTTGATCAACTTTAGTGATGAATAAGGGATGGAAAGACACGACGACTGTGATACC 35019
                                                                                                                                                                                                                                                                                                                                                                       al Similarity
115; Conser
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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join(33403. .33438,34288.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Join(27566. .27635,27677. .27835,28839. .28913,29226. .29
29467. .29631,29755. .29902,29982. .30024,30072. .30293,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGVPLPNDDISLDDTFEETRRKLEKEMKEENERLREMLADEEEENSNDISDIDDDDGI
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56.7%;
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Pred. No. 9.8e-05;
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd
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110000
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T83869
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X13726122
T36122
T85356
Y785356
Y785353
X13033
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         Staphylococcus
Mycoplasma genital
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Location/Qualifiers

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SULT 2 3869/c 3869/c 183869; 183869; 20-AUG-1998 (first entry) 20-AUG-	376 atttggttctttaatggtaatactgatctggcattgatagaaaagctgtgatcgatc	256 tgcagatcttttcttgagtagacgaagttgcgcagctgc	Query Match 3.4%; Score 40; Best Local Similarity 47.9%; Pred. No. Matches 115; Conservative 0; Mismatch	SULT 1 1209_06 ntinuation (7 of 17) of V21209 from base Sequence split into 17 fragments LOCUS Fragment Name Begin End V21209_01 100001 210000 V21209_03 300001 410000 V21209_05 600001 510000 V21209_06 600001 910000 V21209_07 700001 810000 V21209_08 800001 910000 V21209_09 900001 1010000 V21209_10 1010000 V21209_11 1010000 V21209_11 1010001 1210000 V21209_11 1010001 1210000 V21209_11 100001 1210000 V21209_11 100001 1210000 V21209_13 1300001 1310000 V21209_13 1300001 1310000 V21209_14 100001 1510000 V21209_15 1500001 1510000 V21209_15 1500001 1510000 V21209_15 1500001 1510000 V21209_15 1500001 1510000	ALIGNMENTS	35 32.2 2.8 110000 1 X20248_07 36 32 2.8 716 1 X13803 37 32 2.8 1709 1 T84145 38 32 2.8 1709 1 V53488 39 32 2.8 2338 1 Q14183 40 32 2.8 2338 1 V23249 41 32 2.8 3775 1 V74549 42 32 2.8 3787 1 V74686 43 31.8 2.7 3972 1 X03040
hosphate deacetylase. e; antisense sequence; control; t; bacterial gene expression; d poisoning; scaled skin syndrome;	ttgatagaaaagctgtgatcgatcgc 435	cttgagtaaacgaagttgcgcagctgcagcaggttttgctgcggcacc 315	DB 1; Length 110000; 0.54; ches 125; Indels 0; Gaps 0;	600001 (Methanococcus jannaschii circular V21209 Accession V21209	VTS	Continuation (8 of Enterococcus faeca DNA encoding one u DNA encoding a x-p N.clavipes draglin Nephila clavipes s Staphylococcus aur

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RESULT X33788/c ID X337 AC X337 DT 25-J DT 25-J DT S: a a KW S: a KW acut KW card KW card KW toxil KW cell KW cell KW coste KW coste KW ss. OS Stap PN 18-X PF 14-S PF 14-S PR 12-S PR 12-S PR 12-S PR 12-S PR 12-S PR 14-S PR 12-S PR 14-S PR 14-S PR 14-S PR 12-S PR 14-S PR
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Best Local
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                                                                                                                                                                                                                                                                                                                      S. aureus coding sequence SEQ ID NO. 45.

S. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; othicis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis; darcryocystitis; epiddymnits; intrarenal abscess; perinephric abscess; toxic shock syndrome; impetigo; folliculitis; cutaneous abscess; cellulitis; wound infection, bacterial myositis; septic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a Staphylococcus aureus protein, that, based on homology with an Escherichia coli protein, is believed to be a N-acetylglucosamine-6-phosphate deacetylase. The present sequence was obtained from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequence is also useful as a source of regulatory elements for the DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.

180 A; 75 C; 107 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X33788
X33788;
                                                                                                                                                                                                                                                                                                  osteomyelitis;
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                                                               (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                14-SEP-1998; U18987.
12-SEP-1997; US-058710.
                                                                                                                                                                   18-MAR-1999.
                                                                                                                                                                                                                               Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aureus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-424969
P-PSDB; W27907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
      MKR, Lonetto MA, -229138/19.
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                                                                                                                                                                                                                                                                                              Helicobacter pylori infection;
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                                 Warren PV;
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No. 0.83;
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                                                                                                                                                                                                                                                                                              stomach cancer; gastritis;
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AC DTR PRESENTATION OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
X33781/c
ID X33781 standard; DNA; 1182
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s. aureus coding sequence SEQ ID NO. 8.

S. aureus infection; diagnosis; therapy; central nervous system disorder; upper respiratory tract infection; otilis media; bacterial tracheitis; acute epiglottitis; thyroiditis; empyema; lung abscess; splenic abscess; cardiac infection; infective endocarditis; secretory diarrhoea; ulcer; retroperitoneal abscess; cerebral abscess; blepharitis; conjunctivitis; keratitis; endophthalmitis; preseptal cellulitis; orbital cellulitis;
                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus WO9912557-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              darcryocystitis; epididymitis; intrarenal abscess; perinephric abscess; toxic shock syndrome; impetigo; folliculitis; cutaneous abscess; cellulitis; wound infection; bacterial myositis; septic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Staphylococcus aureus polynucleotides Claim 21; Page 90-91; 102pp; English.
This sequence represents a S. aureus polynucleotide of The invention also relates to the polypeptides encoded
                                      New isolated Staphylococcus aureus polynucleotides Claim 20; Page 65-67; 102pp; English.
                                                                                                                       WPI; 99-229138/19.
P-PSDB; Y05308.
                                                                                                                                                                                                        Burnham MKR, Lonetto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X33781;
25-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. aureus polynucleotides.
                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                             12-SEP-1997;
                                                                                                                                                                                                                                                                                                                               14-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1126 aagtgtagtacagaaagcaat 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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the sequence listing in the specification. They
are included to maintain the nucleotide numberi
given in the specification for this DNA sequence
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given in the specification for this DNA seq
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Pred. No. 1
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(BUJA/) BUJARD H. Bujard H, Pan W, T WPI; 98-240088/21.

Tolle

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RESULT
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Best Local
09-APR-1998.
02-OCT-1997;
02-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are
                                                                                                                                                                                                                                            P. falciparum gp190 DNA. gp190; malaria; MSP-1; m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                          Plasmodium falciparum
                                                                                                                                                                                                                     monoclonal antibody; passive
                                                                                                                                                                                                                                                                                                                     V35363 standard;
V35363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.

Sequence 7563 BP; 2584 A; 1028 C; 1476 G; 2229 T;
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Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch
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05-JAN-1996; US-009861.
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                                                                                                                                                                                                                     merozoite surface protein;
assive immunisation; parasi
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Matches 123
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11-SEP-1985;
21-FEB-1985; 301173.
22-FEB-1984; GB-004692.
26-SEP-1984; GB-024340.
21-FEB-1985; GB-004429.
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                      Claim 2; Fig 1; 51pp; English.

The sequence encoding the P195 protein of Plasmodium falciparum (N50530) and a peptide comprising at least one of its epitopes (see P50777) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new DNA sequence, together with a carrier.
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                                                                                                                                                                                                                                                                                Cloned
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     Sequence
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les 123; Conserv
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protein of Plasmodium falciparum
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Pred. No. 3.9;
0; Mismatches
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use in vacci
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428

Query Match Best Local S Matches 72

72; Conser

Conservative

3.0%; 53.7%;

Score 34.8; DE Pred. No. 4.9; 0; Mismatches

62; μ,

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Length 8395;

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Best Local
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04-MAY-1998; U08985.
14-NOV-1997; US-06600
06-MAY-1997; US-04400
16-MAY-1997; US-04669
                                             can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
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WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides and folypeptides and folypeptides and folypeptides are favorable products for the detection of Enterococcus and folypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis genome contig SEQ ID NO:217. Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X13154
X13154;
                         polypeptides encoded by the Enterococcus faecalis nucleotide secan be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                              A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system
Sequence
                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                 use in vaccines
                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
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23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                ; US-066009.
; US-044031.
; US-046655.
B₽;
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RESULT 9

X13342/c

ID X1342;
AC X1342;
AC X1342;
AC X1342;
AC X1342;
BDE Enterococcus faeca
KW Vaccine; attenuati
OS Enterococcus faeca
KW Vaccine; attenuati
OS Enterococcus faeca
PN W0985055-A2.

PD 12-NOV-1998; U0898
PF 04-MAY-1998; U0898
PR 14-NOV-1997; US-04
PR 16-MAY-1997; US-04
PT 1-MAY-1997; US-04
PR 16-MAY-1997; US-04
PR 16-MAY-1998; U08-08
PF 14-MOY-1998; U08-08
PF 14-MOY-1997; U08-08
PF 14-MOY-1997; U08-08
PF 14-MOY-1997; U08-08
PF 14-MOY-198; U08-08
PF 14-MOY-
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Best Local
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
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New isolated Enter
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                                                                                                                                                                                                                                                                                                                      865
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atcataaagacctttcacataaacatgtccttcgaatgcattacgtgtattaaaattgat 1044
                                                                                                                                                                                                                                                                                                    tgttgttacaaaaataccacgtggattcagagatcgtgtacgcgcaacattgcatgaatc 924
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faecalis; contig; detection; Enteroco
enuation; computer readable medium; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevent or attenuate an Enterococcal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34.6;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170;
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В QΥ B Qγ 밁 Qy Вþ Qy

QУ 망 ΩV Вþ δ

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1974

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TAATGCTTCTAATAATAATAAAAGGTATATAATTCCCTTTCTGTTATTTTGTTCAGGA 1798

ttatttagcaaatatttatcaagagcacatccatcagcatttagaatttccacagta

547

490

TACCTTAATTAGTTTGCATACAATTGGATGGCTGCTATTAATAATGTTTACAACTACAGA 1855 tccgcatatttgtatacgtgagcttcttggccagccattaaatctgttggatattccaaa TTGATACATAGTGTTTAAAATAATAATTATATATATGCATTTTTGGAAAATAAACATTCAA 1915

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RESULT
V23659,
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Query Match
Best Local S
Matches 88
                                                                              might be
Sequence
                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding interleukin-1 receptor accessory protein used for therapeutic modulation of II-1 activity Claim 2; Fig 1; 95pp; English.

This cDNA clone codes for human interleukin-1 receptor accessory molecule (III-R ACM) (see W53897), a new member of the immunoglobulin superfamily that forms a complex with type 1 III-R and which has higher affinity forms than the receptor itself, suggesting that the known high and low affinity forms of III-R are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAR-1998.
26-AUG-1996;
26-AUG-1996;
                                                                                                        Nucleic acid fragments are useful as diagnostic probes and primers, for isolation of II1-R AcM-encoding genomic sequences, for in situ hybridisation to determine chromosomal localisation of the gene, for chromosome identification and for identifying mutations that
                                                                                                                                                                      W53898-915) of IL1-R AcM. Recombinant IL1-R AcM can be used to identify IL-1R agonists and antagonists useful for therapeutic modulation of IL-1 activity, and to raise specific antibodies
                                                                                                                                                                                                       and recombinant vectors are claimed. Also claimed are isolated nucleic acid molecules encoding epitope-bearing portions (see W53898-915) of IL1-R ACM. Recombinant IL1-R ACM can be used to
                                                                                                                                                                                                                                                                  in fact the receptor with or without IL1-R AcM, respectively. The 2155 bp sequence is present in clone HMEEJ52 (deposited as ATCC 97666) derived from microvascular epithelium (no details of isolation given). Recombinant expression in Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal transduction; infection; rheumatoid arthritis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1998 (first entry)
Human interleukin-1 receptor accessory molecule cDNA
                                                                                                                                                                                                                                                      mammalian and insect cells is described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W53897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 98-230267/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bednarik DP, Olsen HS, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-1 receptor accessory molecule;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; cDNA; 2155
 88; Conservative
                                                                              linked to disease.
2155 BP; 709
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303..353
/*tag= b
354..1370
.*+>q= c
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                3.0%;
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   0;
Score 34.6; E
Pred. No. 3;
0; Mismatches
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                                                                                                                                                                                                                                                     Recombinant host cells
                               DB 1;
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   ; 68
                                                                              G;
                                Length 2155;
                                                                                584
 0;
   Gaps
   0
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anti-S.aureus vaccines (Claim 1; Page 544-549; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer readable medium; vaccine; S.aureus infection; immunodet cellulitis; eyelid infection; food poisoning; osteomyelitis; the skin infection; surgical wound infection; scalded skin syndrome;
                               be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalled skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                            EP-786519-A2.
30-JUL-1997:
07-JAN-1997: 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                           Polynucleotide(s) and proteins derived stored on computer readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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their fragments) are useful as pa
logues of any of the S.aureus DNA
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"these bases represent a line
the sequence listing in the s
are included to maintain the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "these bases represent a line of missing text the sequence listing in the specification. The are included to maintain the nucleotide number given in the specification for this DNA seque.7980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are
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.6180
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
.2580
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                  primers or probes
 sequences
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used
                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus in the production of
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                    for
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Query Match Best Local

Similarity

513

Score 34.6; Pred. No. 8

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DВ

Length 21252;

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Conservative

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Mismatches

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Query Match
Best Local
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14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                     Claim 1; Page 615-626; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2615
                                                                                                                                                                                                                                                      New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis; contig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       computer readable medium.
                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                          WO9850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis
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                            can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                       WPI; 99-045171/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttccggcaacttgacgtccaccttcatcattacggcaaccttcttgatcataaagacctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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; US-066009.
; US-044031.
; US-046655.
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y; detection; Enteroc
Α;
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                                                                                                                                                 Enterococcus faecalis genome contig SEQ ID NO:859.

Enterococcus faecalis; contig; detection; Enterococca

vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis.

WO985055-A2.

12-WOV-1998.
14-WOV-1998.
16-MAY-1997; US-066009.
R 14-WOV-1997; US-044031.
R 16-MAY-1997; US-046655.
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X20248_01

X20248_03

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X20248_08
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                    olated Enterococcus faecalis polynucleotides and polypeptides to develop products for the detection of Enterococcus and for vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                            HUMAN GENOME SCI INC.
SC, Dillon PJ, Kunsch CA;
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RESULT 15
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31-JAN-1996;
31-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                            Caries; antigen I/II; genetic immunisation; Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 982 nucleotide sequences isolated from the Enterococcus faecalis X12938 to X13919 represent these nucleotide sequences which are nucleotide sequences, also known as contigs. The computer-based
           (W02098), a 185 kDa cell surface protein at least partly responsi for S. mutans adhesion to teeth. The T/II antigen includes a series of overlapping T-cell, B-cell and adhesion epitopes. Fragments (see also T36111-21) of the gene can be used to produce recombinant polypeptides (W02087-97) carrying such epitopes for use in vaccines for immunisation against dental caries. The DNA
                                                                                                                                                                                                             (UNME-) UNITED MEDICAL Kelly C, Lehner T; WPI; 96-371434/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can
                                                                                                                                                                Nucleic acid encoding polypeptide for prevention or treatment of dental caries - which stimulates T or B cell response, and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. mutans antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T36122;
26-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2022-2024; 2084pp;
                                                                                       A Streptococcus mutans go
(W02098), a 185 kDa cell
                                                                                                                     Disclosure;
                                                                                                                                                    adheres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used in vaccines to prevent or attenuate an
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                                                                                                                                                     to tooth
                                                                                                                                                                                                W02098
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 can also
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                                                                                                                                                                                                                                                                                                                    sequence (vqvsrkglvryfyrskmvkrflklstsiqwtl) that differs from amino acids 618-650 given on page 46 of the specification"
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/note= "bases 2001-2049 code for an amino acid
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ION: 7161849 INFORMATION: INFORMATION:	NN FOR SEQ ID NO: S CHARACTERISTICS I: 1867 base pai NUCLEIC ACID DEDNESS: double SQY: linear TYPE: DNA (gen SQURCE: SQURCE: 1: 164A-1	APPLICATION UNMBER: US. APPLICATION UNMBER: US. FILING DATE: 19911008 CLASSIFICATION: 435 ATTORNEY_AGENT INFORMATION NAME: BENT, Stephen A. REGISTRATION NUMBER: 2: REFERENCE_DOCKET NUMBER TELEOMMUNICATION INFORMAT TELEPHONE: (703)836-931 TELEFAX: (703)683-4109 TELEFAX: 899149	ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, CITY: Alexandria STATE: Virginia COUNTRY: USA ZIP: 2313-029 MPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: PC-DOS/MS SOFTWARE: Patentin Release	ILT 1 17-772-087-1/c squence 1, Application 18-18-18-18-18-18-18-18-18-18-18-18-18-1		$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
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; Applicant: Koga, Toshihiko;Okahashi, Nobuo;Takahashi, Ichiro;Shibuya, Koji;Ohta, Hirotaka
;Shibuya, Koji;Ohta, Hirotaka
;Title Of INVENTION: METHOD FOR PREPARING VACCINE FOR DENTAL
;CARIES AND VACCINAL COMPOSITIONS FOR DENTAL CARIES USED AS NASAI
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; APPLICANT: BINNS, MATTHEW M.;BOURSNELL, MICHAEL;CAMPBELL, JOAN I.A.;TOMLEY, FIONA M.
TITLE OF INVENTION: FOWLDOX VIRUS PROMOTERS; NUMBER OF SEQUENCES: 22
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PCT-US96-05320A-705
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Best Local Similarity
Matches 89; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                             APPLICATION NUMBER: 08/476,102
FILLING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            ZIP: 20003-3934

COMPUTER READABLE FORM:
MEDIIM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1528
                                                                                                                                                                                                                                              OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: J. Craig Venter TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1708 TGGTTCTGTTAAGTTTCCGTCTTCATTTTTATGTTTTTCAAGTTCTGCCAGTGCAGCTTT 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1588 TTGATATTTGGCAAGATCTGCTTGATACTTAGCAAGTTTTGCTTCGTAATCAGCTTTAGC 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 tttgtatacgtgagcttcttggccagccattaaatctgttggatattccaaattattag 498
                                                                                                                                                                                                APPLICATION NUMBER: PCT/US FILING DATE: April22, 1996 CLASSIFICATION:
                                          REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New CITY: Washington
                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                             Eric K. Steffe
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                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rockville, MD 20850
United States of America
Johns Hopkins University
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United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Owen White Hamilton O. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720 Rutland Avenue
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                                    1488
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                                                                                                                                                                                                                                                                                    6.2
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US-08-781-802-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.8%;
Best Local Similarity 56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                TELEFAX: 312-913-0002 INFORMATION FOR SEQ ID NO:
                                                                                                       FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
                                                                                                                                                                     FILING DATE: 11-JAN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    FILING DATE: 12-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 07-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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APPLICANT: CASADABAN, Malcolm
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SEQUENCE CHARACTERISTICS:
                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 TATGTCAAAGCCAAAAAGTGCGGTGAAATTTGCATTTTATACGGCA 186
                                             TELEPHONE:
                                                                            REFERENCE/DOCKET NUMBER: 95
                                                                                                                                                                                   APPLICATION NUMBER: US 60
                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/019,580 FILING DATE: 12-JUN-1996
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 300 S. CITY: Chicago
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                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIKENS, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                         10-JAN-1997
                                                                                                                                       UMBER: US 60/001,995
01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stable Biocatalysts for Ester Hydrolysis 12
                                                                                                                                                                                                                                                                                                                   US 08/694,078
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                                                                            95,963-E
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Pred. No. 2.4;
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Best Local Similarity
Matches 129; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DA
TITLE OF INVENTION: PROTEIN, A
TITLE OF INVENTION: CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "E011 sequence of longest
OTHER INFORMATION: open reading frame; other possible start codons ATG/met4;
OTHER INFORMATION: TTG/Leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
FEATURE:
                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2846 TCAATCTGCTGCTATTTTCTTCACCATATGGACGTTATTCAAAAACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2666 GATCCACTCTATTTATGCCCTCTACAGGGTTACAAAACAATTCTTTTGTAACTATATAAA 2725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 catcattacggcaaccttcttgatcataaagacctttcacataaacatgt 1012
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LOCATION: 197..1699
OTHER INFORMATION: /
                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 22046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTTCCATCTGTCTGAGAGTCAAATGGTCGTCTCACCAAGTTAACTTGTTAATGAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOLATED DNA CODING FOR SPIDER SILK PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                             US/08/425,069
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                                                                                                                                                         Version
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REFERENCE/DOCKET NUMBER: 1447-106P TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)

(703) 205-80 03) 205-8050

205-8000

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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08317844B Patent No. 5989894
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                                                                                                                                                                        CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & STREET: 301 No. 598984th Washington CITY: Falls Church
STATE: Virginia
                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1674 TTGTCCAGCACCTTGTCCACCTAATCCTCCTTGTCCAGCACCTCCAGCTGCTGCTGCTGC 1615
                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                            ZIP:
                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: Structure of a protein superfiber: TITLE: drafline silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS: Xu, Ming AUTHORS: Lewis, R
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LOCATION: 1...
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TOPOLOGY: lin
                APPLICATION NUMBER:
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7120-7124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                US/08/317,844B
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Pred. No. 6.4;
0; Mismatches
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Street
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US-08-559-303B-72/c

: Sequence 72, Applicat.

: Patent No. 5824501

: GENERAL INFORMATION:
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Best Local Similarity
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TELEPAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                               TITLE OF ANY TOTAL TRANSPORT OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
AMSTER, ROTHSTEIN & EBENSTEIN
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                      1614 TGCACCTGCACCTTGTCCACCTAATCCTCCTCGACCAGAACCTTGGCTTCCAAGTCCTCC 1555
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                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                  APPLICANT: NATHAN A. APPLICANT: GRODEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,9
CURRENT APPLICATION DATA:
                                                                                                                      STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 ttctgcagatcttttcttgagtaaacgaagttgcgcagctgcaggttttgctgcggc 312
               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII
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PAGES: 7120-7124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
                                                                                                 ZIP:
                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE: Structure of a TITLE: drafline silk
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                                                                                                 10016
                                                                                                                                  NEW YORK
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                                                                                                               U.S.A.
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                                                                INCH 1.44 Mb STORAGE DISKETTE
                                                                                                                                                                                                                METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME 78
                                                                                                                                                                                                                                                                                  ELLIS, JAMES GERMAN, AND JOANNA
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dragline silk protein"
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RESULT 9
US-07-781-034-4/c
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Best Local Similarity 44.4
Matches 127; Conservative
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/07781034 Patent No. 5442050
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 72:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 4437
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                           COUNTRY: UZIP: 02173
                                                                                                            STREET: Two Mil
CITY: Lexington
STATE: Massachu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                  ADDRESSEE:
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                                                                                                              Massachusetts
                                                                                                                                                 Two Militia Drive
                                                                                                                                                                                                                                                          Fishman, Jay A.
                                                                                             USA
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                                                                                                                                                                  Hamilton,
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                                                                                                                                                                                                                       Molecular Cloning of Antigens Shared By Rat- and Human-Derived Pneumocystis Carinii
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                                                                                                                                                                  Brook, Smith & Reynolds, P.C
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Pred. No. 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application PC/TUS9208328 GENERAL INFORMATION:
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Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 861-954
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08328
FILING DATE: 19920930
                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: MGH91-02A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/781,034
FILING DATE: 30-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                           CATY: Lexington
STATE: Masc
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 TTCCTCACATTCATCACATTCGTCA 516
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                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 18-OCT-1991
                                                                                                                                                                                                                                                                                                     ZIP:
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                      Massachusetts
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(617) 861-9540
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                                  30-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular Cloning of Antigens Shared By
                                                   US 07/768,166
                                                                                                      US 07/781,034
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 Mismatches

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REGISTRATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08764100 Patent No. 5773700
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Best Local Similarity 51.0%;
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TELEX: 951794
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 27
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HYPOTHETICAL: NO
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LENGTH: '1189 base pairs
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                                                                                                                                                                                                                                                                                                                                                                STREET: 975 Call
                                                                                                 FILING DATE:
                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74; Conservative
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                                                                                                                                                                                                                                                                                                                                                      CA
                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                        975 California Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gielen L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Haan, Petrus T
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                                                                                                                                                                                                                                                                               Floppy disk
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/08764100 Patent No. 5773700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                        APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION UNMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700ris, Allen E.
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 857-11: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        ZIP: 943U4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TRM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: van Grinsven o...
APPLICANT: De Haan, Petrus T
APPLICANT: Gielen L., Johann
                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Improvementifice OF INVENTION: Compounds
                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LENGTH: 3414 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 354-3592
                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/764,100 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 975 Call
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                     PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peters, Dirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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(415) 354-3592
                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Improvements in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robert W
                                                                                                                                                   US 08/032,235
                                                                                                                                                                                    US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johannes J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.4;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martinus Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137-1061
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                                                                                                                                                                                                                                                                                     Version #1.25
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                                              FILING DATE:

FILING DATE:

17-MAR-1993

APPLICATION NUMBER: GB 9206016.9

FILING DATE: 17-MAR-1992

APPLICATION NUMBER: GB 9206016.9

FILING DATE: 19-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5773700715, Allen E.

REGISTRATION NUMBER: 34,490

REFERENCE/DOCKET NUMBER: 137-1061

TELECOMMUNICATION 19070RMATION:

"PRIRPHONE: (415) 354-3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vuery match 2.7%;
Best Local Similarity 50.3%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO:
                                    TELEFAX: (415) 857-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gielen L., Johannes J.
APPLICANT: Peters, Dirk
APPLICANT: Goldbach, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3414 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/214,064
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o. 5773700
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4970 base pairs
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De Haan, Petrus T.
                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Improvements in or Relating to Organic
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Pred. No. 1:
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US-08-764-100-20
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Sequence 20, App...
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Best Local Similarity
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                                                                                                                                                                                                                                                                                TELEFAX: (415) 857-11: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PALEDITIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,100
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 354-3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: No. 5773700ris, Allen
REGISTRATION NUMBER: 34,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gielen L.,
APPLICANT: Peters, Din
APPLICANT: Goldbach, F
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                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US UN APPLICATION NUMBER: US UN APPLICATION NUMBER: US ON APPLICATION OF APP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                   TOPOLOGY:
                                                                                       STRANDEDNESS:
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                                                                                                                                                                                   LENGTH:
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De Haan, Petrus T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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NFORMATION FOR
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APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
                             NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      APPLICATION NUMBER: US 60/035,022 FILING DATE: 10-JAN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               FILING DATE: 10-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/033,177 FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: No. 5986082artis Corporation
T: 3054 Cornwallis Road
Research Triangle Park
No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%;
Similarity 50.3%;
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10-JAN-1997
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             541-8689
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Pred. No. 14;
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LENGTH: 5655 base pairs
TYPE: nucleic acid
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LOCATION: 4271..4474
OTHER INFORMATION: /
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                  aaacgaaatgacaacagttgttgttacaaaaat 879
                                                                 ttccatgtaaaagcattgtactcgatatgcacgatcaactttggtaacaaataatggatg 846
AAAATTAATTAAAAGAAAACTATTTCATAAAAT 1486
                                                   TAGAAGATAAAAAATTATATCAGATTGATTCAATTAAATTTTATAATAATATCATTTTAA 1453
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ES Description	SUMMARIES	DB	% Query Score Match Length DB ID	% Query Match	Score	Result	Res

larva cDNA

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Onchocerca volvulus.

Onchocerca volvulus

Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;

Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 665)

Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.

Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
                                                                                                                                                                                                                                                                                                                                                                                        mRNA S
                                                         Molecular Parasitology
Smith College Department
Department of Biological
Department of Biological College, Northampton, MA, Tel: 4135853826
Fax: 4135853786
                                                                                                                            Genes expressed in molting L3
Unpublished (1997)
On Sep 12, 1996 this sequence
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                              AII11196 665 bp mRNA EST 31-AUG-1998 SWOV3MCA1232SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1232 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmenybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="SWOv3MCA1232"
/clone_lib="Onchocerca volvulus
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/db_xref="taxon:6282"
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REFERENCE

AUTHORS TITLE

SOURCE ORGANISM VERSION KEYWORDS RESULT 1 AI111196/c

LOCUS DEFINITION

ACCESSION

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AUTHORS
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atttgagtttgaaaagcagttgtgatttcagatacctcaatctgtgcactaactgtttta
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
On Sep 19, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                       The library is available from Dr. slustigm@nybc.org)."
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/db_xref="taxon:6282"
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(SL96MLW-OvmL3)"
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SWOV3WCA1879SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO1879 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405188.
Contact: Steven A. Williams
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                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                       College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science
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              Note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
                                                                                                                                                                                                                                                                                       /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                              /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
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(SL96MLW-OvmL3)"
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and converted to double-stranded cDNA using
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aatgcattacgtgtattaaaattgattgttattgaagttggtccacattcaatttctggc 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTTCATCATTTCGGCATCCTGCCTGATCGTATAAGCCTTTCACGTATACATGTCCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTGTACGTGCTACATTACAGGAATCAAACGGAAGTTCAATTCCGGCTACCTGACGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGGATGGAATGAGNNGACAACAACTGATGTGACAAAAATACCACGTGGATTTAACGAA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aatggatgaaacgaaatgacaacagttgttgttacaaaaaataccacgtggattcagagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAATTTGTGTNGCAAATGCAGTTGTCATTTCGGAAATTTCAAGTTGAGCGCTAACTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACAGGTTGTCCGGGATGGTCCACCATCAAGAATCTCATATCGGCATACAGGCATCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGGATTACGAGTATTAAAGTTGACAGTAATTGATGTTGGACCACATTCAATTTGTGGT
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1 (bases 1 to 639)
Williams, S. A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:l Contact: Steven A. Williams
                                                                                                                                                      Onchocerca volvulus
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                  SWOV3MCAM12G08SK
                                                                                                                                                                                                  Onchocerca volvulus.
                                                                                                                                 Filarioidea; Onchocercidae;
                                                                                                                                                                                                                                               AI322117.1
                                                                                                                                                                                                                                                                                                          SWOV3MCAM12G08SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM12G08 5',
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Pred. No. 1.3e-87;
0; Mismatches 97
                                                                                                                                      Onchocerca.
                                                                                                                                                      Secernentea; Spiruria; Spirurida;
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                      replaced gi:1797212
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                                                                                           Lustigman,
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nes 403; Conser
                                ttggtccacattcaatttctggctcaccttcgacaccattgtcaaccggaatcgaat 1112
                                                                             CTTTCACGTATACATGTCCTTCAAATGGAGTACGAGTATTAAAGTTGACAGTAATTGATG
                                                                                                                                                                                                                                                                       aaataccacgtggattcagagatcgtgtacgcgcaacattgcatgaatcaaatggaagtg
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TTGGACCACATTCAATTTCTGGTTCACCTTCTACACCGTTATCAACCGGAATAGCAT
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2 or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The library is available from slustigm@nybc.org)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="molting
/lab_host="XL1-Blue
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/strain="Kumba, Camero
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Pred. No. 4.2e-86;
""smatches 74;
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     515
                                                         549
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  gcacatccatcagcatttagaatttccacagtatcaccgttaccatcatcgacaaagcag 574
                                                                              tcttggccagccattaaatctgttggatattccaaattatttagcaaatatttatcaaga 514
                                                                                                                                                        ATACTAATCTGGCATGGATAATAAATCTCAGATCGATCAGCGTATTTATAAACATGAGCT 550
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                                                 TCTTGGCCAGCCATTAGATNTGATAGATATTCCAAATTGTTGAGTAAATACTTGTCCACA 490
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SWOV3MCAM02C01SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02C01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
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Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
On Oct 30, 1997 this sequence version replaced gi:2160807.
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/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately down molting larvae (mL3),2000 larvae from day 1, 2 or 3
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a 106 c 138 g 178 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams
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/clone_lib="Onchocerca volvulus
(SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                              Score 355.8; DB 3 Pred. No. 2.4e-85;
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                                                                                                                                                                                                                  Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science Center, College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On May 5, 1995 this sequence version replaced gi:797827
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA585626 776 bp mrNA EST 30-DEC-199/
SW3D9CA349SK Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9) Brugia malayi cDNA clone SW3D9CA349 5', mrNA
                                                                                                                                          Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brugia malayi.
Brugia malayi
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AA585626
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                                                                                                                                                                                                                                                                                             Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                         Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                     arioidea; Onchocercidae; Brugia. (bases 1 to 776)
                                 /clone="SW3D9CA349"
/clone_lib="Brugia malayi L3 molting-day 9 larva cDNA
(SAW97MLW-BmL3d9)"
/dev_stage="third stage larvae, nine
/lab_host="E. coli XL1-Blue MRF'"
                                                                                        /organism="Brugia malayi"
/db_xref="taxon:6279"
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AA668051.1
EST.
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria;
Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 537)
Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lus
Genes expressed in molting L3 larvae of Onchocerca vo
Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:8023
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                               AA668051 537 bp mRNA
SWOv3MCAM02A04SK Onchocerca volvulus
(SU96MLW-OvmL3) Onchocerca volvulus
                                                                                                                                                                                                          Onchocerca volvulus
                                                                                                                                                                                                                                                                                                   mRNA sequence.
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85.2%;

 Mismatches

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                                                                                                                                                                                                       gaaattccggcaacttgacgtccaccttcatcattacggcaaccttcttgatcataaaga 994
                                                                                                              AAAATACCACGTGGATTTAACGAACGTGTACGTGCTACATTACAGGAATCAAACGGAAGT
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/lab_host="XLI-Blue MRF'"
/lab_host="XLI-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Yho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately do molting larvae (mL3),2000 larvae from day 1, 2 or 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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/lab_host="XL1-Blue MRF'"
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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larvae, 13, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-2ap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome@smith.edu
                                                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                            (SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Kumba, Cameroons"
                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="molting L3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Onchocerca volvulus molting L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="SWOv3MCAM06H12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ∕organism="Onchocerca volvulus"
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Best Local Similarity
Matches 367; Conserv
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                                                                                                                                                   Onchocerca volvulus

Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spiruria

Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 531)

1 (bases 1 to 531)

Williams, S.A., Lizotte-Waniewski, M., Laney, S., Lustigman, S., Williams, S.A., Lizotte-Waniewski, M., Geisel, S., Jost, S., Kucaba, Hillier, L., Allen, M., Bowles, L., Geisel, S., Jost, S., Kucaba, Martin, J., Steptoe, M., Theising, B., White, Y., Wylie, T., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S.,
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Scienc
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                   SWOV3MCAM03B05 Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone onch17 5' similar TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR. ;, mRNA
                                                    Molecular Parasitology
                                                                                        Unpublished (1998)
On Jan 19, 1998 this sequence
                                                                                                                            Underwood, K. and Marra, M. Molecular Parasitology OvmL3
                                                                           Contact: Steven A.
                                                                                                                                                                                                                                                                                                                                Onchocerca volvulus.
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124 c 123 g
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Pred. No. 3.2e-70;
0; Mismatches 75;
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please reference the Williams lab clone id -
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The library was constructed by Sara Lustigman and Michel
Lizotte-Waniewski in the Laboratory of Dr. S.A.Williams.
library is available from Dr. Sara Lustigman email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1086 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michalle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigminybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="molting L3"
/lab_host="XL1-Blue MRF/"
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="onch17"
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SWOV3MCA691SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO691 5', mRNA
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Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On May 9, 1995 this sequence version replaced gi:802401 Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S Genes expressed in molting L3 larvae of Onchocerca volvulus
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                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1006 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Wanlewski in the Laboratory of Dr. S. A. Williams.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately cap.
                                                                                                                                                                                                                                                                                                                                                                                              slustigm@nybc.org)."
1 71 c .77 g
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lizotte-Waniewski in the Laboratory of Dr. S. A. William The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The ABI trace of this sequence can be viewed at http://www.sanger.ac.uk/brugia/3D6/MB3D6AA4G10T3.html Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2285052
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
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1 (bases 1 to 354)
Blaxter,M.L., Waterfall,M., Daub,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +44 131 650 6760 Fax: +44 131 670 5450
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Brugia malayi
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                                      /dev_stage="third stage larvae, six days after infection"
/lab_host="E. coli XL1-Blue"
/lab_host="E. coli XL1-Blue"
/lab_host="E. coli XL1-Blue"
/note=""vector: lambdaZapII (UniZap XR); Site_1: Eco R I
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
[5' end); Site_1: Xho I (3' end); Brugia malayi is a
[5' end); Site_1: Xho I (3' end); Brugia malayi is a
[5' end); Site_2: Xho I (3' end); Brugia malayi isolated
from the peritoneal cavity of jirds six days after
infection. The mRNA was converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNASE H and DNAPOI I. The library had 2 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Michelle Lizotte-Waniewski.
The library is available from The Filarial Genome Project
Resource Center: contact Dr. S.A. Williams, Clark Science
Center Gmith College Northampton WA 01063 [18] bbone +1
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/strain="TRS Labs"
                                                                                                                                                                                                                                                                                                                                                                                                          /sex="mixed"
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larvae SAW96MLW-BmL3d6"
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ter, Smith College, Northampton, MA 01063 USA phone +1 585 3826 fax +1 413 585 3786 email genome@smith.edu."
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                                                                                                                                                                                                                                                                                                                      Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 466)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:802407.
Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                    Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onchocerca volvulus
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                                                                                                                                                                                                                                                                     genome@smith.edu
/dev_stage="moiting L3"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1 : Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
Xho I; Filarial nematode from infected black flies in
                                                                                                  /clone="SWmL3CO758"
/clone_lib="Onchocerca volvulus
(SL96MLW-OvmL3)"
                                                                                                                                                         /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                           /organism="Onchocerca volvulus"
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                                                       Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae Unpublished (1997)
On Sep 12, 1996 this sequence version Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                       AA618952.1
EST.
                                                                                                                                                                                                                                                                                                                                 sequence.
                                                                                                                                                                                                                                                                                                                                                                 12-NOV SWOV3NCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO20;
                                                                                                                                                                                                                                            Onchocerca volvulus.
                  Smith College
                                         Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture.
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                                                                                                                                                                                                                                                                                                              GI:2522828
Biological Sciences, Clark Science Center, Smith
                  Department of Biological Sciences
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                                                                                                                                Laney, S. and Lustigman, S. of Onchocerca volvulus
                                                                                  replaced gi:1405277
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(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO318 5', mRNA
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Fax: 4135853786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmenybc.org)."

2 others
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/lab_host="XL1-Blue MRF'"
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(SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 263; DB 36;
Pred. No. 2.1e-60;
                                                                                                 mRNA
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                                                                                               12-NOV-1997
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Best Local Similarity
Matches 305; Conserv
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                                           536
                                                                                                                                476
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135
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                                                                                                                                                                                                                                                                                                                                                      375 GCAGCTGCAGCACCATTTCGTGANCGAACTGCTCCAAATCCTTGTGGTTCTGCACAT 316
                                                                                                                                                                                                                                                                                                                                                                                                  296
                    atttccacagtatcaccgttaccatcatcgacaaagcaggaatggacaaccgcgcgcagaaa
AATTCCACCTTATCACCGTTACCATCATCAACGAAGCATGAATGTACAACAGCACAGAAT 76
                                                                                                            tgtggtcgaacacattcgcttatttggttctttaatggtaatactgatctggcattgatag 415
                                                                                     GTTGGATATTCCAAGTTGTTGAGCAAATATTTGTCCAAAGCACAACCATCAGCATTTAAT 136
                                                                                                                                                                            AACAGTTGTGATCGATCCGCATATTTGTAGACGTGAGCCTTCTTGTCCAGCCATTAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                gcaggttttgctgcggcaccacctgtttttaacagctccgaatccttgtggttctgaacat 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 9, 1995 this sequence version replaced gi:802391 Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Filarioidea; Onchocercidae; Onchocerca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular Parasitology
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primer: pBluescript SK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H
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/db_xref="taxon:6282"
/clone="SWmL3CO318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.4%;
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Pred. No. 1e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
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4, 2003, 09:12:27; search time 1 Seconds (without alignments) 4.131 Million cell updates/sec April ö Run

us-10-054-562a-3 Title: Perfect score:

1 atgatgattcgtcttattgc......ttcgtccaaatcagaaggca 1161 Scoring table: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 0.0

1 seqs, 1779 residues Searched:

of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

us-10-054-562a-1:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description us-10-054-562a-1 a 1161 100.0 1779 1 Query Match Length DB Score Result Š

ALIGNMENTS

RESULT 1 us-10-054-562a-1

Gaps ö Length 1779; Indels DB 1; ö ; Score 1161; I ; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 100.0%;
Matches 1161; Conservative 0;

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1 ATGATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCG 60 ð g

61 227 ò g

121 287 õ a

240 GAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGAT 181 ò . В

347

406

466 TCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACT 241 407 å

1126 1020 1186 1080 1140 1306 1006 1066 886 946 840 540 900 994 999 780 900 960 420 480 646 706 826 CAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCA GTGTCATTTCGTTTCATCCATATTTGTTACCAAAGTTGATCGTGCATATCGAGAACAA TGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACA ACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGT ACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGAT TIGCIAAAIAATITIGGAATATCCAACAGATTIAATGGCTGGCCAAGAAGCTCACGTATAC AAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAA CCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAA CAACCÉGIAAIACITGCIGCAGIACAAAAIGGAAICIGCAIGICACCAIIIIGGCIICICA AIGITTATGGGITTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAA GITGICATITICGITICATCCATTATITICATACCAAAGITGATCGIGCATATCGAGTACAA TTTCGTCCAAATCAGAAGGCA 1161 1001 1067 1127 1187 1247 361 421 587 647 707 827 721 781 947 841 1021 1081 1141 301 467 527 481 541 601 167 661 887 901 961 g ò g ò 용 ò a ò g ò g ò ద ò g ŏ a ò g ò ద ò 윱 à g ò 셤 à ò

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